

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:00:45 ; Search time 11.864 Seconds  
(without alignments)  
30.459 Million cell updates/sec

Title: US-09-674-716B-5  
Perfect score: 31  
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
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2	31	100.0	7	2	US-08-672-345C-36	Sequence 26, Appl
3	31	100.0	7	2	US-08-672-345C-39	Sequence 29, Appl
4	31	100.0	7	3	US-09-214-095D-23	Sequence 23, Appl
5	31	100.0	7	3	US-09-214-095D-26	Sequence 26, Appl
6	31	100.0	7	3	US-09-214-095D-29	Sequence 29, Appl
7	31	100.0	113	2	US-08-672-345C-6	Sequence 6, Appl
8	31	100.0	113	2	US-08-672-345C-7	Sequence 7, Appl
9	31	100.0	113	2	US-08-672-345C-8	Sequence 8, Appl
10	31	100.0	113	2	US-08-672-345C-96	Sequence 96, Appl
11	31	100.0	113	2	US-08-672-345C-97	Sequence 97, Appl
12	31	100.0	113	2	US-08-672-345C-98	Sequence 98, Appl
13	31	100.0	113	3	US-09-214-095D-6	Sequence 6, Appl
14	31	100.0	113	3	US-09-214-095D-7	Sequence 7, Appl
15	31	100.0	113	3	US-09-214-095D-8	Sequence 8, Appl
16	31	100.0	113	3	US-09-214-095D-104	Sequence 104, App
17	31	100.0	113	3	US-09-214-095D-108	Sequence 108, App
18	31	100.0	113	3	US-09-214-095D-112	Sequence 112, App
19	28	90.3	7	2	US-08-672-345C-20	Sequence 20, Appl
20	28	90.3	7	3	US-09-214-095D-20	Sequence 20, Appl
21	28	90.3	113	2	US-08-672-345C-5	Sequence 5, Appl
22	28	90.3	113	2	US-08-672-345C-95	Sequence 95, Appl
23	28	90.3	113	3	US-09-214-095D-5	Sequence 5, Appl
24	28	90.3	113	3	US-09-214-095D-100	Sequence 100, App
25	28	90.3	280	3	US-09-214-095D-119	Sequence 119, App
26	27	87.1	7	2	US-08-672-345C-80	Sequence 80, Appl
27	27	87.1	7	3	US-09-214-095D-80	Sequence 80, Appl

Sequence 14, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 21, Appl  
Sequence 27521, A  
Sequence 32578, A  
Sequence 5240838  
Patent No. 5240838  
Sequence 1003, Ap  
Sequence 999, App  
Sequence 1007, Ap  
Sequence 6926, Ap  
Sequence 21143, A  
Sequence 24241, A  
Sequence 27421, A

## ALIGNMENTS

RESULT 1  
 US-08-672-345C-23  
 Sequence 23, Application US/08672345C  
 Patent No. 5948658  
 GENERAL INFORMATION:  
 APPLICANT: Landry Donald, W.  
 TITLE OF INVENTION: ANTI-OCCAINE CATALYTIC ANTIBODY  
 NUMBER OF SEQUENCES: 108  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper and Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/672,345C  
 FILING DATE: 24-JUN-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 0575/51400  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-278-0400  
 TELEFAX: 212-391-0525  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-672-345C-23

Query Match	100.0%;	Score 31;	DB 2;	Length 7;
Best Local Similarity	100.0%;	Pred. No. 3e+05;		
Matches	7;	Conservative	0;	Mismatches 0;
				Indels

Qy 1 LMSTRAS 7  
| | | | |  
ph 1 LMSTRAS 7

## RESULT 2

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; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-29

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
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Db 1 LMSTRAS 7

RESULT 4
US-09-214-095D-23
; Sequence 23, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-23

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
   |||||
Db 1 LMSTRAS 7

RESULT 5
US-09-214-095D-26
; Sequence 26, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-26

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LMSTRAS 7  
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Db 1 LMSTRAS 7

## RESULT 6

US-09-214-095D-29  
; Sequence 29, Application US/09214095D  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-29

Query Match 100.0%; Score 31; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LMSTRAS 7  
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Db 1 LMSTRAS 7

## RESULT 7

US-08-672-345C-6  
; Sequence 6, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-672-345C-6

Query Match 100.0%; Score 31; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LMSTRAS 7  
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Db 55 LMSTRAS 61

## RESULT 8

US-08-672-345C-7  
; Sequence 7, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-672-345C-7

Query Match 100.0%; Score 31; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
|||||  
Db 55 LMSTRAS 61

## RESULT 9

US-08-672-345C-8  
; Sequence 8, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,345C  
FILING DATE: 24-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-672-345C-8

Query Match 100.0%; Score 31; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
Db 55 LMSTRAS 61

RESULT 10  
US-08-672-345C-96  
; Sequence 96, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 96:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-96

Query Match 100.0%; Score 31; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
Db 55 LMSTRAS 61

RESULT 11  
US-08-672-345C-97  
; Sequence 97, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 97:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-97

Query Match 100.0%; Score 31; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
Db 55 LMSTRAS 61

RESULT 12  
US-08-672-345C-98  
; Sequence 98, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-672-345C-98

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred.No.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 13
US-09-214-095D-6
; Sequence 6, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCES: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-6

Query Match 100.0%; Score 31; DB 3; Length 113;
Best Local Similarity 100.0%; Pred.No.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 14
US-09-214-095D-7
; Sequence 7, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCES: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-7

Query Match 100.0%; Score 31; DB 3; Length 113;
Best Local Similarity 100.0%; Pred.No.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 15
US-09-214-095D-8
; Sequence 8, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCES: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-8

Query Match 100.0%; Score 31; DB 3; Length 113;
Best Local Similarity 100.0%; Pred.No.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

Search completed: September 30, 2004, 06:38:16
Job time : 12.8644 secs
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Blank sheet

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 9.76271 Seconds  
(without alignments)  
88.677 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QOLVEYPPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	43	89.6	383	2	C42622	ubiquinol-cytochrome b
2	42	87.5	74	2	G30538	Ig kappa chain V r
3	42	87.5	112	1	KWS16	Ig kappa chain V r
4	42	87.5	113	1	KWS51	Ig kappa chain V r
5	37	77.1	120	1	KWS67	Ig kappa chain pre
6	37	77.1	467	2	A85363	probable calmoduli
7	36	75.0	108	2	S36277	Ig lambda chain V
8	36	75.0	570	2	T38148	phosphatidyl synth
9	35	72.9	120	2	B29775	Ig kappa chain pre
10	35	72.9	480	2	A86371	hypothetical prote
11	34	70.8	440	2	D82100	meat protein VC224
12	34	70.8	586	2	D89903	hypothetical prote
13	34	70.8	722	2	S76367	hypothetical prote
14	34	70.8	1074	2	T01906	hypothetical prote
15	33	68.8	112	2	I26317	Ig kappa chain V r
16	33	68.8	112	2	D26317	Ig kappa chain V r
17	33	68.8	277	2	A03322	lysozyme (EC 3.2.1
18	33	68.8	315	2	D83163	hypothetical prote
19	33	68.8	323	2	D90527	glycerol 3-phospha
20	33	68.8	379	1	S41834	ubiquinol-cytochro
21	33	68.8	414	2	AG1614	B. subtilis YxiO p
22	33	68.8	414	2	A11251	B. subtilis YxiO p
23	33	68.8	452	2	A25346	3',5'-cyclic-nucle
24	33	68.8	561	1	S41589	long-chain-fatty-a
25	33	68.8	561	2	B90943	long-chain-fatty-a
26	33	68.8	561	2	F85791	long-chain-fatty-a
27	33	68.8	561	2	AC0725	long-chain-fatty-a
28	33	68.8	664	2	F70483	glycine-tRNA ligas
29	33	68.8	726	2	T21138	hypothetical prote

30 33 68.8 816 2 S46268 ataxin-1 - human  
31 32 68.8 817 2 T15138 hypothetical prote  
32 32 66.7 61 4 I65317 hemoglobin delta c  
33 32 66.7 112 2 B49060 Ig light chain V r  
34 32 66.7 120 2 A29775 Ig kappa chain pre  
35 32 66.7 132 2 S40334 Ig kappa chain - h  
36 32 66.7 151 2 G96705 unknown protein, 7  
37 32 66.7 180 2 AF2397 hypothetical prote  
38 32 66.7 242 2 T45421 probable 2-hydroxy  
39 32 66.7 282 2 T49628 biliverdin reducta  
40 32 66.7 295 2 A42268 biliverdin reducta  
41 32 66.7 296 2 G02066 biliverdin reducta  
42 32 66.7 296 2 S62624 biliverdin reducta  
43 32 66.7 298 2 T01948 hypothetical prote  
44 32 66.7 313 1 F69399 conserved hypotet  
45 32 66.7 315 2 A85019 probable bHLH DNA-

#### ALIGNMENTS

##### RESULT 1

C42622 ubiquinol-cytochrome-c reductase (EC 1.1.0.2.2) cytochrome b - honeybee mitochondrion  
C;Species: mitochondrion Apis mellifera (honeybee)  
A;Variety: ligustica  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 03-Jun-2002  
C;Accession: C42622; S52971  
R;Crozier, R.H.; Crozier, Y.C.  
Mol. Biol. Evol. 9, 474-482, 1992  
A;Title: The cytochrome b and ATPase genes of honeybee mitochondrial DNA.  
A;Reference number: A42622; MUID:92261310; PMID:1533894  
A;Accession: C42622  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-383 <CRO>  
A;Cross-references: GB:M87052  
R;Crozier, R.H.; Crozier, Y.C.  
Genetics 133, 97-117, 1993  
A;Title: The mitochondrial genome of the honeybee Apis mellifera: complete sequence and  
A;Reference number: S52960; MUID:93114603; PMID:8417993  
A;Accession: S52971  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-383 <CR2>  
A;Cross-references: EMBL:L06178; NID:G336279; PIDN:AAB96809.1; PID:G552449  
C;Genetics:  
A;Genome: mitochondrion  
A;Genetic code: SGC4  
C;Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol-  
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion;  
F;14-340/Domain: cytochrome b6 homology <CBH>  
F;14-211/Domain: cytochrome b6 homology <CB6>  
F;223-340/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>  
F;85,184/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted  
F;99,198/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 89.6%; Score 43; DB 2; Length 383;

Best Local Similarity 77.8%; Pred. No. 0.55;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOLVEYPPT 9

Db 341 KQLIEYPPT 349

##### RESULT 2

G30538 Ig kappa chain V region (253.15E2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 16-Aug-1996

C;Accession: G30538

R;Clafin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988  
 A>Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae  
 A:Reference number: A30534; MUID:89035545; PMID:3141511

A:Accession: G30538  
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-74 <CLIA>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 42; DB 2; Length 74;  
 Best Local Similarity 88.9%; Pred. No. 0.15;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9  
 |||||  
 Db 63 QQLVEYPLT 71

## RESULT 3

KWS16

Ig kappa chain V region (M167) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 16-Aug-1996  
 C:Accession: A01908

R:Rudikoff, S.; Porter, W.  
 Biochemistry 17, 2703-2707, 1978  
 A>Title: Kappa-Chain variable region from M167, a phosphorylcholine binding myeloma protein  
 A:Reference number: A01908; MUID:79000273; PMID:99160  
 A:Accession: A01908

A:Molecule type: protein  
 A:Residues: 1-112 <RUD>  
 C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:16-95/Domain: immunoglobulin homology <IMM>  
 F:23-93/Disulfide bonds: #status predicted

Query Match 87.5%; Score 42; DB 1; Length 112;  
 Best Local Similarity 88.9%; Pred. No. 0.24;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9  
 |||||  
 Db 94 QQLVEYPLT 102

## RESULT 4

KWS51

Ig kappa chain V region (M511) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000  
 C:Accession: A01910

R:Appella, E.  
 Mol. Immunol. 17, 711-718, 1980  
 A>Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine binding myeloma protein  
 A:Reference number: A01910; MUID:81052016; PMID:6776396  
 A:Accession: A01910

A:Molecule type: protein  
 A:Residues: 1-113 <APP>  
 C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:16-95/Domain: immunoglobulin homology <IMM>  
 F:23-93/Disulfide bonds: #status predicted

Query Match 87.5%; Score 42; DB 1; Length 113;  
 Best Local Similarity 88.9%; Pred. No. 0.24;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9  
 |||||  
 Db 334 QQLVEYPPF 341

Qy 1 QQLVEYPFT 9  
 |||||  
 Db 94 QQLVEYPLT 102

## RESULT 5

KWS67

Ig kappa chain precursor V region (VK167) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 21-Jan-2000  
 C:Accession: A01909  
 R:Selsing, E.; Storb, U.  
 Cell 25, 47-58, 1981  
 A>Title: Somatic mutation of immunoglobulin light-chain variable-region genes.  
 A:Reference number: A01909; MUID:82002223; PMID:6751832  
 A:Accession: A01909

A:Molecule type: DNA  
 A:Residues: 1-120 <SEL>  
 A>Note: the sequence was determined from the germline gene  
 C:Genetics: 17/1  
 A:Introns: 17/1  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>  
 F:36-115/Domain: immunoglobulin homology <IMM>  
 F:43-113/Disulfide bonds: #status predicted

Query Match 77.1%; Score 37; DB 1; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYP 7  
 |||||  
 Db 114 QQLVEYP 120

## RESULT 6

A85363

Probable calmodulin-binding protein [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
 C:Accession: A85363

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory  
 Nature 402, 769-777, 1999  
 A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A:Reference number: A85001; MUID:20083488; PMID:10617198  
 A:Accession: A85363

A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-467 <STO>  
 A:Cross-references: GB:NC\_001268; NID:g7270002; PIDN:CAB79818.1; GSPDB:GN00140  
 C:Genetics:  
 A:Gene: At4g31000  
 A:Map position: 4

Query Match 77.1%; Score 37; DB 2; Length 467;  
 Best Local Similarity 75.0%; Pred. No. 12;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYPPF 8  
 |||||  
 Db 334 QQLVEYPPF 341

## RESULT 7

S36277

Ig lambda chain V region (clone alpha-FOG1-G8) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000

C:Accession: S36277  
 R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
 EMBO J. 12, 725-734, 1993  
 A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A:Reference number: S36256; MUID:193178448; PMID:7679990  
 A:Accession: S36277  
 A>Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-108 <GRI>  
 A:Cross-references: EXBL:Z18829; NID:G33417; PIDN:CAA79281.1; PID:G939910  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 36; DB 2; Length 108;  
 Best Local Similarity 66.7%; Pred. No. 4;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9  
 |||:|  
 Db 89 QQLISYPLT 97

RESULT 8  
 T38148  
 phosphatidyl synthase - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
 C:Accession: T38148  
 R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: Z11774  
 A:Accession: T38148  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-570 <PEA>  
 A:Cross-references: EXBL:Z99295; PIDN:CAB16578.1; GSPDB:GNO0066; SPDB:SPAC22A12.08C  
 A:Experimental source: strain 972h-; cosmid c22A12  
 C:Genetics:  
 A:Gene: SPDB:SPAC22A12.08C  
 A:Map position: 1  
 A:Introns: 43/2; 62/2; 227/2; 483/1

Query Match 75.0%; Score 36; DB 2; Length 570;  
 Best Local Similarity 77.8%; Pred. No. 23;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9  
 :|||:|  
 Db 547 KQLVEYSPT 555

RESULT 9  
 B29775  
 Ig kappa chain precursor V region (mouse 24.1) - shrew mouse  
 C:Species: Mus pahari  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 21-Jan-2000  
 C:Accession: B29775  
 R:Jouvin-Marche, E.; Rudikoff, S.  
 Immunogenetics 24, 191-201, 1986  
 A:Title: Evolution of a V-kappa gene family.  
 A:Reference number: A91751; MUID:87006895; PMID:3093373  
 A:Accession: B29775  
 A:Molecule type: DNA  
 A:Residues: 1-120 <JOU>  
 A:Cross-references: GB:M15553; NID:G197470; PIDN:AAA39037.1; PID:G197471  
 A>Note: this sequence was determined from the germline gene  
 C:Genetics:  
 A:Introns: 17/1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-120/Product: Ig kappa chain V region 24.1 #status predicted <MAT>

F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 120;  
 Best Local Similarity 85.7%; Pred. No. 7.2;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7  
 |||:|  
 Db 114 QQLVEYP 120

RESULT 10  
 A86371  
 hypothetical protein F508.25 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001  
 C:Accession: A86371  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: A86371  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-480 <STO>  
 A:Cross-references: GB:AE005172; NID:G4056452; PIDN:AAC98025.1; GSPDB:GN00141  
 C:Genetics:  
 A:Map position: 1

Query Match 72.9%; Score 35; DB 2; Length 480;  
 Best Local Similarity 85.7%; Pred. No. 31;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQLVEYPP 8  
 |||:|  
 Db 269 QQLVEYPP 275

RESULT 11  
 D82100  
 mesJ protein VC2242 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
 C:Species: Vibrio cholerae  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Dec-2002  
 C:Accession: D82100  
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.  
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A:Reference number: A82035; MUID:20406833; PMID:10952301  
 A:Accession: D82100  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-440 <HEI>  
 A:Cross-references: GB:AE004296; GB:AE003852; NID:G9656799; PIDN:AAF95386.1; GSPDB:GN001  
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C:Genetics:  
 A:Gene: VC2242  
 A:Map position: 1  
 C:Superfamily: Cell cycle protein MesJ

Query Match 70.8%; Score 34; DB 2; Length 440;  
 Best Local Similarity 75.0%; Pred. No. 46;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPP 8

```

Db      10 QQLARYPF 17
|||||
RESULT 12
D89903
hypothetical protein Sall31 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89903
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Haramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89903
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-586 <XUR>
A:Cross-references: GB:BA000018; PID:g13701089; PIDN:BA842384.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: Sall31
C:Superfamily: Halobacterium halobium 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid fer
Query Match 70.8%; Score 34; DB 2; Length 586;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      2 QQLVEYFP 9
|||
Db      109 QQLIEPFT 116
|||||
RESULT 13
S76367
hypothetical protein - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
C.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76367
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-722 <KAN>
A:Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BA10219.1; PID:g100159
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: glycine-tRNA ligase beta chain
Query Match 70.8%; Score 34; DB 2; Length 722;
Best Local Similarity 85.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy      1 QQLVEYFP 7
|||
Db      254 EQLEVEYP 260
|||||
RESULT 14
T01906
hypothetical protein T12H20.3 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Mar-1999
C:Accession: T01906
R:Cotton, M.; Graves, T.; Sutterer, C.; Modde, T.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of A. thaliana T12H20.
A:Reference number: Z14453
A:Accession: T01906
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1074 <COT>
A:Cross-references: EMBL:AF080119; NID:g3600029; PID:g3600033
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Note: T12H20.3
Query Match 70.8%; Score 34; DB 2; Length 1074;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy      2 QQLVEYFP 8
|||
Db      853 ELIEYFP 859
|||||
RESULT 15
I26317
Ig kappa chain V region (H158-89H4) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: I26317
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a de
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: I26317
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Experimental source: strain Balb/c
A:Note: this sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus he
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
P:16-95/Domain: immunoglobulin homology <IMM>
Query Match 68.8%; Score 33; DB 2; Length 112;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      2 QQLVEYFP 9
|||
Db      95 QHLEYFP 102
|||||
Search completed: September 30, 2004, 06:00:35
Job time : 11.7627 secs

```



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 5.49153 Seconds  
(without alignments)  
85.337 Million cell updates/sec

Title: US-09-674-716B-7  
Sequence: 1 QQLVEYFPFT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	43	89.6	383	1	CYB APILI	P34845 apis mellif
2	42	87.5	112	1	KV2A MOUSE	P01626 mus musculu
3	42	87.5	113	1	KV2C MOUSE	P01628 mus musculu
4	37	77.1	120	1	KV2B MOUSE	P01627 mus musculu
5	36	75.0	379	1	CYB AKOJE	P21715 akodon jels
6	36	75.0	379	1	CYB AKOTO	P21721 akodon toba
7	36	75.0	379	1	CYB AKOTO	P21721 akodon toba
8	36	75.0	380	1	CYB DELSU	P21721 akodon toba
9	36	75.0	380	1	CYB MICMS	P21721 akodon toba
10	36	75.0	380	1	CYB THOIS	P21721 akodon toba
11	36	75.0	381	1	CYB AULIM	P21721 akodon toba
12	36	75.0	381	1	CYB ELIMO	P21721 akodon toba
13	36	75.0	381	1	CYB PHIXA	P21721 akodon toba
14	36	75.0	381	1	CYB SIGHI	P21721 akodon toba
15	36	75.0	381	1	CYB THODA	P21721 akodon toba
16	34	70.8	722	1	SYGB SYN3	P21721 akodon toba
17	33	68.8	379	1	CYB MARBB	P21721 akodon toba
18	33	68.8	379	1	CYB MARMR	P21721 akodon toba
19	33	68.8	452	1	CYB DICDI	P21721 akodon toba
20	33	68.8	561	1	LCFA_SCO57	P21721 akodon toba
21	33	68.8	561	1	LCFA_SCOLI	P21721 akodon toba
22	33	68.8	561	1	LCFA_SALTY	P21721 akodon toba
23	33	68.8	664	1	SYGB AQUAE	P21721 akodon toba
24	33	68.8	789	1	ATX1 RAT	P21721 akodon toba
25	33	68.8	792	1	ATX1 MOUSE	P21721 akodon toba
26	33	68.8	816	1	ATX1 HUMAN	P21721 akodon toba
27	32	66.7	295	1	BIEA RAT	P21721 akodon toba
28	32	66.7	296	1	BIEA HUMAN	P21721 akodon toba
29	32	66.7	332	1	NDPA VIBFA	P21721 akodon toba
30	32	66.7	358	1	YCCF BACSU	P21721 akodon toba
31	32	66.7	374	1	Y006 BORBU	P21721 akodon toba
32	32	66.7	379	1	CYB BOLAM	P21721 akodon toba
33	32	66.7	673	1	Z145_HUMAN	P21721 akodon toba

34	31	64.6	130	1	MSRB_PASNU	Q3cmbl pasteurella
35	31	64.6	149	1	CYB_CERN	P82047 cervus nipp
36	31	64.6	153	1	CYB_CERN	P82045 cervus nipp
37	31	64.6	154	1	CYB_CERN	P82049 cervus nipp
38	31	64.6	154	1	CYB_CERN	P82048 cervus nipp
39	31	64.6	154	1	CYB_CERN	P82046 cervus nipp
40	31	64.6	168	1	RR5_CYACA	Q9tlu8 cyanidium c
41	31	64.6	178	1	YP20_BACLI	P05332 bacillus li
42	31	64.6	222	1	TYSY_MENJA	Q57931 methanococ
43	31	64.6	366	1	HNLS_SORBI	P82708 sorghum bic
44	31	64.6	378	1	CYB_CEBAL	Q94zk8 cebus albif
45	31	64.6	379	1	CYB_ALCAA	O47922 alces alces

ALIGNMENTS

RESULT 1  
CYB APILI  
ID CYB APILI STANDARD; PRT; 383 AA.  
AC P34845;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Cytochrome b.  
GN MTCTB OR COB OR CYTB.  
OS Apis mellifera ligustica (Common honeybee).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
OC Apidae; Apis  
OX NCBI\_TaxID=7469;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Thorax;  
RX MEDLINE=92261310; PubMed=1533894;  
RA Crozier R.H.; Crozier Y.C.;  
RT "The cytochrome b and ATPase genes of honeybee mitochondrial DNA.";  
RL Mol. Biol. Evol. 9:474-482(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Thorax;  
RX MEDLINE=93114603; PubMed=8417993;  
RA Crozier R.H.; Crozier Y.C.;  
RT "The mitochondrial genome of the honeybee Apis mellifera: complete  
sequence and genome organization.";  
RL Genetics 133:97-117(1993).  
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase  
complex (complex III or cytochrome b-c1 complex), which is a  
respiratory chain that generates an electrochemical potential  
coupled to ATP synthesis (By similarity).  
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or  
b562) is low-potential and absorbs at about 562, and heme 2 (or BH  
or b566) is high-potential and absorbs at about 566 (By  
similarity).  
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,  
cytochrome c1 and the Rieske protein (By similarity).  
CC -!- SIMILARITY: Belongs to the cytochrome b family.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; L06178; RA06809.1; -;  
CC EMBL; M87052; -; NOT\_ANNOTATED\_CDS.  
CC PIR; C42622; C42622.  
CC InterPro; IPR005798; Cytb\_b6\_C.  
CC InterPro; IPR005797; Cytb\_b6\_N.  
CC Pfam; PF00032; cytochrome\_b\_C; 1.  
CC

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DR PFam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; 1.
KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 85 85 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 99 99 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 184 184 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 198 198 IRON 2 (HEME B566 AXIAL LIGAND).
SQ SEQUENCE 383 AA; 45256 MW; A140A05B6053C2D5 CRC64;

Query Match 79.6%; Score 43; DB 1; Length 383;
Best Local Similarity 77.8%; Pred. No. 0.36;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
Db 341 QQLVEYPFT 349

RESULT 2
KV2A_MOUSE ID KV2A_MOUSE STANDARD; PRT; 112 AA.
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=79000273; PubMed=99160;
RZ Rudikoff S., Potter M.;
RT "Kappa Chain variable region from M167, a phosphorylcholine binding
myeloma protein."
RL Biochemistry 17:2703-2707(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY
CC CHAIN HAS ALSO BEEN DETERMINED.
DR PIR; A01908; KWS16.
DR HSSP; P80362; IWTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR PFam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FRAMEWORK-1.
FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 39 FRAMEWORK-2.
FT DOMAIN 40 54 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 55 61 FRAMEWORK-3.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 94 102 FRAMEWORK-4.
FT DISULFID 103 112 BY SIMILARITY.
FT NON TER 112 112
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;

Query Match 87.5%; Score 42; DB 1; Length 112;
Best Local Similarity 88.9%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
Db 94 QQLVEYPFT 102

RESULT 3
KV2C_MOUSE ID KV2C_MOUSE STANDARD; PRT; 113 AA.
AC P01627;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region V kappa167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8200223; PubMed=6791832;
RZ Selsing E., Storb U.;
RT "Somatic mutation of immunoglobulin light-chain variable-region
genes."
RL Cell 25:47-58(1981).
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AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396;
RZ Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
phosphorylcholine-binding murine myeloma protein."
RL Mol. Immunol. 17:711-718(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A01910; KWS51.
DR HSSP; P80362; IWTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR PFam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FRAMEWORK-1.
FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 39 FRAMEWORK-2.
FT DOMAIN 40 54 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 55 61 FRAMEWORK-3.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 94 102 FRAMEWORK-4.
FT DISULFID 103 112 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match 87.5%; Score 42; DB 1; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
Db 94 QQLVEYPFT 102

RESULT 4
KV2B_MOUSE ID KV2B_MOUSE STANDARD; PRT; 120 AA.
AC P01627;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region V kappa167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8200223; PubMed=6791832;
RZ Selsing E., Storb U.;
RT "Somatic mutation of immunoglobulin light-chain variable-region
genes."
RL Cell 25:47-58(1981).
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CC use by non-profit institutions as long as its content is in no way
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CC DR EMBL; J00562; AAA39032.1; -
CC DR EMBL; K02415; AAA39051.1; -
CC DR PIR; A01909; KWS67.
CC DR HSP; P80362; IWT.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00835; IG LIKE; 1.
CC DR Immunoglobulin V region; Signal.
CC KW SIGNAL 1
CC FT CHAIN 21
CC FT DOMAIN 21
CC FT DOMAIN 21
CC FT DOMAIN 44
CC FT DOMAIN 59
CC FT DOMAIN 60
CC FT DOMAIN 74
CC FT DOMAIN 75
CC FT DOMAIN 81
CC FT DOMAIN 82
CC FT DOMAIN 113
CC FT DOMAIN 114
CC FT DISULFID 43
CC FT DISULFID 113
CC SQ SEQUENCE 120 AA; 63B571F0E4DE3E8 CRC64;

Query Match 77.1%; Score 37; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYP 7
Db 114 QQLVEYP 120

RESULT 5
CYB_AKOJE
ID CYB_AKOJE STANDARD; PRT; 379 AA.
AC P21715;
DT 01-MAY-1991 (Rel. 18, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Akodon jelskii (Jelski's South American field mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Abrothrix.
OX NCBI_TaxID=241142;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Smith M.F.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-267 FROM N.A.
RC TISSUE=Liver;
RA Smith M.F., Patton J.L.;
RL "The diversification of South American murid rodents: evidence from mitochondrial DNA sequence data for the akodontine tribe.";
RN [3]
RP SEQUENCE OF 1-133 FROM N.A.
RC STRAIN=Isolate MVZ 173073, Isolate MVZ 173074, Isolate MVZ 173083, and
RC Isolate MVZ 173084;
RC TISSUE=Liver;
RX MEDLINE=91163325; PubMed=2002767;
RA Smith M.F., Patton J.L.;
RL "Variation in mitochondrial cytochrome b sequence in natural populations of South American akodontine rodents (Muridae: Sigmodontinae).";
RL Mol. Biol. Evol. 8:85-103(1991).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

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CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 (By similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC
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CC
CC EMBL; M35714; AAA16998.2; ALT_TERM.
CC EMBL; M35715; AAA31630.1; -
CC EMBL; M35716; AAA31629.1; -
CC PIR; C41824; C41824.
CC InterPro; IPR005798; Cytb_b6_C.
CC InterPro; IPR005797; Cytb_b6_N.
CC Pfam; PF00032; Cytochrome_b_C; 1.
CC Pfam; PF00033; Cytochrome_b_N; 1.
CC PROSITE; PS00193; CYTOCHROME_B_N; 1.
CC PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 83
FT METAL 97
FT METAL 182
FT METAL 196
FT METAL 118
FT VARIANT 122
FT VARIANT 122
FT VARIANT 122
FT VARIANT 122
FT SEQUENCE 379 AA; 42529 MW; F9F012A46671D59A CRC64;

Query Match 75.0%; Score 36; DB 1; Length 379;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QQLVEYPPT 9
Db 341 QQLVEYPPT 348

RESULT 6
CYB_AKOTB
ID CYB_AKOTB STANDARD; PRT; 379 AA.
AC Q33887;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Akodon toba (Chaco grass mouse).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Akodon.
OX NCBI_TaxID=29101;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate UMMZ 133965; TISSUE=Liver;
RA Smith M.F., Patton J.L.;
RL "Phylogenetic relationships and the radiation of sigmodontine rodents in South America: evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
RN [2]
RP SEQUENCE OF 1-267 FROM N.A.
RC STRAIN=Isolate UMMZ 133965; TISSUE=Liver;
RA Smith M.F., Patton J.L.;

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Thu Sep 30 13:18:56 2004

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RT "Diversification of South American murid rodents: Evidence from
RT mitochondrial DNA sequence data for the akodontine tribe.";
RL Biol. J. Linn. Soc. Lond. 50:149-177(1993).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-cl complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH
CC or b566) is high-potential and absorbs at about 566 (By
CC similarity).
CC -!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC -----
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CC -----
EMBL; U03527; AAD12554.2; -
DR InterPro; IPR005798; Cytb_b6_C.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_OO; 1.
DR Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
SQ SEQUENCE 379 AA; 42689 MW; 8B946C35430FDCD0 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 379;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QLVVEYPT 9
Db 341 QPVEYPT 348

RESULT 7
CYB_AKOTO
ID CYB_AKOTO STANDARD; PRT; 379 AA.
AC P21721;
DT 01-MAY-1991 (Rel. 18, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Akodon torques (Cloud forest grass mouse).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Akodon.
OC NCBI_TaxID=10078;
EN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Smith M.F.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-267 FROM N.A.
RC TISSUE=Liver;
RA Smith M.F.; Patton J.L.;
RT "The diversification of South American murid rodents: evidence from
RT mitochondrial DNA sequence data for the akodontine tribe.";

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RL Biol. J. Linn. Soc. Lond. 50:149-177(1993).
RN [3]
RP SEQUENCE OF 1-133 FROM N.A.
RC STRAIN=Isolate MVZ 171720, Isolate MVZ 171721, Isolate MVZ 174053, and
RC Isolate MVZ 174054;
RC TISSUE=Liver; PubMed=2002767;
RX MEDLINE=91163325;
RA Smith M.F., Patton J.L.;
RT "Variation in mitochondrial cytochrome b sequence in natural
RT populations of South American akodontine rodents (Muridae:
RT Sigmodontinae).";
RL Mol. Biol. Evol. 8:85-103(1991).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-cl complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH
CC or b566) is high-potential and absorbs at about 566 (By
CC similarity).
CC -!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC -----
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CC -----
EMBL; M35700; AAA18997.2; -
DR EMBL; M35701; AAA31624.1; -
DR EMBL; M35702; AAA31625.1; -
DR PIR; G23725; G23725.
DR InterPro; IPR005798; Cytb_b6_C.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00193; CYTOCHROME_B_OO; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
FT VARIANT 108 108 V->A (in isolates MVZ 174053 and MVZ
FT 174054).
FT VARIANT 115 115 V->I (in isolates MVZ 174053 and MVZ
FT 174054).
SQ SEQUENCE 379 AA; 42611 MW; 4C94CF8A92CCC34F CRC64;

Query Match 75.0%; Score 36; DB 1; Length 379;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QLVVEYPT 9
Db 341 QPVEYPT 348

RESULT 8
CYB_DELSU
ID CYB_DELSU STANDARD; PRT; 380 AA.
AC Q9XNV7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Delomys sublineatus (pallid Atlantic forest rat).

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OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Delonys.
OX NCBI_TaxID=89131;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate MVZ 183075;
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-cl complex), which is a
respiratory chain that generates an electrochemical potential
coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
b562) is low-potential and absorbs at about 562, and heme 2 (or BH
or b566) is high-potential and absorbs at about 566 (By
similarity).
CC -!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
DR EMBL; AF108687; AAD45469.1; -
DR InterPro; IPR005798; Cytb_b6 C.
DR InterPro; IPR005797; Cytb_b6 N.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; 1.
KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
SQ SEQUENCE 380 AA; 42820 MW; DE9A0EDA1D4AE785 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 380;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPT 9
DB 341 QPVEYPT 348

RESULT 9
ID CYB MICMS STANDARD; PRT; 380 AA.
AC Q9TFX5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Microzomys minutus (Forest small rice rat).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Microzomys.
OX NCBI_TaxID=37025;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=Isolate MVZ 173975;
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-cl complex), which is a
respiratory chain that generates an electrochemical potential
coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
b562) is low-potential and absorbs at about 562, and heme 2 (or BH
or b566) is high-potential and absorbs at about 566 (By
similarity).
CC -!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC
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or send an email to license@isb-sib.ch).
CC
DR EMBL; AF108698; AAD45480.1; -
DR InterPro; IPR005798; Cytb_b6 C.
DR InterPro; IPR005797; Cytb_b6 N.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; 1.
KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
SQ SEQUENCE 380 AA; 42930 MW; C8C06F18D6F6DE21 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 380;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPT 9
DB 341 QPVEYPT 348

RESULT 10
ID CYB THOIS STANDARD; PRT; 380 AA.
AC Q9XNW9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Thomasomys ischyurus (Strong-tailed oldfield mouse).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Thomasomys.
OX NCBI_TaxID=89110;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate MVZ 181999;
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: Evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-cl complex), which is a

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CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH
CC or b566) is high-potential and absorbs at about 566 (By
CC similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF106675; AAD45457.1; -
CC InterPro; IPR005798; Cytb_b6_C.
CC InterPro; IPR005797; Cytb_b6_N.
CC Pfam; PF00032; cytochrome_b_C; 1.
CC Pfam; PF00033; cytochrome_b_N; 1.
CC PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE; PS00193; CYTOCHROME_B_OO; 1.
CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
CC Heme.
CC METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
CC METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
CC METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
CC METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
CC SEQUENCE 380 AA; 42941 MW; D73B891E41F61438 CRC64;
CC -----
Query Match 75.0%; Score 36; DB 1; Length 380;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 2 QLVSEYPT 9
CC | | | | |
CC 341 QPVEYPT 348
CC
CC Db
CC
CC RESULT 11
CC CYB_AULMI
CC ID CYB_AULMI STANDARD; PRT; 381 AA.
CC Q9XNV4;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Cytochrome b.
CC GN MTCYB OR COB OR CYTB.
CC OS Auliscomys micropus (Southern big-eared mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
CC OC Auliscomys.
CC NCBI_TaxID=89122;
CC [1]
CC SEQUENCE FROM N.A.
CC Smith M.F., Patton J.L.;
CC "Phylogenetic relationships and the radiation of sigmodontine rodents
CC in South America: evidence from cytochrome b.";
CC J. Mammal. Evol. 6:189-128(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH
CC or b566) is high-potential and absorbs at about 566 (By
CC similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).

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CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF106690; AAD45472.1; -
CC InterPro; IPR005798; Cytb_b6_C.
CC InterPro; IPR005797; Cytb_b6_N.
CC Pfam; PF00032; cytochrome_b_C; 1.
CC Pfam; PF00033; cytochrome_b_N; 1.
CC PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE; PS00193; CYTOCHROME_B_OO; 1.
CC Mitochondrion; Electron transport; Respiratory chain; Transmembrane;
CC Heme.
CC METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
CC METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
CC METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
CC METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
CC SEQUENCE 381 AA; 43093 MW; 7DBEBC93338DA2C3 CRC64;
CC -----
Query Match 75.0%; Score 36; DB 1; Length 381;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 2 QLVSEYPT 9
CC | | | | |
CC 341 QPVEYPT 348
CC
CC Db
CC
CC RESULT 12
CC CYB_ELIMO
CC ID CYB_ELIMO STANDARD; PRT; 381 AA.
CC Q9XNV3;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Cytochrome b.
CC GN MTCYB OR COB OR CYTB.
CC OS Eligmodontia morgani (Morgan's gerbil mouse).
CC OC Mitochondrion.
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
CC OC Eligmodontia.
CC NCBI_TaxID=89097;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=Isolate MVZ 182670;
CC Smith M.F., Patton J.L.;
CC "Phylogenetic relationships and the radiation of sigmodontine rodents
CC in South America: evidence from cytochrome b.";
CC J. Mammal. Evol. 6:189-128(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH
CC or b566) is high-potential and absorbs at about 566 (By
CC similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC -----
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CC or send an email to license@isb-sib.ch).

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

CC EMBL; AF108691; AAD45473.1; -  
 CC InterPro; IPR005798; Cytb\_b6\_C.  
 CC InterPro; IPR005797; Cytb\_b6\_N.  
 CC Pfam; PF00032; cytochrome\_b\_c; 1.  
 CC Pfam; PF00033; cytochrome\_b\_N; 1.  
 CC PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
 CC PROSITE; PS00193; CYTOCHROME\_B\_QO; 1.  
 CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;  
 CC Heme.  
 CC METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).  
 CC METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).  
 CC METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).  
 CC METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).  
 CC SEQUENCE 381 AA; 43035 MW; D43D2988EB59486D CRC64;  
 SQ

Query Match 75.0%; Score 36; DB 1; Length 381;  
 Best Local Similarity 87.5%; Pred. No. 9.2;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QLVVEPFT 9  
 | | | | |  
 DB 341 QPVEPFT 348

## RESULT 13

CC CYB\_PHYXA STANDARD; PRT; 381 AA.  
 CC O92Z56;  
 CC 10-OCT-2003 (Rel. 42, Created)  
 CC 10-OCT-2003 (Rel. 42, Last sequence update)  
 CC 10-OCT-2003 (Rel. 42, Last annotation update)  
 CC Cytochrome b.  
 CC MTCYB OR COB OR CYTB.  
 CC Phyllotis xanthopygus (Yellow-rumped leaf-eared mouse).  
 CC Mitochondrion.  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 CC Phyllotis.  
 CC NCBI\_TaxID=59941;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=FMH 133830;  
 CC Steppan S.J.;  
 CC "Phylogenetic relationships and species limits within Phyllotis  
 CC (Rodentia: Sigmodontinae): concordance between mtDNA sequence and  
 CC morphology.";  
 CC J. Mammal. 79:573-593 (1998).  
 CC [2]  
 CC REVISIONS.  
 CC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase  
 CC complex (complex III or cytochrome b-c1 complex), which is a  
 CC respiratory chain that generates an electrochemical potential  
 CC coupled to ATP synthesis (By similarity).  
 CC -!- COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or  
 CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH  
 CC or b566) is high-potential and absorbs at about 566 (By  
 CC similarity).  
 CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,  
 CC cytochrome c1 and the Rieske protein (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome b family.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

CC EMBL; U86931; AAD12358.2; -  
 CC InterPro; IPR005798; Cytb\_b6\_C.  
 CC InterPro; IPR005797; Cytb\_b6\_N.  
 CC Pfam; PF00032; cytochrome\_b\_c; 1.  
 CC Pfam; PF00033; cytochrome\_b\_N; 1.  
 CC PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
 CC PROSITE; PS00193; CYTOCHROME\_B\_QO; 1.  
 CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;  
 CC Heme.  
 CC METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).  
 CC METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).  
 CC METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).  
 CC METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).  
 CC SEQUENCE 381 AA; 43076 MW; CC314C640B7246FB CRC64;  
 SQ

Query Match 75.0%; Score 36; DB 1; Length 381;  
 Best Local Similarity 87.5%; Pred. No. 9.2;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QLVVEPFT 9  
 | | | | |  
 DB 341 QPVEPFT 348

## RESULT 14

CC CYB\_SIGHI STANDARD; PRT; 381 AA.  
 CC O9XNU6;  
 CC 28-FEB-2003 (Rel. 41, Created)  
 CC 28-FEB-2003 (Rel. 41, Last sequence update)  
 CC 10-OCT-2003 (Rel. 42, Last annotation update)  
 CC Cytochrome b.  
 CC MTCYB OR COB OR CYTB.  
 CC Sigmodon hispidus (Hispid cotton rat).  
 CC Mitochondrion.  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 CC Sigmodon.  
 CC NCBI\_TaxID=42415;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC Smith M.F., Patton J.L.;  
 CC "Phylogenetic relationships and the radiation of sigmodontine rodents  
 CC in South America: evidence from cytochrome b.";  
 CC J. Mammal. Evol. 6:89-128 (1999).  
 CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase  
 CC complex (complex III or cytochrome b-c1 complex), which is a  
 CC respiratory chain that generates an electrochemical potential  
 CC coupled to ATP synthesis (By similarity).  
 CC -!- COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or  
 CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH  
 CC or b566) is high-potential and absorbs at about 566 (By  
 CC similarity).  
 CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,  
 CC cytochrome c1 and the Rieske protein (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome b family.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

CC EMBL; AF108702; AAD45484.1; -  
 CC InterPro; IPR005798; Cytb\_b6\_C.  
 CC InterPro; IPR005797; Cytb\_b6\_N.  
 CC Pfam; PF00032; cytochrome\_b\_c; 1.  
 CC Pfam; PF00033; cytochrome\_b\_N; 1.  
 CC PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
 CC PROSITE; PS00193; CYTOCHROME\_B\_QO; 1.

KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;

KW Heme: 83 83 IRON 1 (HEME B562 AXIAL LIGAND).  
FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).  
FT METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).  
FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).  
SQ SEQUENCE 381 AA; 42965 MW; 0472259421B38284 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 381;

Best Local Similarity 87.5%; Pred. No. 9.2; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPPT 9

DB 341 QPVEYPPT 348

## RESULT 15

CYB\_THODA  
ID CYB\_THODA STANDARD; PRT; 381 AA.  
AC Q9XNXL;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Cytochrome b.  
GN MTCYB OR COB OR CYTB.  
OS Thomasomys daphne (Daphne's oldfield mouse).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
OC Thomasomys.  
OX NCBI\_TaxID=89108;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate MVZ 171502;  
RA Smith M.F., Patton J.L.;  
RT "Phylogenetic relationships and the radiation of sigmodontine rodents in South America: evidence from cytochrome b.";  
RL J. Mammal. Evol. 6:89-128(1999).  
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).  
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or EL or b562) is low-potential and absorbs at about 562, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 (By similarity).  
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).  
CC -!- SIMILARITY: Belongs to the cytochrome b family.  
CC -----  
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CC -----  
CC EMBL; AF108673; AAD45455.1; -  
CC InterPro; IPR005798; Cytb\_b6.C.  
CC InterPro; IPR005797; Cytb\_b6.N.  
CC Pfam; PF00032; cytochrome\_b\_C; 1.  
CC Pfam; PF00033; cytochrome\_b\_N; 1.  
CC PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
CC PROSITE; PS00193; CYTOCHROME\_B\_QQ; 1.  
KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;  
KW Heme: 83 83 IRON 1 (HEME B562 AXIAL LIGAND).  
FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).  
FT METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).  
FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).  
SQ SEQUENCE 381 AA; 43035 MW; 351993B27E14502A CRC64;

Query Match 75.0%; Score 36; DB 1; Length 381;  
Best Local Similarity 87.5%; Pred. No. 9.2;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;QY 2 QLVVEYPPT 9  
DB 341 QPVEYPPT 348

Search completed: September 30, 2004, 06:01:18

Job time : 7.49153 secs



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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 29.4407 Seconds  
(without alignments)  
96.454 Million cell updates/sec

Title: US-09-674-716B-7  
Perfect score: 48  
Sequence: 1 QQLVEYPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL 25:\*
- 1: sp\_archea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_protein:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirs:\*
  - 16: sp\_bacteriaph:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	83.3	349	8 Q85TH4	Q85th4 melipona bi
2	39	81.2	506	16 Q87RR4	Q87rr4 vibrio para
3	37	77.1	278	10 Q8W454	Q8w454 arabidopsis
4	37	77.1	467	10 Q85550	Q85550 arabidopsis
5	37	77.1	609	10 Q8H816	Q8h816 oryza sativ
6	36	75.0	84	8 Q9B313	Q9b313 neoceratodu
7	36	75.0	247	8 Q9WBP34	Q9wbp34 bothriomyrm
8	36	75.0	352	8 Q9XNV8	Q9xnv8 delomyes dor
9	36	75.0	371	8 Q8M293	Q8m293 oxymycteru
10	36	75.0	377	8 Q9XNV0	Q9xnv0 reithrodon
11	36	75.0	377	8 Q9XNX5	Q9xnx5 scapteromys
12	36	75.0	379	8 Q8M2A0	Q8m2a0 oxymycteru
13	36	75.0	379	8 Q9TGL4	Q9tgl4 cervus elap
14	36	75.0	379	8 Q8M299	Q8m299 oxymycteru
15	36	75.0	379	8 Q8M296	Q8m296 oxymycteru
16	36	75.0	379	8 Q8M290	Q8m290 oxymycteru

17	36	75.0	379	8 Q9TF12	Q9tf12 spermophilu
18	36	75.0	379	8 Q9TF64	Q9tf64 spermophilu
19	36	75.0	379	8 Q8M294	Q8m294 oxymycteru
20	36	75.0	379	8 Q8M295	Q8m295 oxymycteru
21	36	75.0	379	8 Q8M297	Q8m297 oxymycteru
22	36	75.0	379	8 Q8LU40	Q8lu40 oxymycteru
23	36	75.0	379	8 Q8M292	Q8m292 oxymycteru
24	36	75.0	379	8 Q9TF11	Q9tf11 spermophilu
25	36	75.0	379	8 Q9TF08	Q9tf08 spermophilu
26	36	75.0	379	8 Q33940	Q33940 bolomy uri
27	36	75.0	379	8 Q8H95	Q8h95 cynocephalu
28	36	75.0	379	8 Q94QC8	Q94qc8 carvus timo
29	36	75.0	379	8 Q9Y7J8	Q9y7j8 salmiri sci
30	36	75.0	379	8 Q9Y6T9	Q9y6t9 salmiri sci
31	36	75.0	380	8 Q35970	Q35970 thomasomys
32	36	75.0	380	8 Q9MNS7	Q9mns7 calomys lep
33	36	75.0	380	8 Q9XNX6	Q9xnx6 blarinomys
34	36	75.0	380	8 Q9XNX0	Q9xnx0 thomasomys
35	36	75.0	380	8 Q9XNW3	Q9xnw3 rhipidomys
36	36	75.0	380	8 Q9MNT3	Q9mnt3 tapecomys p
37	36	75.0	380	8 Q94U29	Q94uz9 microtus gu
38	36	75.0	380	8 Q9MNT5	Q9mnt5 andalgomy
39	36	75.0	380	8 Q94V01	Q94v01 microtus oa
40	36	75.0	380	8 Q9MNT0	Q9mnt0 graomys dom
41	36	75.0	380	8 Q8M7E7	Q8m7e7 calomys fec
42	36	75.0	380	8 Q9XNW8	Q9xnw8 thomasomys
43	36	75.0	380	8 Q9T7L7	Q9t7l7 microtus ri
44	36	75.0	380	8 Q9MHP9	Q9mhf9 microtus lo
45	36	75.0	380	8 Q34853	Q34853 lenoxus api

ALIGNMENTS

RESULT 1

Q85TH4	PRELIMINARY;	PRT;	349 AA.
ID	Q85TH4		
AC	Q85TH4;		
DC	01-JUN-2003 (Tremblrel. 24, Created)		
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)		
DE	01-OCT-2003 (Tremblrel. 25, Last annotation update)		
DE	Cytochrome b.		
GN	CYTB.		
OS	Melipona bicolor.		
OG	Mitochondrion.		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;		
OC	Apidae; Melipona.		
OX	NCBI_taxID=60889;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Silvestre D., Arias M.C.;		
RT	"The mitochondrial genome of Melipona bicolor (Apidae, Meliponini).";		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF466146; AAO18422.1; -		
DR	GO; GO:00016020; C:membrane; IEA.		
DR	GO; GO:0005739; P:oxidoreductase activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR005798; Cytb_b6_C.		
DR	InterPro; IPR005797; Cytb_b6_N.		
DR	Pfam; PF00032; cytochrome_b_C; 1.		
DR	Pfam; PF00033; cytochrome_b_N; 1.		
DR	PROSITE; PS00192; CYTOCHROME_B_HEME; 1.		
KW	PROSITE; PS00193; CYTOCHROME_B_QQ; 1.		
KW	Mitochondrion.		
SQ	SEQUENCE 349 AA; 41464 MW; 9B1DC3A6927DADD3 CRC64;		

Query Match 83.3%; Score 40; DB 8; Length 349;  
Best Local Similarity 75.0%; Pred.No. 5.2;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQLVEYPT 9

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Db      311 QMIEYDPT 318
      |::|||
RESULT 2
Q87RR4 ID Q87RR4 PRELIMINARY; PRT; 506 AA.
AC Q87RR4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN VP0713.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; Pubmed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tsgomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RA "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005075; BACS8976.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . . ; IEA.
DR InterPro; IP001867; Trans reg C.
DR Pfam; PF00486; trans reg C_1.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 506 AA; 57784 MW; 7E566E91D449223 CRC64;

Query Match 81.2%; Score 39; DB 16; Length 506;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOLVEYDPT 9
      |::|||
Db      209 QOLVEYDPT 217
      |::|||
RESULT 3
Q8W454 ID Q8W454 PRELIMINARY; PRT; 278 AA.
AC Q8W454;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative calmodulin-binding protein.
GN AT4G31000/F6118.90 OR AT4G31000.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

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RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY062856; AAL32934.1; -.
DR EMBL; AY114575; AAM47894.1; -.
SQ SEQUENCE 278 AA; 31406 MW; 398DCFB65C85A836 CRC64;

Query Match 77.1%; Score 37; DB 10; Length 278;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOLVEYDPT 8
      |::|||
Db      145 QOLVEYDPT 152
      |::|||
RESULT 4
O65550 ID O65550 PRELIMINARY; PRT; 467 AA.
AC O65550;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative calmodulin-binding protein.
GN F6118.90 OR AT4G31000.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoerge W., Hoheisel J.,
RA Mewes H.W., Mayer K., Schueller C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoerge W., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022198; CAAL18193.1; -.
DR EMBL; AL161578; CAB79818.1; -.
DR PIR; A85363; A85363.
SQ SEQUENCE 467 AA; 52831 MW; 4DB1FB318D553B3D CRC64;

Query Match 77.1%; Score 37; DB 10; Length 467;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOLVEYDPT 8
      |::|||
Db      334 QOLVEYDPT 341
      |::|||
RESULT 5
Q8H816 ID Q8H816 PRELIMINARY; PRT; 609 AA.
AC Q8H816;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OJ1743A09.11.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;

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RN SEQUENCE FROM N.A.  
 RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,  
 RA Currie J., Collura K.;  
 RT "Rice Genomic Sequence."  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC105364; AN05331.1; --  
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO: GO:0008152; P:metabolism; IEA.  
 DR InterPro: IPR002086; Aldehyde\_dehydr.  
 DR Pfam: PF00646; F-box; 1.  
 DR PROSITE: PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 DR PROSITE: PS0181; PBOX; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 609 AA; 68105 MW; AEA195731E0BF07C CRC64;

Query Match 77.1%; Score 37; DB 10; Length 609;  
 Best Local Similarity 77.8%; Pred. No. 40;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLVVEPPT 9  
 DB 569 QQLLEPPT 577

RESULT 6  
 Q9B313 PRELIMINARY; PRT; 84 AA.  
 AC Q9B313;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome b (Fragment).  
 GN CYTB.  
 OS Neoceratodus forsteri (Australian lungfish).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.  
 OX NCBI\_TaxID=7892;  
 RN SEQUENCE FROM N.A.  
 RA Frentiu F., Ovenden J.R., Street R.;  
 RT "Australian lungfish (Neoceratodus forsteri) have low genetic  
 RT diversity at allozyme and mitochondrial loci: A conservation alert for  
 RT a living fossil?";  
 RL Conserv. Genet. 0:0-0(2001).  
 CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE  
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A  
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL  
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).  
 CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY  
 CC BOUND TO THE PROTEIN (BY SIMILARITY).  
 CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
 DR EMBL: AF344663; AAK29031.1; --  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO: GO:0005739; C:mitochondrion; IEA.  
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO: GO:0006118; P:electron transport; IEA.  
 DR GO: GO:0006810; P:transport; IEA.  
 DR InterPro: IPR005798; Cytb\_b6\_C.  
 DR Pfam: PF00032; cytochrome\_b\_c; 1.  
 DR Electron transport; Heme; Respiratory chain; Transmembrane; Transport;  
 KW Mitochondrion.  
 FT NON TER 1  
 SQ SEQUENCE 84 AA; 9673 MW; 1E7AFAD921592DAC CRC64;

Query Match 75.0%; Score 36; DB 8; Length 84;  
 Best Local Similarity 87.5%; Pred. No. 8.1;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEPPT 9  
 DB 27 QPVEPPT 34

RESULT 7  
 Q9MP34 PRELIMINARY; PRT; 247 AA.  
 AC Q9MP34;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome b (Fragment).  
 GN CYTB.  
 OS Bothriomyx meridionalis.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Formicidae; Dolichoderinae; Bothriomyrmex.  
 OX NCBI\_TaxID=121499;  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=ACFC;  
 RA Chiotis M., Jermin L.S., Crozier R.H.;  
 RT "A molecular framework for the phylogeny of the ant subfamily  
 RT Dolichoderinae";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE  
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A  
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL  
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).  
 CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY  
 CC BOUND TO THE PROTEIN (BY SIMILARITY).  
 CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
 DR EMBL: AF146714; AAF66714.1; --  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO: GO:0005739; C:mitochondrion; IEA.  
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO: GO:0006118; P:electron transport; IEA.  
 DR GO: GO:0006810; P:transport; IEA.  
 DR InterPro: IPR005798; Cytb\_b6\_C.  
 DR InterPro: IPR005797; Cytb\_b6\_N.  
 DR Pfam: PF00032; cytochrome\_b\_c; 1.  
 DR Pfam: PF00033; cytochrome\_b\_N; 1.  
 DR PROSITE: PS00193; CYTOCHROME\_B\_QQ; 1.  
 KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;  
 KW Mitochondrion.  
 FT NON TER 1  
 SQ SEQUENCE 247 AA; 29263 MW; CC68F8BA0D065B1A CRC64;

Query Match 75.0%; Score 36; DB 8; Length 247;  
 Best Local Similarity 75.0%; Pred. No. 25;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEPPT 9  
 DB 201 QSIEPPT 208

RESULT 8  
 Q9XNV8 PRELIMINARY; PRT; 352 AA.  
 AC Q9XNV8;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome B (Fragment).  
 GN CYTB.  
 OS Delomys dorsalis (striped Atlantic forest rat).

OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Delomys.  
 OX NCBI\_TaxID=89119;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Smith M.F., Patton J.L.;  
 RT "Phylogenetic relationships and the radiation of sigmodontine rodents  
 in South America: Evidence from cytochrome b.";  
 RL J. Mammal. Evol. 6:89-128(1999).  
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE  
 COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A  
 RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL  
 COUPLED TO ATP SYNTHESIS (BY SIMILARITY).  
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY  
 BOUND TO THE PROTEIN (BY SIMILARITY).  
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
 CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
 DR EMBL; AF108686; AAD45468.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR005798; Cytb\_b6\_C.  
 DR InterPro; IPR005797; Cytb\_b6\_N.  
 DR Pfam; PF00033; cytochrome\_b\_N; 1.  
 DR Pfam; PF00032; cytochrome\_b\_C; 1.  
 DR PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
 DR PROSITE; PS00193; CYTOCHROME\_B\_QO; 1.  
 KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;  
 KW Mitochondrion.  
 FT NON\_TER 352  
 FT NON\_TER 352  
 SQ SEQUENCE 352 AA; 39631 MW; AA408DB627140D6C CRC64;  
 Query Match 75.0%; Score 36; DB 8; Length 352;  
 Best Local Similarity 87.5%; Pred. No. 37;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QLVVEYPPT 9  
 DB 341 QPVEYPT 348  
 RESULT 9  
 ID Q8M293 PRELIMINARY; PRT; 371 AA.  
 AC Q8M293;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DE Cytochrome b (Fragment).  
 GN CYTB.  
 OS Oxymycterus quaestor.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Oxymycterus.  
 OX NCBI\_TaxID=196087;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hoffmann F.G., Lessa E.P., Smith M.F.;  
 RT "Systematics of Oxymycterus with description of a new species from  
 Uruguay.";  
 RL J. Mammal. 83:408-420(2002).  
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE  
 COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A  
 RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL  
 COUPLED TO ATP SYNTHESIS (BY SIMILARITY).  
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY

CC -1- BOUND TO THE PROTEIN (BY SIMILARITY).  
 CC SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
 CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
 DR EMBL; AF454772; AAM33839.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR005798; Cytb\_b6\_C.  
 DR InterPro; IPR005797; Cytb\_b6\_N.  
 DR Pfam; PF00033; cytochrome\_b\_N; 1.  
 DR Pfam; PF00032; cytochrome\_b\_C; 1.  
 DR PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
 DR PROSITE; PS00193; CYTOCHROME\_B\_QO; 1.  
 KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;  
 KW Mitochondrion.  
 FT NON\_TER 371  
 FT NON\_TER 371  
 SQ SEQUENCE 371 AA; 41657 MW; 2B0AC6BAEB2DED16 CRC64;  
 Query Match 75.0%; Score 36; DB 8; Length 371;  
 Best Local Similarity 87.5%; Pred. No. 39;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QLVVEYPPT 9  
 DB 333 QPVEYPT 340  
 RESULT 10  
 Q8XNV0  
 ID Q8XNV0 PRELIMINARY; PRT; 377 AA.  
 AC Q8XNV0;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome B (Fragment).  
 GN CYTB.  
 OS Reithrodon auritus (bunny rat).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Reithrodon.  
 OX NCBI\_TaxID=56234;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Smith M.F., Patton J.L.;  
 RT "Phylogenetic relationships and the radiation of sigmodontine rodents  
 in South America: Evidence from cytochrome b.";  
 RL J. Mammal. Evol. 6:89-128(1999).  
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE  
 COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A  
 RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL  
 COUPLED TO ATP SYNTHESIS (BY SIMILARITY).  
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY  
 BOUND TO THE PROTEIN (BY SIMILARITY).  
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
 CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
 DR EMBL; AF108694; AAD45476.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR005798; Cytb\_b6\_C.  
 DR InterPro; IPR005797; Cytb\_b6\_N.  
 DR Pfam; PF00033; cytochrome\_b\_N; 1.  
 DR Pfam; PF00032; cytochrome\_b\_C; 1.

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DR PROSITE; PS00192; CYTOCHROME B HEME; 1.
DR PROSITE; PS00193; CYTOCHROME B_QO; 1.
KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
FT Mitochondrion. 1
FT NON_TER 1
SQ SEQUENCE 377 AA; 42533 MW; 618DB37395E5E97 CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 8; Length 377;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 OLVEYPFT 9
DB 338 QPVEYPFT 345

RESULT 11
Q9XNX5 PRELIMINARY; PRT; 377 AA.
AC Q9XNX5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome B (Fragment).
GN CYTB.
OS Scapteromys tumidus (swamp rat).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Scacteromys.
OX NCBI_TaxID=89126;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents in South America: Evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
EMBL; AF108669; AAD45451.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:000810; P:transport; IEA.
DR InterPro; IPR005798; Cytb_b6_C.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME B_QO; 1.
DR PROSITE; PS00193; CYTOCHROME B_QO; 1.
KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
FT NON_TER 1
SQ SEQUENCE 377 AA; 42392 MW; 692D67AE20B6F3BB CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 8; Length 377;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 OLVEYPFT 9
DB 337 QPVEYPFT 344

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RESULT 12
Q8M2A0 PRELIMINARY; PRT; 379 AA.
AC Q8M2A0;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
GN CYTB.
OS Oxymycterus amazonicus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Oxymycterus.
OX NCBI_TaxID=196085;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoffmann F.G., Lessa E.P., Smith M.F.;
RT "Systematics of Oxymycterus with description of a new species from Uruguay.";
RL J. Mammal. 83:408-420(2002).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
EMBL; AF454765; AAM33832.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:000810; P:transport; IEA.
DR InterPro; IPR005798; Cytb_b6_C.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME B_QO; 1.
KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
FT NON_TER 379
SQ SEQUENCE 379 AA; 42856 MW; E7C010CACE44CE8F CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 8; Length 379;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 OLVEYPFT 9
DB 341 QPVEYPFT 348

RESULT 13
Q9TGL4 PRELIMINARY; PRT; 379 AA.
AC Q9TGL4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Cervus elaphus (Red deer).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]

```

RP SEQUENCE FROM N.A.  
 RX MEDLINE=20229580; PubMed=10764539;  
 RA Kuwayama R., Ozawa T.;  
 RT "Phylogenetic relationships among european red deer, wapiti, and sika  
 deer inferred from mitochondrial DNA sequences.";  
 RL Mol. Phylogenet. Evol. 15:115-123(2000).  
 CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE  
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A  
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL  
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).  
 CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY  
 CC BOUND TO THE PROTEIN (BY SIMILARITY).  
 CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
 DR EMBL; AB021098; BAA83607.1; -;  
 DR HSP; P00157; IBE3.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR005798; Cytb\_b6\_C.  
 DR Pfam; PF00032; cytochrome\_b6\_C; 1.  
 DR Pfam; PF00033; cytochrome\_b\_N; 1.  
 DR PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
 DR PROSITE; PS00193; CYTOCHROME\_B\_OO; 1.  
 DR Electron transport; Heme; Respiratory chain; Transmembrane; Transport;  
 KW Mitochondrion.  
 SQ SEQUENCE 379 AA; 42871 MW; 36F71191E46D263B CRC64;  
 Query Match 75.0%; Score 36; DB 8; Length 379;  
 Best Local Similarity 87.5%; Pred. No. 39;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QLVVEYPT 9  
 DB 341 QPVEYPT 348

RESULT 14  
 Q8M299 PRELIMINARY; PRT; 379 AA.  
 AC Q8M299;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome b (fragment).  
 GN CYTB.  
 OS Oxymycterus delator (sp. holicudo).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Oxymycterus.  
 ON NCBI\_TaxID=29125;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hoffmann F.G., Lessa E.P., Smith M.F.;  
 RT "Systematics of Oxymycterus with description of a new species from  
 Uruguay.";  
 RL J. Mammal. 83:408-420(2002).  
 CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE  
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A  
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL  
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).  
 CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY  
 CC BOUND TO THE PROTEIN (BY SIMILARITY).  
 CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
 DR EMBL; AF454766; AM33833.1; -;  
 DR HSP; P00157; IBE3.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR005798; Cytb\_b6\_C.  
 DR Pfam; PF00032; cytochrome\_b6\_C; 1.  
 DR Pfam; PF00033; cytochrome\_b\_N; 1.  
 DR PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
 DR PROSITE; PS00193; CYTOCHROME\_B\_OO; 1.  
 DR Electron transport; Heme; Respiratory chain; Transmembrane; Transport;  
 KW Mitochondrion.  
 SQ SEQUENCE 379 AA; 42802 MW; BFE22C9B4F985AE1 CRC64;

DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR005798; Cytb\_b6\_C.  
 DR Pfam; PF00032; cytochrome\_b6\_C; 1.  
 DR Pfam; PF00033; cytochrome\_b\_N; 1.  
 DR PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
 DR PROSITE; PS00193; CYTOCHROME\_B\_OO; 1.  
 DR Electron transport; Heme; Respiratory chain; Transmembrane; Transport;  
 KW Mitochondrion.  
 FT NON TER 379  
 SQ SEQUENCE 379 AA; 42855 MW; 55DD10D7D344D8E3 CRC64;  
 Query Match 75.0%; Score 36; DB 8; Length 379;  
 Best Local Similarity 87.5%; Pred. No. 39;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QLVVEYPT 9  
 DB 341 QPVEYPT 348

RESULT 15  
 Q8M296 PRELIMINARY; PRT; 379 AA.  
 AC Q8M296;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome b (fragment).  
 GN CYTB.  
 OS Oxymycterus dasytrichus.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Oxymycterus.  
 ON NCBI\_TaxID=196088;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hoffmann F.G., Lessa E.P., Smith M.F.;  
 RT "Systematics of Oxymycterus with description of a new species from  
 Uruguay.";  
 RL J. Mammal. 83:408-420(2002).  
 CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE  
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A  
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL  
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).  
 CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY  
 CC BOUND TO THE PROTEIN (BY SIMILARITY).  
 CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
 DR EMBL; AF454769; AM33836.1; -;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR005798; Cytb\_b6\_C.  
 DR Pfam; PF00032; cytochrome\_b6\_C; 1.  
 DR Pfam; PF00033; cytochrome\_b\_N; 1.  
 DR PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
 DR PROSITE; PS00193; CYTOCHROME\_B\_OO; 1.  
 DR Electron transport; Heme; Respiratory chain; Transmembrane; Transport;  
 KW Mitochondrion.  
 FT NON TER 379  
 SQ SEQUENCE 379 AA; 42802 MW; BFE22C9B4F985AE1 CRC64;

Query Match 75.0%; Score 36; DB 8; Length 379;  
Best Local Similarity 87.5%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 QLVVEVPFT 9  
DB 341 QPVEVPFT 348

Search completed: September 30, 2004, 05:59:31  
Job time : 32.6073 secs

Blank sheet



QM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 43.9322 Seconds  
(without alignments)  
57.883 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEVPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match %	Score	Length	DB	ID	Description
1	48	100.0	9	3	AA32256	Aay32256 Light cha
2	48	100.0	116	3	AA32262	Aay32262 Humanised
3	48	100.0	145	3	AA32261	Aay32261 Mouse ant
4	45	93.8	19	3	AA32261	Aay32261 Murine an
5	45	93.8	122	3	AA32261	Aay32261 Murine an
6	45	93.8	131	2	AA32232	Aay32232 Mouse Mab
7	45	93.8	132	2	AA32232	Aay32232 Light cha
8	44	91.7	9	2	AA32232	Aay32232 Light cha
9	44	91.7	113	2	AA32232	Aay32232 Light cha
10	44	91.7	113	2	AA32232	Aay32232 Light cha
11	37	77.1	100	4	AA32232	Aay32232 Light cha
12	36	75.0	9	2	AA32232	Aay32232 Light cha
13	36	75.0	113	2	AA32232	Aay32232 Light cha
14	36	75.0	113	2	AA32232	Aay32232 Light cha
15	36	75.0	241	5	AA32232	Aay32232 Light cha
16	36	75.0	241	5	AA32232	Aay32232 Light cha
17	36	75.0	241	5	AA32232	Aay32232 Light cha
18	36	75.0	241	5	AA32232	Aay32232 Light cha
19	36	75.0	253	5	AA32232	Aay32232 Light cha
20	36	75.0	274	2	AA32232	Aay32232 Light cha
21	36	75.0	392	3	AA32232	Aay32232 Light cha
22	36	75.0	510	3	AA32232	Aay32232 Light cha
23	35	72.9	112	3	AA32232	Aay32232 Light cha
24	35	72.9	126	2	AA32232	Aay32232 Light cha
25	35	72.9	425	6	AA32232	Aay32232 Light cha

26	35	72.9	533	3	AA32256	Arabidops
27	35	72.9	536	3	AA32256	Arabidops
28	35	72.9	622	3	AA32256	Arabidops
29	34	70.8	9	3	AA32256	Murine l3
30	34	70.8	113	3	AA32256	Murine l3
31	34	70.8	146	2	AA32256	Murine l3
32	34	70.8	440	6	AA32256	Amino aci
33	34	70.8	585	5	AA32256	Protein e
34	34	70.8	601	6	AA32256	Staphyloc
35	34	70.8	604	4	AA32256	S. epider
36	33	68.8	9	2	AA32256	Ag81648
37	33	68.8	82	4	AA32256	C242:11 M
38	33	68.8	107	4	AA32256	Peptide #
39	33	68.8	107	4	AA32256	Human ant
40	33	68.8	108	2	AA32256	Anti-Rh(D
41	33	68.8	113	2	AA32256	BW 835 VK
42	33	68.8	113	2	AA32256	Sequence
43	33	68.8	113	2	AA32256	Ag90819
44	33	68.8	133	2	AA32256	26Of9 hyb
45	33	68.8	133	2	AA32256	CTW01 Vi.
						GLI varia
						Sequence

#### ALIGNMENTS

RESULT 1

AA32256

ID AA32256 standard; peptide; 9 AA.

XX

AC AA32256;

XX

DT 15-FEB-2000 (first entry)

XX

DE Light chain CDR L3 of mouse anti-CD23 Mab C11.

XX

KW

KW

KW

KW

KW

KW

KW

KW

KW

KW

XX

OS Mus musculus.

XX

PN WO9958679-A1

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99WO-GB001434.

XX

PR 09-MAY-1998; 98GB-00009839.

XX

PA (GLAX ) GLAXO GROUP LTD.

XX

PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX

PT WPI; 2000-053101/04.

XX

DR N-PSDB; AA324741.

XX

PS Cell receptor specific antibodies useful for treating e.g. arthritis,

XX

PS diabetes, multiple sclerosis and psoriasis.

XX

PS Claim 1; Page 40; 81pp; English.

XX

CC This sequence represents complementarity determining region 3 (CDR L3)

CC of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11

CC (see also AA32262). The invention provides altered antibodies, such as

CC chimeric or humanised antibodies, which comprise sufficient of the amino

CC acid sequences of C11 light and heavy chain CDRs (see AA32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents  
 CC  
 XX Sequence 9 AA;  
 SQ

Query Match 100.0%; Score 48; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
 Db 1 QQLVEYPFT 9

RESULT 2  
 AAY32262  
 ID AAY32262 standard; protein; 116 AA.

XX AAY32262;

XX 15-FEB-2000 (first entry)

XX Humanised anti-CD23 Mab C11 light chain variable region.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.  
 XX Homo sapiens.  
 OS Synthetic.

Key	Location/Qualifiers
FT Region	1..23 /note= "framework region 1"
FT Region	24..39 /note= "CDR 1"
FT Region	40..54 /note= "framework region 2"
FT Region	55..61 /note= "CDR 2"
FT Region	62..93 /note= "framework region 3"
FT Region	94..102 /note= "CDR 3"
FT Region	103..113 /note= "framework region 4"

XX WO9958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX ) GLAXO GROUP LTD.

XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 XX WPI; 2000-053101/04.  
 DR N-PSDB; AAZ34747.  
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 XX diabetes, multiple sclerosis and psoriasis.  
 XX Claim 9; Fig 3; Sipp; English.

XX This sequence represents the light chain variable region (VL) of  
 CC humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human  
 CC framework (H5IGKVII) and the light chain complementarity determining  
 CC regions (see AAY32254-56) of murine antibody C11. The DNA was constructed  
 CC by splice overlap PCR. The invention provides altered antibodies, such as  
 CC chimeric or humanised antibodies, which comprise sufficient of the amino  
 CC acid sequences of the C11 light and heavy chain complementarity  
 CC determining regions to render them capable of binding to the CD23 type II  
 CC molecule expressed on haematopoietic cells. The antibodies are used to  
 CC block soluble CD23 formation in human therapy, for the treatment of  
 CC arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents  
 XX

XX Sequence 116 AA;

Query Match 100.0%; Score 48; DB 3; Length 116;  
 Best Local Similarity 100.0%; Pred. NO. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
 Db 94 QQLVEYPFT 102

RESULT 3  
 AAY32261  
 ID AAY32261 standard; protein; 145 AA.

XX AAY32261;

XX 15-FEB-2000 (first entry)

XX Mouse anti-CD23 Mab C11 light chain variable region.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.  
 XX Mus musculus.

Key	Location/Qualifiers
FT Region	55..70 /note= "CDR L1"
FT Region	83..92 /note= "CDR L2"
FT Region	125..134 /note= "CDR L3"

PN WO9958679-A1.  
 XX 18-NOV-1999.  
 XX 07-MAY-1999; 99WO-CB001434.  
 XX 09-MAY-1998; 98GB-00009839.  
 XX (GLAXO) GLAXO GROUP LTD.  
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 XX WPI; 2000-053101/04.  
 XX DR N-PSDB; AA234746.  
 XX  
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 XX diabetes, multiple sclerosis and psoriasis.  
 XX Claim 8; Fig 2; 81pp; English.  
 XX This sequence represents the light chain variable region (VL) of murine  
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides  
 CC altered antibodies, such as chimeric or humanised antibodies (see  
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions (see AAY32254-59) to render them capable of binding to the CD23  
 CC type II molecule expressed on haematopoietic cells. The antibodies are  
 CC used to block soluble CD23 formation in human therapy, for the treatment  
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, sinusitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents  
 XX  
 XX Sequence 145 AA;  
 Query Match 100.0%; Score 48; DB 3; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 0.11;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQLVEYPFT 9  
 DB 125 QQLVEYPFT 133  
 RESULT 4  
 AAY70804  
 ID AAY70804 standard; peptide; 19 AA.  
 XX  
 XX AAY70804;  
 XX  
 XX 31-JUL-2000 (first entry)  
 XX Murine anti-PAB-421 IDI-1 mAb light chain CDR based peptide IDI-1 L3.  
 XX  
 XX Murine; p53 protein; monoclonal antibody; mAb; PAB-421; IDI-1 L3;  
 XX light chain variable region; VL; complementarity determining region; CDR;  
 XX dermatological; immunosuppressive; antiinflammatory; autoimmune response;  
 XX SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;  
 XX DNA-binding domain; anti-idiotypic antibody.  
 XX  
 XX Mus sp.  
 XX  
 XX WO200023082-A1.  
 XX 27-APR-2000.  
 XX 19-OCT-1999; 99WO-US024443.

PR 19-OCT-1998; 98US-0104816P.  
 XX (VEDA) YEDA RES & DEV CO LTD.  
 XX Cohen IR, Rotter V, Erez-Alon N, Herkel J;  
 XX WPI; 2000-339512/29.  
 XX Treatment of systemic lupus erythematosus by down-regulating the  
 PT autoimmune response to the C-terminal DNA-binding domain of the p53  
 PT protein by an active compound comprising of antibodies to p53 or  
 PT fragments of p53.  
 XX Claim 78; Fig 10; 87pp; English.  
 XX The patent discloses a method for the treatment of systemic lupus  
 CC erythematosus (SLE) by down-regulating the autoimmune response to the C-  
 CC terminal DNA-binding domain of p53 protein by an active compound. The  
 CC present sequence is a IDI-1 L3 peptide which comprises the  
 CC complementarity determining region (CDR) of the light chain of IDI-1  
 CC monoclonal antibody (mAb). The IDI-1 mAb is an anti-idiotypic  
 CC antibody/Ab2 mAb specific for PAB-421 which is an Ab1 mAb specific to the  
 CC C-terminal DNA-binding domain of murine p53 protein. The peptide  
 CC corresponds to residues 92-110 of IDI-1 light chain variable region. It  
 CC is an example of the active compound useful in the diagnosis, prevention  
 CC and treatment of SLE in humans  
 XX Sequence 19 AA;  
 SQ  
 Query Match 93.8%; Score 45; DB 3; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 0.051;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQLVEYPFT 9  
 DB 6 QQLVEYPFT 14  
 RESULT 5  
 AAY70790  
 ID AAY70790 standard; protein; 122 AA.  
 XX  
 XX AAY70790;  
 XX 31-JUL-2000 (first entry)  
 XX Murine anti-PAB-421 IDI-1 mAb light chain variable region.  
 XX  
 XX Murine; p53 protein; PAB-421; monoclonal antibody; mAb; IDI-1;  
 XX anti-idiotypic antibody; DNA-binding domain; dermatological;  
 XX immunosuppressive; antiinflammatory; autoimmune response; SLE;  
 XX systemic lupus erythematosus; diagnosis; treatment; autoantigen;  
 XX light chain variable region; VL; complementarity determining region; CDR.  
 XX  
 XX Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 XX Region 27..42  
 XX /label= CDR  
 XX /note= "Complementarity determining region"  
 XX Region 58..64  
 XX /label= CDR  
 XX /note= "Complementarity determining region"  
 XX Region 97..105  
 XX /label= CDR  
 XX /note= "Complementarity determining region"  
 XX  
 XX WO200023082-A1.  
 XX 27-APR-2000.  
 XX 19-OCT-1999; 99WO-US024443.

PR 19-OCT-1998; 98US-0104816P.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Cohen IR, Rotter V, Erez-Alon N, Herkel J;  
 XX WPI; 2000-339512/29.  
 XX  
 PT Treatment of systemic lupus erythematosus by down-regulating the  
 PT autoimmune response to the C-terminal DNA-binding domain of the p53  
 PT protein by an active compound comprising of antibodies to p53 or  
 XX fragments of p53.  
 XX  
 PS Claim 78; Fig 9; 87pp; English.  
 XX  
 CC The patent discloses a method for the treatment of systemic lupus  
 CC erythematosus (SLE) by down-regulating the autoimmune response to the C-  
 CC terminal DNA-binding domain of p53 protein by an active compound. The  
 CC present sequence is a light chain variable region of IDI-1 an anti-  
 CC idiotype antibody/Ab2 monoclonal antibody (mAb) specific for PAb-421  
 CC which is an Ab1 mAb specific to the C-terminal DNA-binding domain of  
 CC murine p53 protein. The Ab1 and Ab2 mAbs and peptides based on  
 CC complementarity determining regions of light and heavy chain variable  
 CC regions of these antibodies, are examples of active compounds useful in  
 CC the diagnosis, prevention and treatment of SLE in humans  
 XX  
 SQ Sequence 122 AA;  
 Query Match 93.8%; Score 45; DB 3; Length 122;  
 Best Local Similarity 88.9%; Pred. No. 0.38;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQLVEYPPT 9  
 Db 97 QQLVEYPPT 105  
 RESULT 6  
 AAR12232  
 ID AAR12232 standard; protein; 131 AA.  
 AC AAR12232;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 19-AUG-1991 (first entry)  
 XX  
 DE Mouse MAB 2E12 L chain V region.  
 XX  
 KW HIV-1; chimera.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9107494-A.  
 XX  
 PD 30-MAY-1991.  
 XX  
 PF 13-NOV-1989; 89US-00433703.  
 XX  
 PR 13-NOV-1989; 89US-00433703.  
 XX  
 PA (XOMA ) XOMA CORP.  
 PA (GREG ) GREEN CROSS CORP.  
 PA (ZOMA-) ZOMA CORP.  
 XX  
 PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;  
 XX WPI; 1991-178106/24.  
 DR N-PSDB; AAQ12012.  
 XX  
 PT New chimeric mouse human antibodies - used in treatment, diagnosis and  
 PT prophylaxis of HIV infections.  
 XX  
 PS Disclosure; Fig 1; 108pp; English.

XX The mouse VL gene product may be used to produce chimeric mouse-human  
 CC Abs against HIV-1 comprising human Ig constant regions and murine  
 CC variable regions. These novel sequence are useful in treatment, diagnosis  
 CC and prophylaxis of HIV infections, and may be produced by a bacterial,  
 CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct  
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 131 AA;  
 Query Match 93.8%; Score 45; DB 2; Length 131;  
 Best Local Similarity 88.9%; Pred. No. 0.41;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQLVEYPPT 9  
 Db 114 QQLVEYPPT 122  
 RESULT 7  
 AAR12354  
 ID AAR12354 standard; protein; 132 AA.  
 XX  
 AC AAR12354;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 15-AUG-1991 (first entry)  
 XX  
 DE Light (kappa) chain variable region of murine 2E12 immunoglobulin.  
 XX  
 KW Chimeric antibodies; immunoconjugates; HIV; AIDS.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9107493-A.  
 XX  
 PD 30-MAY-1991.  
 XX  
 PF 13-NOV-1989; 89US-00433730.  
 XX  
 PR 13-NOV-1989; 89US-00433730.  
 XX  
 PA (XOMA ) XOMA CORP.  
 PA (GREG ) GREEN CROSS CORP.  
 XX  
 PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;  
 XX WPI; 1991-178105/24.  
 DR N-PSDB; AAQ12056.  
 XX  
 PT New chimeric mouse-human antibodies - used to detect, kill and remove HIV  
 PT -1 antigen from sample.  
 XX  
 PS Disclosure; Fig 1; 107pp; English.  
 XX  
 CC This is the light (kappa)- chain variable (V) region of a mouse  
 CC monoclonal antibody (Mab), 2E12, and is specific for an HIV-1 vital  
 CC antigen. It is used in the construction of a chimeric MAb comprising  
 CC heavy and light chains having murine V regions and human C regions. The  
 CC chimeric MABs are more effective than murine MAB 2E12 since they have an  
 CC increased compatibility in humans. The heavy and light chain V-regions  
 CC are joined by manipulating their respective joining (J) regions, to  
 CC generate restriction enzyme recognition sites. The chimeric MABs can be  
 CC used as immuno- conjugates, in association with e.g. toxins for HIV  
 CC treatment. They can also be used in diagnosis of HIV. See also AAQ12057-  
 CC 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003  
 CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)  
 XX  
 SQ Sequence 132 AA;  
 Query Match 93.8%; Score 45; DB 2; Length 132;  
 Best Local Similarity 88.9%; Pred. No. 0.41;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
 DB 114 QQLVEYPFT 122  
 RESULT 8  
 AAW39823  
 ID AAW39823 standard; peptide; 9 AA.  
 AC AAW39823;  
 XX  
 DT 16-JUN-1998 (first entry)  
 DE Light chain CDR3 of catalytic antibody 2A10.  
 XX  
 KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9749800-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 PF 25-JUN-1997; 97WO-US010965.  
 XX  
 PR 25-JUN-1996; 96US-00672345.  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 PI Landry DW;  
 XX  
 DR WPI; 1998-077166/07.  
 DR N-PSDB; AAV09789.  
 XX  
 PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 PS Disclosure; Fig 21; 147pp; English.  
 XX  
 CC The present sequence represents the light chain of a catalytic antibody  
 CC which is capable of degrading cocaine. A series of cocaine transition  
 CC state analogues (TSAs) were prepared and used to immunise mice for  
 CC production of hybridomas. Catalytic antibodies were identified by their  
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The  
 CC antibodies reduce the concentration of cocaine in a subject, and are used  
 CC particularly for the treatment of an overdose. They are also used for  
 CC treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)  
 XX  
 SQ Sequence 113 AA;  
 Query Match 91.7%; Score 44; DB 2; Length 113;  
 Best Local Similarity 88.9%; Pred. No. 0.55;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QQLVEYPFT 9  
 DB 94 QQLVEYPFT 102  
 RESULT 10  
 AAW39804  
 ID AAW39804 standard; protein; 113 AA.  
 XX  
 AC AAW39804;  
 XX  
 DT 16-JUN-1998 (first entry)  
 DE Variable domain of the Kappa light chain of catalytic antibody 2A10.  
 XX  
 KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9749800-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 PF 25-JUN-1997; 97WO-US010965.  
 XX  
 PR 25-JUN-1996; 96US-00672345.  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 PI Landry DW;  
 XX  
 DR WPI; 1998-077166/07.  
 DR N-PSDB; AAV09789.  
 XX  
 PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 PS Claim 15; Page 82; 147pp; English.  
 XX  
 CC AAW39821-23 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 2A10, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)  
 XX  
 SQ Sequence 9 AA;  
 Query Match 91.7%; Score 44; DB 2; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QQLVEYPFT 9  
 DB 1 QQLVEYPFT 9  
 RESULT 9  
 AAW39882  
 ID AAW39882 standard; protein; 113 AA.  
 XX  
 AC AAW39882;  
 XX

XX 25-JUN-1997; 97WO-US010965.  
 XX 25-JUN-1996; 96US-00672345.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Landry DW;  
 XX WPI; 1998-077166/07.  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX Claim 16; Page 73-74; 147pp; English.  
 XX AA39801-05 represent the amino acid sequences of the variable domain of  
 CC the kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809  
 CC represents the heavy chain) was identified using TSA1, which is an  
 CC immunogenic conjugate of a phosphate monoester transition state analogue.  
 CC Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the  
 CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved)  
 XX Sequence 113 AA;  
 SQ Query Match 91.7%; Score 44; DB 2; Length 113;  
 Best Local Similarity 88.9%; Pred. No. 0.55;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QQLVEVPFT 9  
 Db 94 QQFVEVPFT 102  
 RESULT 11  
 AA06969  
 ID AA06969 standard; protein; 100 AA.  
 AC AA06969;  
 DT 16-OCT-2001 (first entry)  
 DE Mouse germline kappa light chain variable (VK) region, 167/24.  
 XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherosclerosis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angiodysplasia; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; VK; kappa light chain variable region.  
 OS Mus sp.  
 XX WO200157226-A1.  
 PN 09-AUG-2001.  
 XX 02-FEB-2001; 2001WO-US003537.  
 XX 03-FEB-2000; 2000US-00497625.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX

PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
 XX WPI; 2001-488888/53.  
 XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
 PT disorder in a patient, comprises a binding specificity for CCR2, and a  
 PT non-human antigen binding region and human immunoglobulin.  
 XX Disclosure; Page 151; 183pp; English.  
 XX The patent discloses a humanised antibody or its antigen-binding  
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
 CC comprising an antigen binding region of non-human origin and at least a  
 CC portion of an immunoglobulin of human origin. The humanised antibodies  
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They  
 CC are useful for inhibiting or treating HIV infection. The proteins of the  
 CC invention are useful for inhibiting leukocyte trafficking, for treating  
 CC CCR2-mediated disorders such as inflammatory disorder, autoimmune  
 CC disorders such as rheumatoid arthritis and multiple sclerosis,  
 CC atherosclerosis and atherosclerosis, and for inhibiting restenosis. They  
 CC are useful in therapy or diagnosis, and in the manufacture of a  
 CC medicament for treating CCR-2 mediated disease. They are also useful for  
 CC treating allergy, anaphylaxis, malignancy, chronic and acute  
 CC inflammation, histamine and IgE mediated allergic reaction, shock,  
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
 CC associated with vascular intervention, including angioplasty and/or stent  
 CC placement in a mammal. Humanised antibodies are also useful for  
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated  
 CC with vascular intervention. The present sequence is mouse germline kappa  
 CC light chain variable (VK) region, 167/24  
 XX Sequence 100 AA;  
 SQ Query Match 77.1%; Score 37; DB 4; Length 100;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQLVEYP 7  
 Db 94 QQLVEYP 100  
 RESULT 12  
 AA39817  
 ID AA39817 standard; peptide; 9 AA.  
 AC AA39817;  
 DT 16-JUN-1998 (first entry)  
 DE Light chain CDR3 of catalytic antibody 3B9.  
 XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX Mus sp.  
 OS WO9749800-A1.  
 PN 31-DEC-1997.  
 XX 25-JUN-1997; 97WO-US010965.  
 XX 25-JUN-1996; 96US-00672345.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Landry DW;  
 XX

DR WPI; 1998-077166/07.  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX Claim 11; Page 81; 147pp; English.  
 PS  
 XX AAW39815-17 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)  
 XX  
 XX SQ Sequence 9 AA;  
 Query Match 75.0%; Score 36; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 QQLVEYPFT 9  
 | : |||||  
 Db 1 QHFVDYPT 9  
 | : |||||  
 RESULT 13  
 AAW39803  
 ID AAW39803 standard; protein; 113 AA.  
 AC AAW39803;  
 XX  
 XX 16-JUN-1998 (first entry)  
 DE  
 XX Variable domain of the Kappa light chain of catalytic antibody 12H1.  
 DE  
 XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX  
 OS Mus sp.  
 XX  
 XX WO9749800-A1.  
 PN  
 XX 31-DEC-1997.  
 PD  
 XX 25-JUN-1997; 97WO-US010965.  
 PF  
 XX 25-JUN-1996; 96US-00672345.  
 PR  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 XX Landry DW;  
 PI  
 XX WPI; 1998-077166/07.  
 DR  
 XX P-PSDB; AAV09802.  
 DR  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 XX Claim 18; Page 73; 147pp; English.  
 PS  
 XX AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the Kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were

CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808  
 CC represents the heavy chain) was identified using TSA2, and has a per  
 CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine  
 CC in a subject, and are used particularly for the treatment of an overdose.  
 CC They are also used for treating addiction (by reducing the in vivo  
 CC concentration that can be achieved)  
 XX  
 XX SQ Sequence 113 AA;  
 Query Match 75.0%; Score 36; DB 2; Length 113;  
 Best Local Similarity 66.7%; Pred. No. 23;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 QQLVEYPFT 9  
 | : |||||  
 Db 94 QHFVDYPT 102  
 | : |||||  
 RESULT 14  
 AAW39801  
 ID AAW39801 standard; protein; 113 AA.  
 AC AAW39801;  
 XX  
 XX 16-JUN-1998 (first entry)  
 DT  
 XX Variable domain of the Kappa light chain of catalytic antibody 3B9.  
 DE  
 XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX  
 OS Mus sp.  
 XX  
 XX WO9749800-A1.  
 PN  
 XX 31-DEC-1997.  
 PD  
 XX 25-JUN-1997; 97WO-US010965.  
 PF  
 XX 25-JUN-1996; 96US-00672345.  
 PR  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 XX Landry DW;  
 PI  
 XX WPI; 1998-077166/07.  
 DR  
 XX P-PSDB; AAV09791.  
 DR  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 XX Claim 12; Page 71-72; 147pp; English.  
 PS  
 XX AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the Kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806  
 CC represents the heavy chain) was identified using TSA1, which is an  
 CC immunogenic conjugate of a phosphate monoester transition state analogue.  
 CC Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the  
 CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved)  
 XX  
 XX SQ Sequence 113 AA;

Query Match 75.0%; Score 36; DB 2; Length 113;  
Best Local Similarity 66.7%; Pred. No. 23;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
| : : : :  
Db 94 QHEVDYPT 102

QY 1 QQLVEYPFT 9  
| : : : :  
Db 223 QQLISYPLT 231

Search completed: September 30, 2004, 06:06:15  
Job time : 46.9322 secs

## RESULT 15

AAW24063  
ID AAW24063 standard; protein; 241 AA.

XX AC AAW24063;

XX DT 17-MAR-1998 (first entry)

XX DE Human WSX receptor agonist antibody clone #17.

XX KW Human; WSX receptor; clone #17; identification; purification; ligand;

XX KW activator; antibody; agonist; proliferation; obesity; differentiation;

XX KW anaemia; treatment; neoplasia; arteriosclerosis; Type II diabetes;

XX KW polycystic ovarian disease; cardiovascular disease; osteoarthritis;

XX KW dermatological disorder; hypertension; insulin resistance;

XX KW hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis.

XX OS Homo sapiens.

XX PN WO9725425-A1.

XX PD 17-JUL-1997.

XX PF 07-JAN-1997; 97WO-US000325.

XX PR 08-JAN-1996; 96US-00585005.

XX PR 20-JUN-1996; 96US-00667197.

XX PA (GETH ) GENENTECH INC.

XX PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;

XX PI Rodrigues ML;

XX DR WPI; 1997-372864/34.

XX PT WSX receptor and related antibodies and ligands - used to develop

XX PT products for diagnosis and therapy, e.g. for improving haematopoiesis or

XX PT for treating tumours.

XX PS Example 14; Page 122-123; 219pp; English.

XX CC The present sequence is an agonist antibody clone to the human WSX

XX CC receptor, which can be used to identify and purify ligands and

XX CC activators. An anti-WSX receptor antibody can be used as an agonist to

XX CC activate the WSX receptor, leading to enhanced proliferation or

XX CC differentiation of a cell expressing the WSX receptor. It can also be

XX CC used to decrease body weight and/or fat-depot weight and/or food intake

XX CC in an obese mammal. WSX receptor ligands can be used to enhance

XX CC proliferation or differentiation of lymphoid, myeloid or erythroid blood

XX CC cell lineages. This is useful when a mammal, especially a human, is

XX CC suffering from decreased blood cell levels, i.e. anaemia, caused by

XX CC chemotherapy, radiation therapy or bone marrow transplantation therapy.

XX CC It can also be used to repopulate blood cells in a mammal. The products

XX CC can also be used to treat, e.g. neoplastic disorders, arteriosclerosis,

XX CC Type II diabetes, polycystic ovarian disease, cardiovascular diseases,

XX CC osteoarthritis, dermatological disorders, hypertension, insulin

XX CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer and

XX CC cholelithiasis

XX SQ Sequence 241 AA;

Query Match 75.0%; Score 36; DB 2; Length 241;

Best Local Similarity 66.7%; Pred. No. 51;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:01:30 ; Search time 151.017 Seconds  
(without alignments)  
19.178 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEYPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/prodata1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/prodata1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	91.7	9	10	US-09-940-727B-27
2	44	91.7	113	10	US-09-940-727B-8
3	44	91.7	113	10	US-09-940-727B-108
4	37	77.1	100	9	US-09-840-459-32
5	37	77.1	100	16	US-10-766-773-32
6	37	77.1	100	16	US-10-766-610-32
7	37	77.1	100	16	US-10-733-563-32
8	37	77.1	609	16	US-10-437-963-104782
9	36	75.0	9	10	US-09-940-727B-21
10	36	75.0	9	16	US-10-632-706-134
11	36	75.0	113	10	US-09-940-727B-5
12	36	75.0	113	10	US-09-940-727B-7
13	36	75.0	113	10	US-09-940-727B-100
14	36	75.0	113	10	US-09-940-727B-112
15	36	75.0	241	8	US-08-779-457-50

16	36	75.0	251	10	US-09-880-748-1310	Sequence 1310, Ap
17	36	75.0	251	12	US-10-293-418-1310	Sequence 1310, Ap
18	36	75.0	253	10	US-09-880-748-936	Sequence 936, App
19	36	75.0	253	12	US-10-293-418-936	Sequence 936, App
20	36	75.0	280	10	US-09-940-727B-119	Sequence 119, App
21	35	72.9	90	16	US-10-767-701-56894	Sequence 56894, A
22	35	72.9	298	12	US-10-425-114-71736	Sequence 71736, A
23	35	72.9	569	12	US-10-425-114-72355	Sequence 72355, A
24	34	70.8	440	12	US-10-282-122A-77411	Sequence 77411, A
25	34	70.8	1074	16	US-10-389-566-2371	Sequence 2371, Ap
26	33	68.8	79	12	US-10-425-114-44597	Sequence 44597, A
27	33	68.8	82	9	US-09-864-761-47635	Sequence 47635, A
28	33	68.8	82	12	US-10-424-599-280477	Sequence 280477, A
29	33	68.8	83	12	US-10-424-599-212368	Sequence 212368, A
30	33	68.8	107	10	US-09-848-798-40	Sequence 40, Appl
31	33	68.8	199	12	US-10-424-599-246437	Sequence 246437, A
32	33	68.8	243	16	US-10-437-963-161157	Sequence 161157, A
33	33	68.8	250	16	US-10-333-235A-55	Sequence 55, Appl
34	33	68.8	337	16	US-10-437-963-190847	Sequence 190847, A
35	33	68.8	368	16	US-10-333-235A-58	Sequence 58, Appl
36	33	68.8	441	12	US-10-282-122A-45037	Sequence 45037, A
37	33	68.8	465	16	US-10-333-235A-59	Sequence 59, Appl
38	33	68.8	561	15	US-10-369-493-870	Sequence 870, Appl
39	33	68.8	726	9	US-09-973-451-10	Sequence 10, Appl
40	33	68.8	789	14	US-10-207-706-5	Sequence 5, Appl
41	33	68.8	792	14	US-10-207-706-4	Sequence 4, Appl
42	33	68.8	816	14	US-10-207-706-3	Sequence 3, Appl
43	33	68.8	849	16	US-10-437-963-114890	Sequence 114890, A
44	33	68.8	899	12	US-10-282-122A-68696	Sequence 68696, A
45	32	66.7	70	12	US-10-424-599-215810	Sequence 215810, A

#### ALIGNMENTS

#### RESULT 1

US-09-940-727B-27  
; Sequence 27, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 27  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-27

Query Match 91.7%; Score 44; DB 10; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.2e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9  
DB 1 QQLVEYPT 9

#### RESULT 2

US-09-940-727B-8  
; Sequence 8, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:

; APPLICANT: Landry, Donald W  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 0575/51400-B  
 ; CURRENT APPLICATION NUMBER: US/09/940,727B  
 ; CURRENT FILING DATE: 2002-09-04  
 ; PRIOR FILING DATE: 1998-12-28  
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965  
 ; PRIOR FILING DATE: 1997-06-25  
 ; PRIOR APPLICATION NUMBER: 08/672,345  
 ; PRIOR FILING DATE: 1996-06-25  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 8  
 ; LENGTH: 113  
 ; TYPE: PRT  
 ; ORGANISM: mouse  
 US-09-940-727B-8

Query Match 91.7%; Score 44; DB 10; Length 113;  
 Best Local Similarity 88.9%; Pred.No. 0.87;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
 Db 94 QQFVEYPFT 102

RESULT 3  
 US-09-940-727B-108  
 ; Sequence 108, Application US/09940727B  
 ; Publication No. US2003007793A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald W  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 0575/51400-B  
 ; CURRENT APPLICATION NUMBER: US/09/940,727B  
 ; CURRENT FILING DATE: 2002-09-04  
 ; PRIOR FILING DATE: 1998-12-28  
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965  
 ; PRIOR FILING DATE: 1997-06-25  
 ; PRIOR APPLICATION NUMBER: 08/672,345  
 ; PRIOR FILING DATE: 1996-06-25  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 108  
 ; LENGTH: 113  
 ; TYPE: PRT  
 ; ORGANISM: mouse  
 US-09-940-727B-108

Query Match 91.7%; Score 44; DB 10; Length 113;  
 Best Local Similarity 88.9%; Pred.No. 0.87;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
 Db 94 QQFVEYPFT 102

RESULT 4  
 US-09-840-459-32  
 ; Sequence 32, Application US/09840459  
 ; Patent No. US20020150576A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Larosa, Gregory J.  
 ; APPLICANT: Horvath, Christopher  
 ; APPLICANT: Newman, Walter  
 ; APPLICANT: Jones, S. Tarran  
 ; APPLICANT: O'Brien, Siobhan H.  
 ; APPLICANT: O'Keefe, Theresa  
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; TITLE OF INVENTION: METHODS OF USE THEREFOR  
 ; FILE REFERENCE: 1855.1052-012  
 ; CURRENT APPLICATION NUMBER: US/09/840,459  
 ; CURRENT FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: PCT/US01/03537  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: 09/497,625  
 ; PRIOR FILING DATE: 2000-02-03  
 ; PRIOR APPLICATION NUMBER: 09/359,193  
 ; PRIOR FILING DATE: 1999-07-22  
 ; PRIOR APPLICATION NUMBER: 09/121,781  
 ; PRIOR FILING DATE: 1998-07-23  
 ; NUMBER OF SEQ ID NOS: 107  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 32  
 ; LENGTH: 100  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-840-459-32

Query Match 77.1%; Score 37; DB 9; Length 100;  
 Best Local Similarity 100.0%; Pred.No. 1.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7  
 Db 94 QQLVEYP 100

RESULT 5  
 US-10-766-773-32  
 ; Sequence 32, Application US/10766773  
 ; Publication No. US20040126851A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Larosa, Gregory J.  
 ; APPLICANT: Horvath, Christopher  
 ; APPLICANT: Newman, Walter  
 ; APPLICANT: Jones, S. Tarran  
 ; APPLICANT: O'Brien, Siobhan H.  
 ; APPLICANT: O'Keefe, Theresa  
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
 ; TITLE OF INVENTION: METHODS OF USE THEREFOR  
 ; FILE REFERENCE: 1855.1052-028  
 ; CURRENT APPLICATION NUMBER: US/10/766,773  
 ; CURRENT FILING DATE: 2004-01-27  
 ; PRIOR APPLICATION NUMBER: 09/497,625  
 ; PRIOR FILING DATE: 2000-02-03  
 ; PRIOR APPLICATION NUMBER: 09/359,193  
 ; PRIOR FILING DATE: 1999-07-22  
 ; PRIOR APPLICATION NUMBER: 09/121,781  
 ; PRIOR FILING DATE: 1998-07-23  
 ; NUMBER OF SEQ ID NOS: 106  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 32  
 ; LENGTH: 100  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-766-773-32

Query Match 77.1%; Score 37; DB 16; Length 100;  
 Best Local Similarity 100.0%; Pred.No. 1.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7  
 Db 94 QQLVEYP 100

RESULT 6  
 US-10-766-610-32  
 ; Sequence 32, Application US/10766610  
 ; Publication No. US20040132980A1  
 ; GENERAL INFORMATION:

APPLICANT: LaRosa, Gregory J.  
APPLICANT: Hervath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
FILE REFERENCE: 1855.1052-029  
CURRENT APPLICATION NUMBER: US/10/766,610  
CURRENT FILING DATE: 2004-01-27  
PRIOR APPLICATION NUMBER: 09/840,459  
PRIOR FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-766-610-32

Query Match 77.1%; Score 37; DB 16; Length 100;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7  
|||  
DB 94 QQLVEYP 100

RESULT 7  
US-10-733-563-32  
Sequence 32, Application US/10733563  
Publication No. US20040151721A1  
GENERAL INFORMATION:  
APPLICANT: O'Keefe, Theresa  
APPLICANT: Ponath, Paul  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
FILE REFERENCE: 10448-213001  
CURRENT APPLICATION NUMBER: US/10/733,563  
CURRENT FILING DATE: 2003-12-10  
PRIOR APPLICATION NUMBER: US 10/272,899  
PRIOR FILING DATE: 2002-10-17  
PRIOR APPLICATION NUMBER: US 60/392,364  
PRIOR FILING DATE: 2002-06-26  
PRIOR APPLICATION NUMBER: US 60/350,166  
PRIOR FILING DATE: 2001-10-19  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-733-563-32

Query Match 77.1%; Score 37; DB 16; Length 100;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7  
|||  
DB 94 QQLVEYP 100

## RESULT 8

US-10-437-963-104782  
Sequence 104782, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 104782  
LENGTH: 609  
TYPE: PRT  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_102083C.1.pep  
US-10-437-963-104782

Query Match 77.1%; Score 37; DB 16; Length 609;  
Best Local Similarity 77.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
|||  
DB 569 QQLVEIPFT 577

## RESULT 9

US-09-940-727B-21  
Sequence 21, Application US/09940727B  
Publication No. US2003007793A1  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald W  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 0575/51400-B  
CURRENT APPLICATION NUMBER: US/09/940,727B  
CURRENT FILING DATE: 2002-09-04  
PRIOR APPLICATION NUMBER: 09/214,095  
PRIOR FILING DATE: 1998-12-28  
PRIOR APPLICATION NUMBER: PCT/US97/10965  
PRIOR FILING DATE: 1997-06-25  
PRIOR APPLICATION NUMBER: 08/672,345  
PRIOR FILING DATE: 1996-06-25  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 21  
LENGTH: 9  
TYPE: PRT  
ORGANISM: mouse  
US-09-940-727B-21

Query Match 75.0%; Score 36; DB 10; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
|||  
DB 1 QHFDVDPFT 9

## RESULT 10

US-10-632-706-134  
Sequence 134, Application US/10632706  
Publication No. US20040175385A1

```
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROFOXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 134
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-134

Query Match 75.0%; Score 36; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 1,2e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 1 QQLISYPLT 9

RESULT 11
US-09-940-727B-5
; Sequence 5, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-5

Query Match 75.0%; Score 36; DB 10; Length 113;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 94 QHFVDYEPFT 102

RESULT 12
US-09-940-727B-7
; Sequence 7, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
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; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-7

Query Match 75.0%; Score 36; DB 10; Length 113;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 94 QHFVDYEPFT 102

RESULT 13
US-09-940-727B-100
; Sequence 100, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-100

Query Match 75.0%; Score 36; DB 10; Length 113;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 94 QHFVDYEPFT 102

RESULT 14
US-09-940-727B-112
; Sequence 112, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
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NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 112  
LENGTH: 113  
TYPE: PRT  
ORGANISM: mouse  
US-09-940-727B-112

Query Match 75.0%; Score 36; DB 10; Length 113;  
Best Local Similarity 66.7%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
Db 94 QHFDYPT 102

RESULT 15  
US-08-779-457-50  
Sequence 50, Application US/08779457  
Publication No. US20020193571A1  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
APPLICANT: Chiang, Nancy Y.  
APPLICANT: Kyung, Jin Kim  
APPLICANT: Matthews, William  
APPLICANT: Rodrigues, Maria L.  
TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/779,457  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/667197  
FILING DATE: 06/20/96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585005  
FILING DATE: 01/08/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0986P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-779-457-50

Query Match 75.0%; Score 36; DB 8; Length 241;  
Best Local Similarity 66.7%; Pred. No. 67;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
Db 223 QQLISYPLT 231

Search completed: September 30, 2004, 06:54:52  
Job time : 152.017 secs

Blank sheet

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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:00:45 ; Search time 15.2542 Seconds  
(without alignments)  
30.459 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEYPPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	91.7	9	2	US-08-672-345C-27
2	44	91.7	9	3	US-09-214-095D-27
3	44	91.7	113	2	US-08-672-345C-8
4	44	91.7	113	2	US-08-672-345C-98
5	44	91.7	113	3	US-09-214-095D-8
6	44	91.7	113	3	US-09-214-095D-108
7	36	75.0	9	2	US-08-672-345C-21
8	36	75.0	9	3	US-09-214-095D-21
9	36	75.0	113	2	US-08-672-345C-5
10	36	75.0	113	2	US-08-672-345C-7
11	36	75.0	113	2	US-08-672-345C-95
12	36	75.0	113	2	US-08-672-345C-97
13	36	75.0	113	3	US-09-214-095D-5
14	36	75.0	113	3	US-09-214-095D-7
15	36	75.0	113	3	US-09-214-095D-100
16	36	75.0	113	3	US-09-214-095D-112
17	36	75.0	280	3	US-09-214-095D-119
18	35	72.9	112	3	US-08-483-749A-4
19	34	70.8	9	4	US-09-406-532-20
20	34	70.8	113	4	US-09-406-532-14
21	34	70.8	585	4	US-09-134-001C-4914
22	33	68.8	9	1	US-08-438-123-3
23	33	68.8	11	1	US-08-438-123-11
24	33	68.8	107	3	US-09-240-274-40
25	33	68.8	108	1	US-08-468-661-3
26	33	68.8	108	1	US-08-466-272A-3
27	33	68.8	108	1	US-08-478-857-3

28 33 68.8 108 2 US-08-471-771-3 Sequence 3, Appli  
29 33 68.8 108 3 US-09-130-783-3 Sequence 3, Appli  
30 33 68.8 113 3 US-08-483-749A-16 Sequence 16, Appli  
31 33 68.8 113 5 PCT-US93-11611-5 Sequence 5, Appli  
32 33 68.8 133 1 US-08-253-877C-10 Sequence 10, Appli  
33 33 68.8 133 1 US-08-253-877C-28 Sequence 28, Appli  
34 33 68.8 133 2 US-08-452-164A-10 Sequence 10, Appli  
35 33 68.8 133 2 US-08-452-164A-28 Sequence 28, Appli  
36 33 68.8 133 3 US-08-603-024-4 Sequence 4, Appli  
37 33 68.8 133 3 US-08-603-024-27 Sequence 27, Appli  
38 33 68.8 133 4 US-08-450-809-23 Sequence 23, Appli  
39 33 68.8 133 5 PCT-US93-11611-2 Sequence 2, Appli  
40 33 68.8 133 5 PCT-US93-11611-9 Sequence 9, Appli  
41 33 68.8 141 1 US-08-438-123-7 Sequence 7, Appli  
42 33 68.8 437 4 US-09-252-991A-20209 Sequence 20209, A  
43 33 68.8 442 4 US-09-328-352-5748 Sequence 5748, Ap  
44 33 68.8 584 4 US-09-489-039A-14137 Sequence 14137, A  
45 33 68.8 598 4 US-09-252-991A-25875 Sequence 25875, A

ALIGNMENTS

RESULT 1  
US-08-672-345C-27  
; Sequence 27, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-27

Query Match 91.7%; Score 44; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 3e-05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QQLVEYPPT 9

Db 1 QQLVEYPT 9

RESULT 2

US-09-214-095D-27  
 ; Sequence 27, Application US/09214095D  
 ; Patent No. 6280987  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 51400-A-PCT-US  
 ; CURRENT APPLICATION NUMBER: US/09/214,095D  
 ; CURRENT FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 27  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Murinae gen. sp.  
 US-09-214-095D-27

Query Match 91.7%; Score 44; DB 3; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 38+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9  
 || |||||

Db 1 QQFVEYPFT 9

## RESULT 3

US-08-672-345C-8  
 ; Sequence 8, Application US/08672345C  
 ; Patent No. 5948658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald, W.  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; NUMBER OF SEQUENCES: 108  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper and Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/672,345C  
 ; FILING DATE: 24-JUN-1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 0575/51400  
 ; TELEPHONE: 212-278-0400  
 ; TELEFAX: 212-391-0525  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 113 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-672-345C-8

Query Match 91.7%; Score 44; DB 2; Length 113;  
 Best Local Similarity 88.9%; Pred. No. 0.25;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9  
 || |||||

Db 94 QQFVEYPFT 102

## RESULT 4

US-08-672-345C-98  
 ; Sequence 98, Application US/08672345C  
 ; Patent No. 5948658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald, W.  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; NUMBER OF SEQUENCES: 108  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper and Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/672,345C  
 ; FILING DATE: 24-JUN-1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 0575/51400  
 ; TELEPHONE: 212-278-0400  
 ; TELEFAX: 212-391-0525  
 ; INFORMATION FOR SEQ ID NO: 98:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 113 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-672-345C-98

Query Match 91.7%; Score 44; DB 2; Length 113;  
 Best Local Similarity 88.9%; Pred. No. 0.25;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9  
 || |||||

Db 94 QQFVEYPFT 102

## RESULT 5

US-09-214-095D-8  
 ; Sequence 8, Application US/09214095D  
 ; Patent No. 6280987  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 51400-A-PCT-US  
 ; CURRENT APPLICATION NUMBER: US/09/214,095D  
 ; CURRENT FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 8  
 ; LENGTH: 113  
 ; TYPE: PRT  
 ; ORGANISM: Murinae gen. sp.  
 US-09-214-095D-8

Query Match 91.7%; Score 44; DB 3; Length 113;  
 Best Local Similarity 88.9%; Pred. No. 0.25;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



```
QY      1 QQLVEYPFT 9
      |||||
Db     94 QQVEYEPFT 102

RESULT 6
US-09-214-095D-108
; Sequence 108, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-108

Query Match      91.7%; Score 44; DB 3; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QQLVEYPFT 9
      |||||
Db     94 QQVEYEPFT 102

RESULT 7
US-08-672-345C-21
; Sequence 21, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-21

Query Match      75.0%; Score 36; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 QQLVEYPFT 9
      |||||
Db     1 QHEVDYEPFT 9

RESULT 8
US-09-214-095D-21
; Sequence 21, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen.sp.
US-09-214-095D-21

Query Match      75.0%; Score 36; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 QQLVEYPFT 9
      |||||
Db     1 QHEVDYEPFT 9

RESULT 9
US-08-672-345C-5
; Sequence 5, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-672-345C-5

Query Match 75.0%; Score 36; DB 2; Length 113;  
 Best Local Similarity 66.7%; Pred. No. 8.5;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPFT 9  
 DB 94 QHFVDYPPFT 102

RESULT 10

US-08-672-345C-7  
 ; Sequence 7, Application US/08672345C  
 ; Patent No. 5948658

; GENERAL INFORMATION:  
 ; APPLICANT: Landry Donald, W.

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/672,345C

; FILING DATE: 24-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/51400

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400

; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 113 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-672-345C-7

Query Match

Best Local Similarity 75.0%; Score 36; DB 2; Length 113;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPFT 9  
 DB 94 QHFVDYPPFT 102

RESULT 11

US-08-672-345C-95  
 ; Sequence 95, Application US/08672345C  
 ; Patent No. 5948658

; GENERAL INFORMATION:  
 ; APPLICANT: Landry Donald, W.

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-672-345C-95

Query Match

75.0%; Score 36; DB 2; Length 113;  
 Best Local Similarity 66.7%; Pred. No. 8.5;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPFT 9  
 DB 94 QHFVDYPPFT 102

RESULT 12

US-08-672-345C-97

; Sequence 97, Application US/08672345C

; Patent No. 5948658

; GENERAL INFORMATION:

; APPLICANT: Landry Donald, W.

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/672,345C

; FILING DATE: 24-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/51400

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400

; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 97:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 113 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

FILE REFERENCE: 51400-A-PCT-US  
CURRENT APPLICATION NUMBER: US/09/214,095D  
CURRENT FILING DATE: 1999-07-19  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 100  
LENGTH: 113  
TYPE: PRT  
ORGANISM: Murine  
US-09-214-095D-100

Query Match 75.0%; Score 36; DB 3; Length 113;  
Best Local Similarity 66.7%; Pred. No. 8.5;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
DB 94 QHFVDYPFT 102

Search completed: September 30, 2004, 06:38:17  
Job time : 16.2542 secs

MOLECULE TYPE: peptide  
US-08-672-345C-97

Query Match 75.0%; Score 36; DB 2; Length 113;  
Best Local Similarity 66.7%; Pred. No. 8.5;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
DB 94 QHFVDYPFT 102

RESULT 13  
US-09-214-095D-5  
Sequence 5, Application US/09214095D  
Patent No. 6280987  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 51400-A-PCT-US  
CURRENT APPLICATION NUMBER: US/09/214,095D  
CURRENT FILING DATE: 1999-07-19  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 113  
TYPE: PRT  
ORGANISM: Murinae gen. Sp.  
US-09-214-095D-5

Query Match 75.0%; Score 36; DB 3; Length 113;  
Best Local Similarity 66.7%; Pred. No. 8.5;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
DB 94 QHFVDYPFT 102

RESULT 14  
US-09-214-095D-7  
Sequence 7, Application US/09214095D  
Patent No. 6280987  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 51400-A-PCT-US  
CURRENT APPLICATION NUMBER: US/09/214,095D  
CURRENT FILING DATE: 1999-07-19  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7  
LENGTH: 113  
TYPE: PRT  
ORGANISM: Murinae gen. sp  
US-09-214-095D-7

Query Match 75.0%; Score 36; DB 3; Length 113;  
Best Local Similarity 66.7%; Pred. No. 8.5;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
DB 94 QHFVDYPFT 102

RESULT 15  
US-09-214-095D-100  
Sequence 100, Application US/09214095D  
Patent No. 6280987  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

Blank sheet

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: September 30, 2004, 05:55:56 ; Search time 5.42373 Seconds  
(without alignments)  
88.677 Million cell updates/sec

Title: US-09-674-716B-9  
Perfect score: 33  
Sequence: 1 GYWS 5

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	67	2 A84376	hypothetical prote
2	33	100.0	117	1 GZMSU1	Ig heavy chain V r
3	33	100.0	444	2 S09681	citrate transport
4	33	100.0	1043	2 F97302	hypothetical prote
5	30	90.9	86	2 T42185	conserved hypothet
6	30	90.9	298	2 AE1752	hypothetical prote
7	30	90.9	298	2 AH1728	Abid phage protein
8	30	90.9	315	2 H86836	carbamate kinase (
9	30	90.9	348	2 G69142	GDP-D-mannose dehy
10	30	90.9	358	2 H83554	hypothetical prote
11	30	90.9	375	2 E83163	hypothetical prote
12	30	90.9	417	2 T08724	hypothetical prote
13	30	90.9	448	2 B9249	PTS system, IIC co
14	30	90.9	448	2 G98113	conserved hypothet
15	30	90.9	452	2 T00113	undecaprenyl-phosp
16	30	90.9	464	2 T28818	hypothetical prote
17	30	90.9	475	2 T46745	arginine/ornithine
18	30	90.9	476	2 D84505	probable membrane
19	30	90.9	480	2 S39978	scRA protein - Sta
20	30	90.9	480	2 D90038	PTS system, sucros
21	30	90.9	490	2 C88879	arginine/ornithine
22	30	90.9	518	1 G69804	multidrug-efflux t
23	30	90.9	535	2 S78598	D-ribulokinase (SC
24	30	90.9	583	2 C72544	probable glycol-tr
25	30	90.9	592	1 IKBBCA	colicin A - Citrob
26	30	90.9	592	2 T15600	hypothetical prote
27	30	90.9	608	2 JQ1462	phosphoenolpyruvat
28	30	90.9	667	1 VCUJGL	env polyprotein.pr
29	30	90.9	847	2 JC4836	alpha-glucuronidas

30	30	90.9	851	2 T47495	hypothetical prote
31	30	90.9	1063	2 A33830	cation efflux syst
32	30	90.9	1063	2 JC4700	cadmium, zinc, cob
33	30	90.9	1215	2 A85595	SWI/SNF family hel
34	30	90.9	1215	2 B72029	helicase, Snf2/Rad
35	30	90.9	1502	2 T42216	multidrug resistan
36	29	87.9	71	2 AFO683	hypothetical prote
37	29	87.9	101	2 S13692	Ig heavy chain V r
38	29	87.9	102	2 B72742	hypothetical prote
39	29	87.9	111	2 S13693	Ig heavy chain V r
40	29	87.9	112	2 S13690	Ig heavy chain V r
41	29	87.9	115	2 S13694	Ig heavy chain V r
42	29	87.9	116	2 S13691	Ig heavy chain V r
43	29	87.9	122	2 A83756	hypothetical prote
44	29	87.9	137	2 S03326	Ig heavy chain pre
45	29	87.9	152	2 D84436	hypothetical prote

## ALIGNMENTS

### RESULT 1

A84376  
hypothetical protein Vng2253h [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C;Accession: A84376  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.C.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;  
Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebbardt, H.; Lowe, T.M.; Lia  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: A84376  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-67 <STO>  
A;Cross-references: GB:AE004437; NID:g10581666; PIDN:AG20373.1; GSPDB:GN00138  
C;Genetics:  
A;Gene: VNG2253H

Query Match 100.0%; Score 33; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
|  
|  
|  
|  
|  
Db 59 GYWS 63

### RESULT 2

GZMSU1  
Ig heavy chain V region (UPC10) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 23-Mar-2001  
C;Accession: A02081  
R;Auffray, C.; Sikorav, J.L.; Ollo, R.; Rougeon, F.  
Ann. Immunol. (Paris) 132D, 77-88, 1981  
A;Title: Correlation between D region structure and antigen-binding specificity: evidences  
A;Reference number: A02081; MUID:83021113; PMID:6181731  
A;Accession: A02081  
A;Molecule type: mRNA  
A;Residues: 1-117 <AUF>  
C;Comment: This chain was isolated from an Ig gamma-2a myeloma protein binding 2,6-levan.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
F;22-96/Disulfide bonds: #status predicted  
Query Match 100.0%; Score 33; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||||  
Db 31 GYWS 35

RESULT 3  
S09681  
citrate transport protein - Klebsiella pneumoniae plasmid pES1  
N:Alternate names: citrate carrier  
C:Species: Klebsiella pneumoniae  
C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 26-Aug-1999  
C:Accession: S09681  
R:van der Rest, M.E.; Schwarz, E.; Oesterheld, D.; Konings, W.N.  
Eur. J. Biochem. 189, 401-407, 1990  
A:Title: DNA sequence of a citrate carrier of Klebsiella pneumoniae.  
A:Reference number: S09681; MUID:90249385; PMID:2186908  
A:Accession: S09681  
A:Molecule type: DNA  
A:Residues: 1-444 <RES>  
A:Cross-references: EMBL:X51479; NID:G43800; PIDN:CAA35944.1; PID:G43801  
C:Genetics:  
A:Genome: plasmid pES1  
C:Superfamily: citrate utilization determinant  
C:Keywords: membrane protein

Query Match 100.0%; Score 33; DB 2; Length 444;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||||  
Db 415 GYWS 419

RESULT 4  
F97302  
hypothetical protein CAC3275 [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C:Accession: F97302  
R:Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: F97302  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1043 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK81209.1; PID:G15026351; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC3275

Query Match 100.0%; Score 33; DB 2; Length 1043;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||||  
Db 580 GYWS 584

RESULT 5  
T42185  
conserved hypothetical protein L7085 - Escherichia coli plasmid pO157  
C:Species: Escherichia coli  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T42185  
R:Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.  
Nucleic Acids Res. 26, 4196-4204, 1998  
A:Title: The complete DNA sequence and analysis of the large virulence plasmid of Escherichia coli O157

A:Reference number: Z22068; MUID:98391744; PMID:9722640  
A:Accession: T42185  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-86 <EUR>  
A:Cross-references: EMBL:AF074613; PIDN:AAC70153.1  
A:Experimental source: strain EDL933; serotype O157:H7  
C:Genetics:  
A:Genome: plasmid pO157  
A:Note: L7085

Query Match 90.9%; Score 30; DB 2; Length 86;  
Best Local Similarity 80.0%; Pred. No. 69;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||||  
Db 72 GYWS 76

RESULT 6  
AE1752  
hypothetical protein homolog lin2562 [imported] - Listeria innocua (strain Clp11262)  
C:Species: Listeria innocua  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AE1752  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, A.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AE1752  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-298 <GLA>  
A:Cross-references: GB:AL592022; PIDN:CAC97789.1; PID:G16415084; GSPDB:GN00178  
A:Experimental source: strain Clp11262  
C:Genetics:  
A:Gene: lin2562

Query Match 90.9%; Score 30; DB 2; Length 298;  
Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||||  
Db 45 GYWS 49

RESULT 7  
AB1728  
AbiD phage protein homolog lin2373 [imported] - Listeria innocua (strain Clp11262)  
C:Species: Listeria innocua  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AB1728  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, A.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AB1728  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-238 <GLA>  
A:Cross-references: GB:AL592022; PIDN:CAC97600.1; PID:G16414896; GSPDB:GN00178  
A:Experimental source: strain Clp11262  
C:Genetics:

A:Gene: lin2373

Query Match 90.9%; Score 30; DB 2; Length 298;  
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
 Db 45 GYWS 49

RESULT 8

H86836  
 carbamate kinase (EC 2.7.2.2) [imported] - Lactococcus lactis subsp. lactis (strain IL14  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
 C:Accession: H86836  
 R:Boletan, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich  
 Genome Res. 11, 731-753, 2001  
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
 A:Reference number: A86625; MUID:21235186; PMID:11337471  
 A:Accession: H86836  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-315 <STO>  
 A:Cross-references: GB:AE005176; PID:gl2724712; PIDN:AAK05794.1; GSPDB:GN00146  
 A:Experimental source: strain IL1403  
 C:Genetics:  
 A:Gene: arcC3  
 C:Superfamily: carbamate kinase  
 C:Keywords: phosphotransferase

Query Match 90.9%; Score 30; DB 2; Length 315;  
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
 Db 88 GYWS 92

RESULT 9

G69142  
 GDP-D-mannose dehydratase - Methanobacterium thermoautotrophicum (strain Delta H)  
 C:Species: Methanobacterium thermoautotrophicum  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 29-Sep-1999  
 C:Accession: G69142  
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
 Qi, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997  
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct  
 A:Reference number: A69000; MUID:98037514; PMID:9371463  
 A:Accession: G69142  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-348 <MTH>  
 A:Cross-references: GB:AE000818; GB:AE000666; NID:g2621384; PIDN:AB84839.1; PID:g262138  
 A:Experimental source: strain Delta H  
 C:Genetics:  
 A:Gene: MTH333  
 C:Superfamily: GDP-D-mannose dehydratase

Query Match 90.9%; Score 30; DB 2; Length 348;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
 Db 156 GYWS 160

RESULT 10

H83554  
 hypothetical protein PA0736 [imported] - Pseudomonas aeruginosa (strain PA01)  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: H83554  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
 .; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
 A:Reference number: A82950; MUID:20437337; PMID:10984043  
 A:Accession: H83554  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STO>  
 A:Cross-references: GB:AE004508; GB:AE004091; NID:g9946611; PIDN:AAG04125.1; GSPDB:GN001  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA0736

Query Match 90.9%; Score 30; DB 2; Length 358;  
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
 Db 203 GYWS 207

RESULT 11

E83163  
 hypothetical protein PA3863 [imported] - Pseudomonas aeruginosa (strain PA01)  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: E83163  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
 .; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
 A:Reference number: A82950; MUID:20437337; PMID:10984043  
 A:Accession: E83163  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-375 <STO>  
 A:Cross-references: GB:AE004803; GB:AE004091; NID:g9950035; PIDN:AAG07250.1; GSPDB:GN001  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA3863

Query Match 90.9%; Score 30; DB 2; Length 375;  
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
 Db 19 GYWS 23

RESULT 12

T08724  
 hypothetical protein DKFZp566D213.1 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 13-Aug-1999  
 C:Accession: T08724  
 R:Koehler, K.; Beyer, A.; Mewes, H.W.; Cassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, May 1999  
 A:Reference number: Z16468  
 A:Accession: T08724  
 A:Molecule type: mRNA  
 A:Residues: 1-417 <KOE>  
 A:Cross-references: EMBL:AL050275  
 A:Experimental source: fetal kidney; clone DKFZp566D213

C;Genetics:  
A;Note: DKFZp566D213.1

Query Match 90.9%; Score 30; DB 2; Length 417;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 402 GYWLS 406

## RESULT 13

B95249  
PTS system, IIC component, probable [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001

C;Accession: B95249  
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,  
son, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A;Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: B95249  
A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-448 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK76187.1; PID:gl4973641; GSPDB:GN00164; TIGR.SP4

A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP2129

Query Match 90.9%; Score 30; DB 2; Length 448;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 186 GYWLS 190

## RESULT 14

G98113  
conserved hypothetical protein spr1938 [imported] - Streptococcus pneumoniae (strain R6)

C;Species: Streptococcus pneumoniae  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001

C;Accession: G98113  
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 193, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: G98113  
A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-448 <KUR>

A;Cross-references: GB:AE007317; PIDN:AAL00740.1; PID:gl5459636; GSPDB:GN00174

C;Genetics:  
A;Gene: spr1938

Query Match 90.9%; Score 30; DB 2; Length 448;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 186 GYWLS 190

## RESULT 15

T00113

undecaprenyl-phosphate galactosephosphotransferase homolog - Actinobacillus actinomycetec  
C;Species: Actinobacillus actinomycetecomitans

C;Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 21-Jul-2000

C;Accession: T00113  
R;Nakano, Y.; Yoshida, Y.; Yanashita, Y.; Koga, T.

Biochim. Biophys. Acta 1442, 409-414, 1998

A;Title: A gene cluster for 6-deoxy-L-talan synthesis in Actinobacillus actinomycetecomi  
A;Reference number: Z14111; MUID:99023768; PMID:9805002

A;Accession: T00113  
A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA  
A;Residues: 1-452 <NAK>

A;Cross-references: EMBL:AB010415; NID:g3132248; PIDN:BAA28142.1; PID:g3132265

A;Experimental source: strain NCTC 9710  
C;Superfamily: xps2A protein

Query Match 90.9%; Score 30; DB 2; Length 452;  
Best Local Similarity 80.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 11 GYWLS 15

Search completed: September 30, 2004, 06:00:37  
Job time : 7.42373 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 3.05085 Seconds  
(without alignments)  
85.337 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	117	1 HV41_MOUSE	P01811 mus musculus
2	33	100.0	444	1 CITI_KLEPN	P16482 klebsiella
3	30	90.9	214	1 CAPA_KLULA	O74232 kluyveromyc
4	30	90.9	292	1 AMPR_PROST	O69772 providencia
5	30	90.9	309	1 ARCI_ENTFA	P35836 enterococcu
6	30	90.9	475	1 ARCD_LACSK	O53092 lactobacill
7	30	90.9	478	1 ARCD_CLOPE	O46170 clostridium
8	30	90.9	480	1 PTGB_STAXY	P51184 staphylococ
9	30	90.9	583	1 SVG_AERPE	O9ybf8 aeropyrum p
10	30	90.9	592	1 CEA_CITFR	P01480 citrobacter
11	30	90.9	608	1 PPCK_NEOPR	P21330 neocallinas
12	30	90.9	667	1 ENV_GALV	P21415 gibbon ape
13	30	90.9	847	1 AGUA_TRIRE	O99024 trichoderma
14	30	90.9	936	1 CAPP_RHOMR	O59757 rhodothermu
15	30	90.9	1063	1 CZCA_ALCEP	P13511 alcaligenes
16	30	90.9	1063	1 CZCA_ALCSP	P94177 alcaligenes
17	30	90.9	1502	1 MRPE_RAT	O88269 rattus norv
18	30	90.9	1503	1 MRPE_HUMAN	O95255 homo sapien
19	29	87.9	252	1 PRIO_ATEPA	P51446 ateles pani
20	29	87.9	252	1 PRIO_RABIT	O95211 oryctolagus
21	29	87.9	270	1 GPRI_YARLI	P41943 yarrowia li
22	29	87.9	271	1 YAB8_SCHPO	O09834 schizosacch
23	29	87.9	287	1 LEF4_LEGPN	O68433 legionella
24	29	87.9	305	1 F334_HUMAN	O9rnw3 homo sapien
25	29	87.9	313	1 ARCC_OBNOE	O8VW54 oenococcus
26	29	87.9	314	1 ARCC_LACSK	O53090 lactobacill
27	29	87.9	318	1 ARCC_LACHI	O8G997 lactobacill
28	29	87.9	363	1 MPG1_SCHPO	O74484 schizosacch
29	29	87.9	388	1 TSGA_BUCAL	P57601 buchnera ap
30	29	87.9	394	1 AR22_DROME	P45888 drosophila
31	29	87.9	482	1 ARCD_FSEAE	P18275 pseudomonas
32	29	87.9	494	1 AMY1_SACFI	P21567 saccharomyc
33	29	87.9	503	1 PRI9_YEAST	P32523 saccharomyc

#### ALIGNMENTS

##### RESULT 1

HV41\_MOUSE  
ID HV41\_MOUSE STANDARD; PRT; 117 AA.  
AC P01811;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE IG heavy chain V region UPC10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83021113; PubMed=6181731;  
RA Auffray C., Sikorav J.L., Ollio R., Rougeon F.;  
RT "Correlation between D region structure and antigen-binding  
RT specificity: evidences from the comparison of closely related  
RT immunoglobulin VH sequences";  
RL Ann. Immunol. (Paris) 132D:77-85(1981)  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG GAMMA-2A MYELOMA  
CC PROTEIN BINDING 2.6-LEVAN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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DR EMBL; M36531; AAA38078.1; -  
DR PIR; A02081; G2MSU.  
DR HSPP; P01810; 2PBU.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF000047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 116 IG-LIKE.  
FT NON TER 117  
SQ SEQUENCE 117 AA; 13001 MW; B20A1074F8E99E7F CRC64;

Query Match 100.0%; Score 33; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 12; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 1 GYWMS 5

Db 31 GYWMS 35

##### RESULT 2

CITI\_KLEPN

```
ID CIT1_KLPPN STANDARD; PRT; 444 AA.
AC P16482;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Citrate-proton symporter (Citrate transporter) (Citrate carrier
DE protein).
GN CITH OR CIT.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13882;
RX MEDLINE=90249385; PubMed=2186908;
RA van der Rest M.E., Schwarz E., Oesterhelth D., Konings W.N.;
RT "DNA sequence of a citrate carrier of Klebsiella pneumoniae.";
RL Eur. J. Biochem. 189:401-407(1990)
CC -!- FUNCTION: UPTAKE OF CITRATE ACROSS THE BOUNDARY MEMBRANE WITH
CC THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
CC -!- PATHWAY: Allows the utilization of citrate as a sole source of
CC carbon and energy.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- SIMILARITY: TO CIT IN TN3411 AND PWR60 FOUND IN E. COLI AND TO
CC CIT IN CITROBACTER AMALONATICS.
CC -!- SIMILARITY: Belongs to the sugar transporter family.
CC
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CC
CC EMBL; X51479; CAA35844.1; -.
CC PIR; S09681; S09681.
CC
CC InterPro; IPR004736; Cit_H_symport.
CC InterPro; IPR007114; MFS.
CC InterPro; IPR005828; Sub_transporter.
CC InterPro; IPR005829; Sug_transporter.
CC Pfam; PF00083; sugar_tr; 1.
CC TIGRFAMs; TIGR00883; 2A0106; 1.
CC PROSITE; PS00850; MFS; 1.
CC PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
CC PROSITE; PS00317; SUGAR_TRANSPORT_2; 1.
CC
CC Transport; Transmembrane; Inner membrane; Citrate utilization;
CC Symport.
KW DOMAIN 1 41 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 62 1 (POTENTIAL).
FT TRANSMEM 63 72 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 73 93 2 (POTENTIAL).
FT TRANSMEM 94 114 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 115 135 3 (POTENTIAL).
FT TRANSMEM 136 137 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 138 158 4 (POTENTIAL).
FT TRANSMEM 159 177 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 178 198 5 (POTENTIAL).
FT TRANSMEM 199 199 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 200 220 6 (POTENTIAL).
FT TRANSMEM 221 251 7 (POTENTIAL).
FT DOMAIN 252 272 8 (POTENTIAL).
FT TRANSMEM 273 289 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 290 310 9 (POTENTIAL).
FT TRANSMEM 311 318 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 319 339 10 (POTENTIAL).
FT TRANSMEM 340 340 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 341 361 11 (POTENTIAL).
FT TRANSMEM 362 379 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 380 400 12 (POTENTIAL).
FT TRANSMEM 401 411 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 412 432 13 (POTENTIAL).
FT TRANSMEM 413 432 14 (POTENTIAL).

FT DOMAIN 433 444 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 444 AA; 48142 MW; D431F732EEDA3EC2 CRC64;

Query Match 100.0%; Score 33; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 415 GYWMS 419
|||||

RESULT 3
CAPA_KLJLA STANDARD; PRT; 214 AA.
AC 074232;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE F-actin capping protein alpha subunit (Fragment).
GN CAP1.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RA Banfield D.K.;
RT "DNA sequence of the SFT1 gene from Kluyveromyces lactis.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: F-actin capping proteins bind in a Ca(2+)-independent
CC manner to the fast growing ends of actin filaments (barbed end)
CC thereby blocking the exchange of subunits at these ends. Unlike
CC other capping proteins (such as gelsolin and severin), these
CC proteins do not sever actin filaments (By similarity).
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit (By
CC similarity).
CC -!- SIMILARITY: Belongs to the F-actin capping protein alpha subunit
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF072674; AAC24885.1; -.
CC InterPro; IPR002189; F-actin_cap_A.
CC Pfam; PF01267; F-actin_cap_A; 1.
CC PRINTS; PR00191; FACTINCAPA.
CC PRODOM; PD006960; F-actin_cap_A; 1.
CC PROSITE; PS00748; F-actin_capping_A; 1.
CC PROSITE; PS00749; F-actin_capping_A_2; 1.
CC
CC Actin-binding; Actin capping.
KW NON TER 1
FT NON TER 1
SQ SEQUENCE 214 AA; 24380 MW; 31851D6573630C02 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 214;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 111 GYWMS 115
|||||

RESULT 4
AMPR_PROST STANDARD; PRT; 292 AA.
ID AMPR_PROST
AC O69772;
DT 30-MAY-2000 (Rel. 39, Created)
```

DT 30-MAY-2000 (Rel. 39, last sequence update)  
 DT 15-MAR-2004 (Rel. 43, last annotation update)  
 GN HTH-type transcriptional activator ampR.  
 GN AMPR.  
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Providencia.  
 OC NCBI\_TaxID=588;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VDG 96;  
 RA Koec J.L., Bamacogullari S., Parzy D., Barnaud G., Teyssou R.,  
 RA Buissou V., Philippot A., Arlet G.J.;  
 RT Cloning and sequencing of ampC and ampR genes from Providencia  
 RT stuartii.;  
 RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RL FUNCTION: THIS PROTEIN IS A POSITIVE REGULATOR OF GENE EXPRESSION  
 CC OF BETA-LACTAMASE (AMP).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.  
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 CC EMBL; Y17315; CAA76738.1; -  
 CC InterPro; IPR000847; HTH\_LysR.  
 CC InterPro; IPR005119; LysR\_subst.  
 CC Pfam; PF00126; HTH\_1; 1.  
 CC Pfam; PF03466; LysR\_substrate; 1.  
 CC PRINTS; PR00039; HTHLYSR.  
 CC PROSITE; PS00931; HTH\_LysR; 1.  
 CC Transcription regulation; DNA-binding; Activator.  
 CC DOMAIN 9 66  
 CC FT H-T-H MOTIF (POTENTIAL).  
 CC FT DNA BIND 26 45  
 CC SEQUENCE 292 AA; 32741 MW; 982CEFF667E112F0 CRC64;  
 SQ  
 Query Match 90.9%; Score 30; DB 1; Length 292;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYVMS 5  
 |||||  
 Db 264 GYVLS 268  
 RESULT 5  
 ID -ARCI ENTFA STANDARD; PRT; 309 AA.  
 AC P35836; OS4531;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DE 10-OCT-2003 (Rel. 42, last annotation update)  
 DE Carbamate kinase 1 (EC 2.7.2.2).  
 GN ARCC1 OR ARCC-1 OR ARCC OR EF0106.  
 OS Enterococcus faecalis (Streptococcus faecalis), and  
 OS Enterococcus faecium (Streptococcus faecium).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OC NCBI\_TaxID=1351, 1352;  
 RN [1]  
 RP SEQUENCE FROM N.A.; CHARACTERIZATION, AND MASS SPECTROMETRY.  
 RC SPECIES=E.faecalis, and E.faecium; STRAIN=ATCC 29212, and D10;  
 RX MEDLINE=98237599; PubMed=9578487;  
 RA Marina A., Uriarte M., Barcelona B., Fresquet V., Cervera J.,  
 RA Rubio V.;  
 RT "Carbamate kinase from Enterococcus faecalis and Enterococcus faecium.  
 RT Cloning of the genes, studies on the enzyme expressed in Escherichia  
 RT coli, and sequence similarity with N-acetyl-L-glutamate kinase.";  
 RT Eur. J. Biochem. 253:280-291(1998).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.faecalis; STRAIN=ATCC 29212;  
 RX MEDLINE=2286540; PubMed=12399499;  
 RA Barcelona-Andres B., Marina A., Rubio V.;  
 RT "Gene structure, organization, expression, and potential regulatory  
 RT mechanisms of arginine catabolism in Enterococcus faecalis.";  
 J. Bacteriol. 184:6289-6300(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.faecalis; STRAIN=V583 / ATCC 700802;  
 RX MEDLINE=22550857; PubMed=12663927;  
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,  
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,  
 RA Tetelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,  
 RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,  
 RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,  
 RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;  
 RT "Role of mobile DNA in the evolution of vancomycin-resistant  
 RT Enterococcus faecalis.";  
 RL Science 299:2071-2074(2003).  
 RN [4]  
 RP SEQUENCE OF 1-32 AND 158-168, AND CHARACTERIZATION.  
 RC SPECIES=E.faecium; STRAIN=D10;  
 RX MEDLINE=94141928; PubMed=8308697;  
 RA Marina A., Bravo J., Fita I., Rubio V.;  
 RT "Crystallization, characterization and preliminary crystallographic  
 RT studies of carbamate kinase of Streptococcus faecium.";  
 J. Mol. Biol. 235:1345-1347(1994).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND MUTAGENESIS OF GLU-135;  
 RC GLU-137; LYS-139; GLU-140; ASP-207 AND ASP-209.  
 RX SPECIES=E.faecium; STRAIN=D10;  
 RC MEDLINE=99226823; PubMed=10211841;  
 RA Marina A., Alzari P.M., Bravo J., Uriarte M., Barcelona B., Fita I.,  
 RA Rubio V.;  
 RT "Carbamate kinase: new structural machinery for making carbamoyl  
 RT phosphate, the common precursor of pyrimidines and arginine.";  
 RL Protein Sci. 8:934-940(1999).  
 CC -1- FUNCTION: Catalyzes the reversible synthesis of carbamate and ATP  
 CC from carbamoyl phosphate and ADP. Can also catalyze, although with  
 CC low efficiency, the phosphorylation of bicarbonate, leading to the  
 CC formation of carboxyphosphate, an unstable intermediate found in  
 CC the reactions catalyzed by carbamoyl-phosphate synthase and biotin  
 CC carboxylase. Can also use acetate.  
 CC -1- CATALYTIC ACTIVITY: ATP + NH(3) + CO(2) = ADP + carbamoyl  
 CC phosphate.  
 CC -1- ENZYME REGULATION: Inhibited by  
 CC adenosine(5')pentaphospho(5')adenosine (ApsA), ApsA and to a much  
 CC lower extent by Ap4A.  
 CC -1- PATHWAY: Arginine degradation via arginine deiminase; third step.  
 CC -1- SUBUNIT: Homodimer (predominantly) and homotetramer.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -1- INDUCTION: By arginine.  
 CC -1- MASS SPECTROMETRY: MW=32803; MW ERR=10; METHOD=Electrospray.  
 CC -1- SIMILARITY: Belongs to the carbamate kinase family.  
 CC  
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 CC  
 CC EMBL; AJ223331; CAA11270.1; -  
 CC EMBL; AJ223332; CAA11271.1; -  
 CC EMBL; AJ312276; CAC41343.1; -  
 CC EMBL; AE016947; AAO79981.1; -  
 CC PIR; S44002; S44002.  
 CC DR PDB; 1B7B; 26-SEP-01.  
 CC TIGR; EF0106; -.  
 CC InterPro; IPR001048; Aa\_Kinase.

DR InterPro; IPR003964; Bac\_carb\_kinase.  
 DR Pfam; PF00696; aakinasase; 1.  
 DR PRINTS; PRO1469; CARYOTKINASE.  
 DR TIGRFAMs; TIGR00746; arcc; 1.  
 KW Transferase; Kinase; Arginine metabolism; 3D-structure;  
 KW Complete proteome.  
 FT INIT MET 0  
 FT MUTAGEN 135 135 E->A: NO CHANGE IN ACTIVITY; WHEN  
 FT MUTAGEN 137 137 ASSOCIATED WITH A-137, A-139 AND A-140.  
 FT MUTAGEN 137 137 E->A: NO CHANGE IN ACTIVITY; WHEN  
 FT MUTAGEN 139 139 ASSOCIATED WITH A-135, A-139 AND A-140.  
 FT MUTAGEN 139 139 K->A: NO CHANGE IN ACTIVITY; WHEN  
 FT MUTAGEN 140 140 ASSOCIATED WITH A-135, A-137 AND A-140.  
 FT MUTAGEN 140 140 E->A: NO CHANGE IN ACTIVITY; WHEN  
 FT MUTAGEN 207 207 ASSOCIATED WITH A-135, A-137 AND A-139.  
 FT MUTAGEN 209 209 D->A: ALMOST NO ACTIVITY; WHEN ASSOCIATED  
 FT MUTAGEN 209 209 WITH A-209.  
 FT CONFLICT 168 168 I -> D (IN REF. 4).  
 SQ SEQUENCE 309 AA; 32795 MW; 50145147FEED290 CRC64;  
 Query Match 90.9%; Score 30; DB 1; Length 309;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYVMS 5  
 DB 86 GYVLS 90  
 RESULT 6  
 ID ARCD\_LACSK STANDARD; PRT; 475 AA.  
 AC O53092;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Arginine/ornithine antiporter.  
 GN ARCD.  
 OS Lactobacillus sakei.  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OX NCBI\_TaxID=15599;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98361904; PubMed=9696763;  
 RA Zuniga M., Champomier-Verges M., Zagrec M., Perez-Martinez G.;  
 RT "Structural and functional analysis of the gene cluster encoding the  
 enzymes of the arginine deiminase pathway of Lactobacillus sakei";  
 RL J. Bacteriol. 180:4154-4159(1998).  
 CC -!- FUNCTION: Catalyzes an electronneutral exchange between arginine  
 and ornithine to allow high-efficiency energy conversion in the  
 arginine deiminase pathway (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- SIMILARITY: Belongs to the amino acid permease family.  
 CC Arcd/cadB/lysI subfamily.  
 CC  
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 CC  
 CC EMBL; AJ001330; CAA04686.1;  
 CC PIR; T46745; T46745.  
 CC InterPro; IPR002293; AA/rel\_permease1.  
 CC InterPro; IPR004841; Permease\_region.  
 CC Pfam; PF00324; aa\_permeases; 1.  
 CC TIGRFAMs; TIGR00905; 2A0302; 1.

KW Transport; Antiport; Amino-acid transport; Transmembrane.  
 FT TRANSMEM 10 30 POTENTIAL.  
 FT TRANSMEM 42 62 POTENTIAL.  
 FT TRANSMEM 74 94 POTENTIAL.  
 FT TRANSMEM 101 121 POTENTIAL.  
 FT TRANSMEM 157 177 POTENTIAL.  
 FT TRANSMEM 205 225 POTENTIAL.  
 FT TRANSMEM 238 258 POTENTIAL.  
 FT TRANSMEM 283 303 POTENTIAL.  
 FT TRANSMEM 333 353 POTENTIAL.  
 FT TRANSMEM 361 381 POTENTIAL.  
 FT TRANSMEM 397 417 POTENTIAL.  
 FT TRANSMEM 451 471 POTENTIAL.  
 SQ SEQUENCE 475 AA; 51881 MW; 8E91A01F6A2203CC CRC64;  
 Query Match 90.9%; Score 30; DB 1; Length 475;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYVMS 5  
 DB 94 GYVLS 98  
 RESULT 7  
 ID ARCD\_CLOPE STANDARD; PRT; 478 AA.  
 AC Q46170;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Arginine/ornithine antiporter.  
 GN ARCD OR CPE0170.  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97199138; PubMed=9053381;  
 RA Ohtani K., Bando M., Swe T., Banu S., Oe M., Hayashi H., Shimizu T.;  
 RT "Collagenase gene (colA) is located in the 3'-flanking region of the  
 perfringolysin O (pfoA) locus in Clostridium perfringens.";  
 RL FEMS Microbiol. Lett. 146:155-159(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=13 / Type A;  
 RX MEDLINE=21664373; PubMed=11792842;  
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,  
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 flesh-eater";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 CC -!- FUNCTION: Catalyzes an electronneutral exchange between arginine  
 and ornithine to allow high-efficiency energy conversion in the  
 arginine deiminase pathway (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- SIMILARITY: Belongs to the amino acid permease family.  
 CC Arcd/cadB/lysI subfamily.  
 CC  
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 CC  
 CC EMBL; X97768; CAA66366.1;  
 CC EMBL; AF003185; BAB79876.1;  
 CC InterPro; IPR002293; AA/rel\_permease1.  
 CC InterPro; IPR004841; Permease\_region.



DR InterPro; IPR004154; HGTP anticodon.  
 DR InterPro; IPR002314; tRNA-synt 2b.  
 DR InterPro; IPR002315; tRNA-synt\_gly.  
 DR InterPro; IPR006195; tRNA\_ligase\_II.  
 DR Pfam; PF03129; HGTP-anticodon; 1.  
 DR Pfam; PF00567; tRNA-synt 2b; 1.  
 DR PRINTS; PR01043; TRNASYNTHGLY.  
 DR TIGRFAMs; TIGR00389; GLYS dimeric; 1.  
 DR PROSITE; PS00862; AA tRNA LIGASE II; 1.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis, Ligase; ATP-binding;  
 KW Complete proteome.  
 SQ SEQUENCE 583 AA; 66395 MW; 7D75DE7B5AA3F999 CRC64;  
 Query Match 90.9%; Score 30; DB 1; Length 583;  
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYWS 5  
 Db 277 GYWS 281  
 RESULT 10  
 CEA\_CITFR  
 ID\_CEA\_CITFR STANDARD; PRT; 592 AA.  
 AC P04180;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Colicin A.  
 GN CAA.  
 OS Citrobacter freundii.  
 OC Plasmid ColA-Ca31.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Citrobacter.  
 OX NCBI\_TaxID=546;  
 [1] SEQUENCE FROM N.A.  
 RP MEDLINE=84036205; PubMed=6313941;  
 RA Morlon J., Lioubes R., Varenne S., Chartier M., Lazdunski C.;  
 RT "Complete nucleotide sequence of the structural gene for colicin A, a  
 RT gene translated at non-uniform rate.";  
 RL J. Mol. Biol. 170:271-285(1983).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=88174422; PubMed=2832701;  
 RA Morlon J., Chartier M., Bidaud M., Lazdunski C.;  
 RT "The complete nucleotide sequence of the colicinogenic plasmid ColA.  
 RT High extent of homology with ColE1.";  
 RL Mol. Gen. Genet. 211:231-243(1988).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 389-592.  
 RP MEDLINE=92235820; PubMed=1273773;  
 RA Parker M.W., Poscma J.P.M., Pattus F., Tucker A.D., Tsernoglou D.;  
 RT "Refined structure of the pore-forming domain of colicin A at 2.4-A  
 RT resolution.";  
 RL J. Mol. Biol. 224:639-657(1992).  
 CC -!- FUNCTION: This colicin is a channel-forming colicin. This class of  
 CC transmembrane toxins depolarize the cytoplasmic membrane, leading  
 CC to dissipation of cellular energy.  
 CC -!- FUNCTION: COLICINS ARE POLYPEPTIDE TOXINS PRODUCED BY AND ACTIVE  
 CC AGAINST ESCHERICHIA COLI AND CLOSELY RELATED BACTERIA.  
 CC -!- SIMILARITY: Belongs to the channel forming colicin family.  
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 CC EMBL; X01008; CAA25503.1; -.

DR EMBL; M37402; AAA72879.1; -.  
 DR PIR; I40784; IKBBCA.  
 DR PUB; LCOL; 15-JUL-93.  
 DR InterPro; IPR000293; Channel\_colicin.  
 DR Pfam; PF01024; Colicin; 1.  
 DR PRINTS; PR00280; CHANCOLICIN.  
 DR PROSITE; PS002657; Channel\_colicin; 1.  
 DR PROSITE; PS00276; CHANNEL COLICIN; 1.  
 KW Antibiotic; Bacteriocin; Plasmid; Transmembrane; 3D-structure.  
 KW TRANSMEM 528 548  
 FT TRANSMEM 555 575  
 FT HELIX 396 418  
 FT HELIX 420 434  
 FT TURN 435 435  
 FT TURN 437 438  
 FT HELIX 444 455  
 FT TURN 456 456  
 FT HELIX 458 460  
 FT HELIX 464 475  
 FT TURN 476 476  
 FT HELIX 479 489  
 FT HELIX 491 493  
 FT TURN 495 497  
 FT HELIX 498 515  
 FT TURN 519 530  
 FT TURN 531 532  
 FT HELIX 535 552  
 FT HELIX 557 575  
 FT TURN 577 577  
 FT HELIX 578 586  
 FT TURN 587 588  
 SQ SEQUENCE 592 AA; 62992 MW; B80FAIP52A8CFC5D CRC64;  
 Query Match 90.9%; Score 30; DB 1; Length 592;  
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYWS 5  
 Db 136 GYWS 140  
 RESULT 11  
 PCKK\_NEOFR  
 ID\_PCKK\_NEOFR STANDARD; PRT; 609 AA.  
 AC P22130;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphoenolpyruvate carboxylase (GTP) (EC 4.1.1.32)  
 DE (Phosphoenolpyruvate carboxylase) (PEPCK).  
 OS Neocallimastix frontalis (Rumen fungus).  
 OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;  
 OC Neocallimastixaceae; Neocallimastix.  
 OX NCBI\_TaxID=4757;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=92164115; PubMed=1339359;  
 RA Raymond P., Gecunjon C., Roux B., Durand R., Fevre M.;  
 RT "Sequence of the phosphoenolpyruvate carboxylase-encoding cDNA from  
 RT the rumen anaerobic fungus Neocallimastix frontalis: comparison of  
 RT the amino acid sequence with animals and yeast.";  
 RL Gene 110:57-63(1992).  
 CC -!- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate  
 CC + CO(2).  
 CC -!- PATHWAY: Rate-limiting gluconeogenic enzyme.  
 CC -!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxylase (GTP)  
 CC family.  
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CC EMBL; M59372; AAA33553.1; --  
 DR PIR; JQ1462; JQ1462.  
 DR InterPro; IPR008209; PEP\_carboxykin.  
 DR InterPro; IPR008210; PEPCK\_N.  
 DR Pfam; PF00821; PEPCK; 1.  
 DR ProDom; PD004738; PEPCK\_N; 1.  
 DR ProSITE; PS00505; PEPCK\_GTP; 1.  
 KW Glucuronogenesis; Lyase; Decarboxylase; GTP-binding.  
 FT NP\_BIND 217 224 GTP (POTENTIAL).  
 FT ACT\_SITE 269 269 POTENTIAL.  
 SQ SEQUENCE 608 AA; 66904 MW; C4D2B249A2B7D26 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 608;  
 Best Local Similarity 80.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
 DB 478 GYWS 482

RESULT 12  
 ID ENV\_GALV STANDARD; PRT; 667 AA.  
 AC P21415;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ENV polyprotein precursor (Contains: Knob protein GP70; Spike protein P15B).  
 GN ENV.  
 OS Gibbon ape leukemia virus.  
 CC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.  
 CC NCBI\_TaxID=11840;  
 CC [1]\_TaxID=11840;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90051069; PubMed=2683360;  
 RA Delassus S., Sonigo P., Wain-Hobson S.;  
 RT "Genetic organization of gibbon ape leukemia virus.";  
 RL Virology 173:205-213(1989).

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CC EMBL; M26927; AAA46811.1; --  
 DR PIR; C32595; VCLJGL.  
 DR HSP; P03385; 1MOP.  
 DR InterPro; IPR002050; Env polyprotein.  
 DR InterPro; IPR008981; F\_MuLV bind.  
 DR Pfam; PF00429; ENV\_polyprotein; 1.  
 KW Coat protein; Glycoprotein; Polyprotein; Transmembrane; Signal.  
 FT SIGNAL 1 42  
 FT CHAIN 43 489 KNOB PROTEIN GP70.  
 FT CHAIN 490 567 SPIKE PROTEIN P15E.  
 FT TRANSMEM 637 653 POTENTIAL.  
 FT TRANSMEM 637 653 POTENTIAL.  
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 667 AA; 73729 MW; 5FEB32F00D8631BE CRC64;

Query Match 90.9%; Score 30; DB 1; Length 667;  
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
 DB 180 GYWS 184

RESULT 13  
 ID AGUA\_TRIRE STANDARD; PRT; 847 AA.  
 AC Q99024;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Alpha-glucuronidase precursor (EC 3.2.1.139) (Alpha-glucosiduronase) (GLR).  
 DE (GLR).  
 OS Trichoderma reesei (Hypocrea jecorina).  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 CC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
 CC NCBI\_TaxID=51453;  
 RN [1]  
 RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.  
 RC STRAIN=QM9414 / Rut C-30;  
 RX MEDLINE=96257277; PubMed=8654984;  
 RA Margolles-Clark E., Saloheimo M., Siika-Aho M., Penttilae M.;  
 RT "The alpha-glucuronidase-encoding gene of Trichoderma reesei.";  
 RL Gene 172:171-172(1996).  
 CC -1- FUNCTION: RELEASES 4-O-METHYLGLUCURONIC ACID FROM XYLAN.  
 CC -1- CATALYTIC ACTIVITY: An alpha-D-glucuronoside + H(2)O = an alcohol + D-glucuronate.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 67 OF GLYCOSYL HYDROLASES.

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CC EMBL; Z68706; CAA92949.1; --  
 DR PIR; JC4836; JC4836.  
 DR InterPro; IPR005154; Glyco\_hydro\_67.  
 DR Pfam; PF03648; Glyco\_hydro\_67; 1.  
 KW Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 847 ALPHA-GLUCURONIDASE.  
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 586 586 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 692 692 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 740 740 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 767 767 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 847 AA; 93424 MW; 214AAE487382FDB4 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 847;  
 Best Local Similarity 80.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
 DB 119 GYWS 123

RESULT 14  
 ID CAPP\_RHOMR STANDARD; PRT; 936 AA.  
 AC Q59757;

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Enophenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).  
 GN PPC OR PEPC.  
 OS Rhodothermus marinus (Rhodothermus obamensis).  
 CC Bacteria; Bacteroidetes; Sphingobacteriales;  
 CC Crenotrichaceae; Rhodothermus.  
 OX NCBI\_TaxID=29549;  
 RN [1]\_TaxID=29549;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OKD7;  
 RX MEDLINE=97420683; PubMed=9276668;  
 RA Takai K., Sako Y., Uchida A., Ishida Y.;  
 RT "Extremely thermostable phosphoenolpyruvate carboxylase from an  
 extreme thermophile, Rhodothermus obamensis.";  
 RL J. Biochem. 122:32-40 (1997).  
 CC -!- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)  
 CC it forms oxaloacetate, a four-carbon dicarboxylic acid source for  
 CC the tricarboxylic acid cycle.  
 CC -!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +  
 CC phosphoenolpyruvate + CO(2).  
 CC -!- COFACTOR: Absolute requirement for divalent cations.  
 CC -!- ENZYME REGULATION: Exhibits positive allosteric property with  
 CC acetyl-CoA and fructose 1,6-bisphosphate, and a negative one with  
 CC L-aspartate and L-malate.  
 CC -!- PATHWAY: Tricarboxylic acid cycle.  
 CC -!- SUBUNIT: Homotetramer.  
 CC -!- MISCELLANEOUS: The optimum temperature for activity is 75 degrees  
 CC Celsius. The enzyme exhibits a pH optimum of 8.0.  
 CC -!- SIMILARITY: Belongs to the PEPCase family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X99379; CAA67760.1; --  
 DR HSP; P00864; 1FTV.  
 DR HAMAP; MF 00595; -; 1.  
 DR InterPro; IPR001449; PEPCase.  
 DR Pfam; P00311; PEPCase; 1.  
 DR PRINTS; PR00150; PEPCARXLA.  
 DR PROSITE; PS00393; PEPCASE 2; 1.  
 DR PROSITE; PS00781; PEPCASE 1; 1.  
 DR Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle;  
 KW Allosteric enzyme.  
 FT ACT\_SITE 155 155 BY SIMILARITY.  
 FT ACT\_SITE 595 595 BY SIMILARITY.  
 FT ACT\_SITE 936 936 BY SIMILARITY.  
 SQ SEQUENCE 936 AA; 107886 MW; C9AA94C3F26C345A CRC64;  
 Query Match 90.9%; Score 30; DB 1; Length 936;  
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYWS 5  
 |||||:  
 Db 598 GYWSA 602  
 RESULT 15  
 CZCA\_ALCEU STANDARD; PRT; 1063 AA.  
 ID CZCA\_ALCEU  
 AC P13511; P94142;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cobalt-zinc-cadmium resistance protein czca (Cation efflux system  
 DE protein czca).  
 GN CZCA.

OS Alkaligenes eutrophus (Ralstonia eutropha).  
 OG Plasmid pMOU30.  
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 CC Burkholderiaceae; Ralstonia.  
 OX NCBI\_TaxID=510;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CH34;  
 RX MEDLINE=90017477; PubMed=2678100;  
 RA Nies D.H., Nies A., Chu L., Silver S.;  
 RT "Expression and nucleotide sequence of a plasmid-determined divalent  
 cation efflux system from Alkaligenes eutrophus.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7351-7355 (1989).  
 RN [2]  
 RP REVISIONS TO 318 AND 959-960.  
 RC STRAIN=CH34;  
 RA van der Lelie D., Schwuchow T., Wuerz S., Schwidetzky U.,  
 RA Baeyens W., Scheel P.O., Nies D.H.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: HAS A LOW CATION TRANSPORT ACTIVITY FOR CO(2+). IT IS  
 CC ESSENTIAL FOR THE EXPRESSION OF COBALT, ZINC, AND CADMIUM  
 CC RESISTANCE. CZCA AND CZCB TOGETHER WOULD ACT IN ZN(2+) EFFLUX  
 CC NEARLY AS EFFECTIVELY AS THE COMPLETE CZC EFFLUX SYSTEM (CZCABC).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -!- INDUCTION: By cadmium, copper and zinc.  
 CC -!- SIMILARITY: BELONGS TO THE ACRB/ACRD/ACRF FAMILY.  
 CC  
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 CC  
 CC EMBL; X38451; CAA67084.1; --  
 DR PIR; A33830; A33830.  
 DR InterPro; IPR001036; Acrflvin\_res.  
 DR InterPro; IPR004763; Czca.  
 DR Pfam; PF00873; ACR tran; 1.  
 DR PRINTS; PR00702; ACRIFLAVINRP.  
 DR TIGRfam; TIGR00914; 2A0601.1  
 KW Plasmid; Transport; Zinc; Cobalt; Cadmium resistance; Transmembrane.  
 FT TRANSMEM 14 29 POTENTIAL.  
 FT TRANSMEM 350 370 POTENTIAL.  
 FT TRANSMEM 452 472 POTENTIAL.  
 FT TRANSMEM 487 507 POTENTIAL.  
 FT TRANSMEM 534 554 POTENTIAL.  
 FT TRANSMEM 883 903 POTENTIAL.  
 FT TRANSMEM 906 926 POTENTIAL.  
 FT TRANSMEM 937 957 POTENTIAL.  
 FT TRANSMEM 962 1004 POTENTIAL.  
 FT TRANSMEM 1013 1033 POTENTIAL.  
 SQ SEQUENCE 1063 AA; 115668 MW; 1E95B7923996AEBB CRC64;  
 Query Match 90.9%; Score 30; DB 1; Length 1063;  
 Best Local Similarity 80.0%; Pred. No. 3.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYWS 5  
 |||||:  
 Db 862 GYWSM 865

Search completed: September 30, 2004, 06:01:20  
 Job time : 5.05085 secs



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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 16.3559 Seconds  
(without alignments)  
96.454 Million cell updates/sec

Title: US-09-674-716B-9  
Perfect score: 33  
Sequence: 1 GYMS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	67	Q9HN48	Q9hn48 halobacteri
2	33	100.0	73	Q8PR71	Q8pr71 xanthomonas
3	33	100.0	85	Q8PEB4	Q8peb4 xanthomonas
4	33	100.0	285	Q8W52	Q8w52 lactobacill
5	33	100.0	377	Q9IAF9	Q9iaf9 ivindomyrus
6	33	100.0	377	Q9IAH9	Q9iaeh9 mormyru ru
7	33	100.0	377	Q9IAH4	Q9iaeh4 brieniomyru
8	33	100.0	377	Q9IAF0	Q9iaf0 mormyru ov
9	33	100.0	377	Q9IAH2	Q9iaeh2 brieniomyru
10	33	100.0	377	Q9I867	Q9iaeh7 campylnorm
11	33	100.0	377	Q9IAG1	Q9iaeh1 hyperopisus
12	33	100.0	377	Q9IAF4	Q9iaeh4 marcusenius
13	33	100.0	377	Q9IAD8	Q9iaeh8 stomatorhin
14	33	100.0	377	Q9IAH1	Q9iaeh1 brieniomyru
15	33	100.0	377	Q9IAE0	Q9iaeh0 pollimyru
16	33	100.0	377	Q9IAF6	Q9iaeh6 marcusenius

17	33	100.0	377	Q9IAD9	Q9iaeh9 pollimyru
18	33	100.0	377	Q9IAH0	Q9iaeh0 campylnorm
19	33	100.0	377	Q9IAE1	Q9iaeh1 pollimyru
20	33	100.0	377	Q9IAG4	Q9iaeh4 hippopotamy
21	33	100.0	377	Q9IAF5	Q9iaeh5 marcusenius
22	33	100.0	377	Q9IAE6	Q9iaeh6 paramomyro
23	33	100.0	377	Q9IAG3	Q9iaeh3 hippopotamy
24	33	100.0	377	Q9IAD5	Q9iaeh5 stomatorhin
25	33	100.0	377	Q9IAF7	Q9iaeh7 marcusenius
26	33	100.0	377	Q9IAG6	Q9iaeh6 gnathonemus
27	33	100.0	377	Q9IAD7	Q9iaeh7 stomatorhin
28	33	100.0	377	Q9IAG2	Q9iaeh2 hippopotamy
29	33	100.0	377	Q9IAD6	Q9iaeh6 stomatorhin
30	33	100.0	377	Q9IAF8	Q9iaeh8 marcusenius
31	33	100.0	377	Q9IAG7	Q9iaeh7 genyomyru
32	33	100.0	377	Q9IAG9	Q9iaeh9 campylnorm
33	33	100.0	377	Q9IAH3	Q9iaeh3 brieniomyru
34	33	100.0	377	Q9IAH6	Q9iaeh6 boulengerom
35	33	100.0	377	Q8AWR8	Q8awr8 pollimyru
36	33	100.0	396	Q7SY78	Q7sy78 xenopus lae
37	33	100.0	721	Q9FRN4	Q9frn4 cryza sativ
38	33	100.0	721	Q7XB20	Q7xb20 cryza sativ
39	33	100.0	1028	Q8SXA6	Q8sxa6 drosophila
40	33	100.0	1043	Q97E41	Q97e41 clostridium
41	33	100.0	1254	Q9VF51	Q9vf51 drosophila
42	33	100.0	1254	Q8GNS1	Q8gns1 drosophila
43	30	90.9	77	Q9S4W3	Q9s4w3 escherichia
44	30	90.9	79	Q9WTF7	Q9wtf7 escherichia
45	30	90.9	79	Q9JMR3	Q9jmr3 escherichia

ALIGNMENTS

RESULT 1

Q9HN48 PRELIMINARY; PRT; 67 AA.  
ID Q9HN48;  
AC Q9HN48;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Vng2253h.  
GN VNG2253h.  
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).  
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
OC Halobacteriaceae; Halobacterium.  
CX NCBI\_TaxID=64091;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2050483; PubMed=11016950;  
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,  
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
RA Maddocks D.G., Jablonaki P.E., Krebs M.P., Angevine C.M., Dale H.,  
RA Isenbarger T.A., Beck R.P., Pohlschroder M., Spudich J.L., Jung K.-H.,  
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Oner A.D.,  
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassa S.,  
RT "Genome sequence of Halobacterium species NRC-1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
EMBL: AE005110; AAG20373.1; -;  
DR PIR; A84376; A84376.  
KW Complete proteome.  
SQ SEQUENCE 67 AA; 6601 MW; A8BAP23FCBEBB648 CRC64;

Query Match 100.0%; Score 33; DB 17; Length 67;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYMS 5  
Db 59 GYMS 63

```

RESULT 2
Q8PR71 PRELIMINARY; PRT; 73 AA.
AC Q8PR71;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein XAC0095.
GN XAC0095.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011632; AA034987.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 73 AA; 8296 MW; 89C3771680F46C3D CRC64;

Query Match 100.0%; Score 33; DB 16; Length 73;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 6 GYWS 10

RESULT 3
Q8PEB4 PRELIMINARY; PRT; 85 AA.
AC Q8PEB4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein XCC0067.
GN XCC0067.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=2022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011632; AA034987.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 85 AA; 8296 MW; 89C3771680F46C3D CRC64;

Query Match 100.0%; Score 33; DB 16; Length 73;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 6 GYWS 10

RESULT 4
Q88W52 PRELIMINARY; PRT; 285 AA.
AC Q88W52;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Integral membrane protein.
GN LP 1809.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezen M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935257; CAD64219.1; -.
DR InterPro; IPR007163; DUF368.
DR Pfam; PF04018; DUF368; 1.
KW Complete proteome.
SQ SEQUENCE 285 AA; 30888 MW; D93DB9353EA9D881 CRC64;

Query Match 100.0%; Score 33; DB 16; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 274 GYWS 278

RESULT 5
Q9IAF9 PRELIMINARY; PRT; 377 AA.
AC Q9IAF9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (fragment).
OS Iivindomyrus opdenboschi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012100; AA039386.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 85 AA; 9609 MW; C6FDC29D07155274 CRC64;

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Query Match 100.0%; Score 33; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GYWS 5
DB 18 GYWS 22

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OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
OC Osteoglossiformes; Mormyridae; Iivindomyrus.  
OX NCB1\_TaxID=91727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20115608; PubMed=10648209;  
RA Sullivan J.P., Lavoue S., Hopkins C.D.;  
RT "Molecular systematics of the African electric fishes (Mormyroidea;  
RT Teleostei) and a model for the evolution of their electric organs.";  
RL J. Exp. Biol. 203:665-683(2000).  
DR EMBL; AF201635; AAF43346.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0006310; P:DNA recombination; IEA.  
DR InterPro; IPR004321; RAG2.  
DR Pfam; PF03089; RAG2; 1.  
DR NON\_TER 377 377  
FT NON TER 1  
SQ SEQUENCE 377 AA; 41428 MW; B60EDE613EAFDBE CRC64;  
Query Match 100.0%; Score 33; DB 13; Length 377;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYWS 5  
Db 368 GYWS 372  
RESULT 6  
Q9IAE9 PRELIMINARY; PRT; 377 AA.  
AC Q9IAE9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 25, Last annotation update)  
DE Recombination-activating protein 2 (Fragment).  
OS Mormyrus rume.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
OC Osteoglossiformes; Mormyridae; Mormyrus.  
OX NCB1\_TaxID=91731;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20115608; PubMed=10648209;  
RA Sullivan J.P., Lavoue S., Hopkins C.D.;  
RT "Molecular systematics of the African electric fishes (Mormyroidea;  
RT Teleostei) and a model for the evolution of their electric organs.";  
RL J. Exp. Biol. 203:665-683(2000).  
DR EMBL; AF201645; AAF43356.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0006310; P:DNA recombination; IEA.  
DR InterPro; IPR004321; RAG2.  
DR Pfam; PF03089; RAG2; 1.  
DR NON\_TER 377 377  
FT NON TER 1  
SQ SEQUENCE 377 AA; 41364 MW; D59BAC6D739ABE56 CRC64;  
Query Match 100.0%; Score 33; DB 13; Length 377;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYWS 5  
Db 368 GYWS 372  
RESULT 7  
Q9IAH4 PRELIMINARY; PRT; 377 AA.  
AC Q9IAH4;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Recombination-activating protein 2 (Fragment).  
OS Brienomyrus hopkinsi.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
OC Osteoglossiformes; Mormyridae; Brienomyrus.  
OX NCB1\_TaxID=112141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20115608; PubMed=10648209;  
RA Sullivan J.P., Lavoue S., Hopkins C.D.;  
RT "Molecular systematics of the African electric fishes (Mormyroidea;  
RT Teleostei) and a model for the evolution of their electric organs.";  
RL J. Exp. Biol. 203:665-683(2000).  
DR EMBL; AF201618; AAF43329.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0006310; P:DNA recombination; IEA.  
DR InterPro; IPR004321; RAG2.  
DR Pfam; PF03089; RAG2; 1.  
DR NON\_TER 377 377  
FT NON TER 1  
SQ SEQUENCE 377 AA; 41403 MW; 0A4599C6604C8123 CRC64;  
Query Match 100.0%; Score 33; DB 13; Length 377;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYWS 5  
Db 368 GYWS 372  
RESULT 8  
Q9IAFO PRELIMINARY; PRT; 377 AA.  
AC Q9IAFO;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Recombination-activating protein 2 (Fragment).  
OS Mormyrus ovis.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
OC Osteoglossiformes; Mormyridae; Mormyrus.  
OX NCB1\_TaxID=112155;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20115608; PubMed=10648209;  
RA Sullivan J.P., Lavoue S., Hopkins C.D.;  
RT "Molecular systematics of the African electric fishes (Mormyroidea;  
RT Teleostei) and a model for the evolution of their electric organs.";  
RL J. Exp. Biol. 203:665-683(2000).  
DR EMBL; AF201644; AAF43355.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0006310; P:DNA recombination; IEA.  
DR InterPro; IPR004321; RAG2.  
DR Pfam; PF03089; RAG2; 1.  
DR NON\_TER 377 377  
FT NON TER 1  
SQ SEQUENCE 377 AA; 41431 MW; 7EB7C6C644E569DB CRC64;  
Query Match 100.0%; Score 33; DB 13; Length 377;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYWS 5  
Db 368 GYWS 372

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RESULT 9
Q9IAH2
ID Q9IAH2 PRELIMINARY; PRT; 377 AA.
AC Q9IAH2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Brienomyrus niger.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Brienomyrus.
OX NCBI_TaxID=42637;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20115608; PubMed=10648209;
RX Sullivan J.P., Lavoue S., Hopkins C.D.;
RA "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201620; AAF43331.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
DR NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41522 MW; 2E93DC79A8B6EC4A CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 368 GYWS 372

RESULT 10
Q9I867
ID Q9I867 PRELIMINARY; PRT; 377 AA.
AC Q9I867;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Campylomormyrus tamandua.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Campylomormyrus.
OX NCBI_TaxID=91719;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20115608; PubMed=10648209;
RX Sullivan J.P., Lavoue S., Hopkins C.D.;
RA "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201625; AAF43336.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
DR NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41387 MW; D52A9E361A56AB43 CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 368 GYWS 372

RESULT 11
Q9IAG1
ID Q9IAG1 PRELIMINARY; PRT; 377 AA.
AC Q9IAG1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Hyperopisus bebe.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Hyperopisus.
OX NCBI_TaxID=91725;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20115608; PubMed=10648209;
RX Sullivan J.P., Lavoue S., Hopkins C.D.;
RA "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201633; AAF43344.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
DR NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41324 MW; C3C5A2B8E34EF6FC CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 368 GYWS 372

RESULT 12
Q9IAF4
ID Q9IAF4 PRELIMINARY; PRT; 377 AA.
AC Q9IAF4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Marcusenius senegalensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Marcusenius.
OX NCBI_TaxID=42650;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20115608; PubMed=10648209;
RX Sullivan J.P., Lavoue S., Hopkins C.D.;
RA "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201640; AAF43351.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
DR NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41324 MW; C3C5A2B8E34EF6FC CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 368 GYWS 372

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DR GO: 0006310; P:DNA recombination; IEA.  
 DR InterPro; IPR004321; RAG2.  
 DR Pfam; PF03089; RAG2; 1.  
 FT NON\_TER 1 377  
 FT NON\_TER 377 377  
 SQ SEQUENCE 377 AA; 41475 MW; 735853EEA67408FE CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
 Db 368 GYWS 372

RESULT 13  
 Q9IAH1 PRELIMINARY; PRT; 377 AA.  
 ID Q9IAH1  
 AC Q9IAH1  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Recombination-activating protein 2 (Fragment).  
 OS Stomatolobus walkeri.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
 OC Osteoglossiformes; Mormyridae; Stomatolobus.  
 OX NCBI\_TaxID=112160;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20115608; PubMed=10648209;  
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;  
 RT "Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs.";  
 RL J. Exp. Biol. 203:665-683(2000).  
 DR EMBL; AF201656; AAF43367.1; -;  
 DR GO: 0005634; C:nucleus; IEA.  
 DR GO: 0003677; F:DNA binding; IEA.  
 DR GO: 0006310; P:DNA recombination; IEA.  
 DR InterPro; IPR004321; RAG2.  
 DR Pfam; PF03089; RAG2; 1.  
 FT NON\_TER 1 377  
 FT NON\_TER 377 377  
 SQ SEQUENCE 377 AA; 41529 MW; 4FD1CC06990F0E2F CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
 Db 368 GYWS 372

RESULT 14  
 Q9IAH1 PRELIMINARY; PRT; 377 AA.  
 ID Q9IAH1  
 AC Q9IAH1  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Recombination-activating protein 2 (Fragment).  
 OS Brienomyrus sp. CU79740.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
 OC Osteoglossiformes; Mormyridae; Brienomyrus.  
 OX NCBI\_TaxID=112278;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20115608; PubMed=10648209;  
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;  
 RT "Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs.";  
 RL J. Exp. Biol. 203:665-683(2000).  
 DR EMBL; AF201621; AAF43332.1; -;  
 DR GO: 0005634; C:nucleus; IEA.  
 DR GO: 0003677; F:DNA binding; IEA.

Qy 1 GYWS 5  
 Db 368 GYWS 372

RESULT 15  
 Q9IAE0 PRELIMINARY; PRT; 377 AA.  
 ID Q9IAE0  
 AC Q9IAE0  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Recombination-activating protein 2 (Fragment).  
 OS Pollimyrus isidori.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
 OC Osteoglossiformes; Mormyridae; Pollimyrus.  
 OX NCBI\_TaxID=91713;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20115608; PubMed=10648209;  
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;  
 RT "Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs.";  
 RL J. Exp. Biol. 203:665-683(2000).  
 DR EMBL; AF201654; AAF43365.1; -;  
 DR GO: 0005634; C:nucleus; IEA.  
 DR GO: 0003677; F:DNA binding; IEA.  
 DR GO: 0006310; P:DNA recombination; IEA.  
 DR InterPro; IPR004321; RAG2.  
 DR Pfam; PF03089; RAG2; 1.  
 FT NON\_TER 1 377  
 FT NON\_TER 377 377  
 SQ SEQUENCE 377 AA; 41457 MW; 393E1B1FA938E9C8 CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
 Db 368 GYWS 372

Search completed: September 30, 2004, 05:59:33  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 24.4068 Seconds  
(without alignments)  
57.883 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33  
Sequence: 1 GYWS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Geneseq1980s:\*  
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3: Geneseq2000s:\*  
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6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	33	100.0	5	3	AA32257	Light Cha
2	33	100.0	137	3	AA32260	Mouse ant
3	33	100.0	163	7	ABM73967	DNA clone
4	33	100.0	345	7	ABM73656	DNA clone
5	33	100.0	444	3	AA32263	Humanised
6	33	100.0	1254	4	ABE62006	Drosophil
7	30	90.9	40	4	ABG07533	Novel hum
8	30	90.9	43	2	AA95472	V39, mono
9	30	90.9	63	6	ABR48102	Human sec
10	30	90.9	63	6	ABR00271	Human gen
11	30	90.9	63	7	ABE91793	Human sec
12	30	90.9	63	7	ADC74531	Human sec
13	30	90.9	64	2	AA307813	Human sec
14	30	90.9	181	2	AA335482	Chlamydia
15	30	90.9	210	4	AAU17327	Novel sig
16	30	90.9	210	7	ABD94035	Human nov
17	30	90.9	242	3	AA376114	Rat HT gl
18	30	90.9	242	4	AAE56053	Skin cell
19	30	90.9	242	5	ABE72253	Rat prote
20	30	90.9	242	5	ABE72301	Rat prote
21	30	90.9	242	5	ABE72290	Rat prote
22	30	90.9	243	5	ABP39269	Staphyloc
23	30	90.9	287	6	ABM72990	Staphyloc
24	30	90.9	310	4	AAU35317	Enterococ
25	30	90.9	310	4	AAE19867	GALV retr

26	30	90.9	310	6	ABU29423	Protein e
27	30	90.9	315	5	ABE55045	Lactococc
28	30	90.9	359	3	AA31982	Arabidops
29	30	90.9	374	4	AA119870	Activatin
30	30	90.9	379	3	AA31981	Arabidops
31	30	90.9	392	3	AA31981	Human sec
32	30	90.9	392	6	ADA41195	Human sec
33	30	90.9	392	6	ABR48101	Human gen
34	30	90.9	392	6	ABR00270	Human sec
35	30	90.9	392	7	ABE91792	Human sec
36	30	90.9	392	7	ADC74530	Human sec
37	30	90.9	392	7	ADC74397	Human sec
38	30	90.9	408	7	ADC97365	B. faeciu
39	30	90.9	420	2	AA305281	EGF-like
40	30	90.9	420	2	AA313362	Amino aci
41	30	90.9	420	3	AA318569	Human PRO
42	30	90.9	420	3	ABD24396	Human PRO
43	30	90.9	420	3	ADC78429	Human PRO
44	30	90.9	420	4	ABE80230	Human PRO
45	30	90.9	420	4	ABE27228	Human EXM

## ALIGNMENTS

RESULT 1  
AA32257  
ID AA32257 standard; peptide; 5 AA.

XX  
AC AA32257;  
DT 15-FEB-2000 (first entry)  
TX  
DE Light chain CDR H1 of mouse anti-CD23 MAB C11.

XX  
KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;  
KW monoclonal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;  
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
therapy.

OS Mus musculus.

XX WO9558679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

(GLAX ) GLAXO GROUP LTD.

PI Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

DR WPI; 2000-053101/04.

DR N-PSDB; AA234742.

PT Cell receptor specific antibodies useful for treating e.g. arthritis,  
diabetes, multiple sclerosis and psoriasis.

XX Claim 1; Page 40; 81pp; English.

XX This sequence represents complementarity determining region 1 (CDR H1)  
of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11  
(see also AA32263). The invention provides altered antibodies, such as  
chimeric or humanised antibodies, which comprise sufficient of the amino  
acid sequences of C11 light and heavy chain CDRs (see AA32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents

XX Sequence 5 AA;

Query Match 100.0%; Score 33; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
 |||||  
 Db 1 GYWS 5

RESULT 2

ID AAY32260 standard; protein; 137 AA.

XX AAY32260;

XX 15-FEB-2000 (first entry)

DE Mouse anti-CD23 MAb C11 heavy chain variable region.

KW CD23; FCER1; IGE receptor; monoclonal antibody; C11; mouse;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.

XX Mus musculus.

Key Location/Qualifiers  
 Region 59..63  
 /note= "CDR H1"  
 Region 78..96  
 /note= "CDR H2"  
 Region 129..131  
 /note= "CDR H3"

XX WO9958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAXO) GLAXO GROUP LTD.

XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX N-PSDE; AAZ34745.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 XX diabetes, multiple sclerosis and psoriasis.

PS Claim 8; Fig 1; 81pp; English.

XX This sequence represents the heavy chain variable region (VH) of murine  
 CC anti-CD23 (PCER1) monoclonal antibody C11. The invention provides  
 CC altered antibodies, such as chimeric or humanised antibodies (see  
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions (see AAY32254-59) to render them capable of binding to the CD23  
 CC type II molecule expressed on haematopoietic cells. The antibodies are  
 CC used to block soluble CD23 formation in human therapy, for the treatment  
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents

XX Sequence 137 AA;

Query Match 100.0%; Score 33; DB 3; Length 137;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
 |||||  
 Db 59 GYWS 63

RESULT 3

ABM73967

ID ABM73967 standard; protein; 163 AA.

XX ABM73967;

XX 17-OCT-2003 (first entry)

DE DNA clone originating in barley containing SNP sequence #377.  
 XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.

XX Hordeum vulgare.

XX WO2003057877-A1.

XX 17-JUL-2003.

XX 16-DEC-2002; 2002WO-IB005403.

XX 20-DEC-2001; 2001JP-00387059.

XX 20-DEC-2001; 2001JP-00387131.

XX 20-DEC-2001; 2001JP-00403299.

XX 20-DEC-2001; 2001JP-00403300.

XX 27-SEP-2002; 2002JP-00327515.

XX (UYN1-) UNIV JAPAN OKAYAMA.

XX Sato K, Takeda K, Kohara Y;

XX WPI; 2003-587127/55.

XX Single nucleotide polymorphism sites in barley varieties and DNA  
 CC sequences containing them for analysis and identification of barley  
 CC varieties and production of barley transformants with desired  
 CC characteristics.

XX Disclosure; SEQ ID XX; 284pp; Japanese.

XX The present invention relates to oligonucleotide clones originating in  
 CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms  
 CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley





CC (HSIGKVII) and the heavy chain complementarity determining regions. (see  
 CC AAY32257-59) of murine antibody C11. The DNA was constructed by splice  
 CC overlap PCR. The invention provides altered antibodies, such as chimeric  
 CC or humanised antibodies, which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions to render them capable of binding to the CD23 type II molecule  
 CC expressed on haematopoietic cells. The antibodies are used to block  
 CC soluble CD23 formation in human therapy, for the treatment of arthritis,  
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,  
 CC diabetes, urveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,  
 CC glomerulonephritis, inflammatory bowel disease, ulcerative colitis,  
 CC Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute aschmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type I diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents  
 CC  
 XX Sequence 444 AA;

Query Match 100.0%; Score 33; DB 3; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
 |||||  
 Db 31 GYWMS 35

RESULT 6  
 ABB62006  
 ID ABB62006 standard; protein; 1254 AA.  
 XX AC ABB62006;  
 XX AC ABB62006;  
 DT 26-MAR-2002 (first entry)  
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 12810.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX KW pharmaceutical.  
 XX OS Drosophila melanogaster.

XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US009231.  
 XX PF 23-MAR-2000; 2000US-0191637P.  
 XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE ) PE CORP NY.  
 XX PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX WPI; 2001-656860/75.  
 XX DR N-PSDB; ABL06109.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 XX genes from Drosophila and for elucidating cell signaling and cell-cell  
 XX interactions.  
 XX PS Disclosure; SEQ ID NO 12810; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA  
 CC sequences (ABU01840-ABU16175) and the encoded proteins (ABB57737-

CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 1254 AA;

Query Match 100.0%; Score 33; DB 4; Length 1254;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
 |||||  
 Db 1139 GYWMS 1143

RESULT 7  
 ABG07533  
 ID ABG07533 standard; protein; 40 AA.

XX AC ABG07533;  
 XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #7524.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX DR N-PSDB; AAS71720.

XX PT New isolated polynucleotide and encoded polypeptides, useful in  
 XX diagnostics, forensics, gene mapping, identification of mutations  
 XX responsible for genetic disorders or other traits and to assess  
 XX biodiversity.

XX PS Claim 20; SEQ ID NO 37892; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pot\_sequences

XX Sequence 40 AA;

SQ

Query Match 90.9%; Score 30; DB 4; Length 40;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5  
|||:  
Db 33 GYWLS 37

RESULT 8  
AAR95472  
ID AAR95472 standard; peptide; 43 AA.

XX AC AAR95472;  
XX DT 05-NOV-1996 (first entry)  
XX V39, monoclonal antibody SM-3 derived antigen binding peptide.  
DE Abtide; prostate specific mucin antigen; human prostate cancer; LNCaP;  
XX diagnostic; detection; imaging; tumour; phage; peptide library; breast;  
KW polymorphic; epithelial.  
XX Synthetic.

XX WO9609411-A1.  
XX 28-MAR-1996.  
XX 20-SEP-1995; 95WO-US011934.

XX 21-SEP-1994; 94US-00310192.  
XX 07-JUN-1995; 95US-00488161.  
XX (CYTO-) CYTOGEN CORP.

XX Alvarez VL;  
XX WPI; 1996-188471/19.

XX New isolated peptide(s) with specific binding activities - obtd. by  
PT screening random peptide libraries, for use in diagnostic and therapeutic  
PT compsns.

XX Claim 38; Page 75; 106pp; English.

XX AAR95459-R95509 are antigen binding peptides ("abtides") derived from the  
CC monoclonal antibody SM-3 which recognises a specific polymorphic  
CC epithelial mucin tumour antigen found on human breast cancer cells. The  
CC abtides are identified from random peptide libraries using specific  
CC ligand binding. Abtides mimic the binding specificity of large molecules  
CC such as antibodies and receptors but have a much smaller size allowing  
CC their production at a lower cost and reducing the extent of their  
CC immunogenicity aiding in vivo delivery. The abtides are useful for the  
CC diagnosis, detection, imaging and treatment of disease, e.g. tumours,  
CC prostate cancer and breast cancer

XX Sequence 43 AA;

Query Match 90.9%; Score 30; DB 2; Length 43;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5  
|||:  
Db 6 GYWLS 10

RESULT 9

ABR48102  
ID ABR48102 standard; protein; 63 AA.

XX AC ABR48102;

XX DT 12-JUN-2003 (first entry)

XX DE Human secreted protein, SEQ ID 993.

XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;  
KW vulnery; antiinflammatory; noctropic; neuroprotective;  
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.

XX Homo sapiens.

XX WO200295010-A2.

XX PD 28-NOV-2002.

XX PF 19-MAR-2002; 2002WO-US009785.

XX PR 21-MAR-2001; 2001US-0277340P.

XX PR 19-JUL-2001; 2001US-0306171P.

XX PR 13-NOV-2001; 2001US-0331287P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-129429/12.

XX Novel human secreted proteins, useful for detecting, preventing,  
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular  
PT disorders such as arrhythmia.

XX Claim 13; SEQ ID NO 993; 1881pp; English.

XX The present invention relates to novel human secreted proteins (ABR47633-  
ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins  
and their coding sequences are useful for the preparation of a diagnostic  
or pharmaceutical composition for diagnosing or treating a cardiovascular  
disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary  
arteriosclerosis and myocardial ischaemia), neural disorders, immune  
system disorders, muscular disorders, reproductive disorders,  
gastrointestinal disorders, pulmonary disorders, renal disorders,  
proliferative disorders and/or cancerous diseases and conditions, for  
infection, for treating thrombosis and arteriosclerosis, for treating or  
preventing neural damage which occurs in neuronal disorders or  
neurodegenerative conditions such as Alzheimer's disease and Parkinson's  
disease, to enhance bone and periodontal regeneration and aid in tissue  
transplants or bone grafts, to prevent skin aging or hair loss, to  
stimulate growth and differentiation of haematopoietic cells and bone  
marrow cells when used in combination with other cytokines, to maintain  
organs before transplantation or for supporting cell culture of primary  
tissues, to increase or decrease differentiation or proliferation of  
embryonic stem cells, or to modulate mammalian characteristics or  
metabolism. Note: The sequence data for this patent was published in  
electronic format and is available from WIPO at  
ftp.wipo.int/pub/published\_pot\_sequences

XX Sequence 63 AA;

Query Match 90.9%; Score 30; DB 6; Length 63;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5  
|||:  
Db 45 GYWLS 49

RESULT 10

```
ABR00271
ID ABR00271 standard; protein; 63 AA.
AC ABR00271;
XX
XX
DT 03-APR-2003 (first entry)
XX
XX Human gene 139 encoded secreted protein HPRAL78, SEQ ID NO:560.
DE
DE Human; secreted protein; digestive disorder; gastrointestinal disorder;
KW mouth; oesophagus; stomach; small intestine; large intestine; liver;
KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
KW immune disorder; inflammation; infection; wound healing; drug screening;
KW chromosome identification; chromosome mapping; cytostatic; gene therapy;
KW antiinflammatory; immunosuppressive; vulnery; chromosome 3p25.2.
XX
OS Homo sapiens.
XX WO200276488-A1.
XX
XX 03-OCT-2002.
XX
XX 19-MAR-2002; 2002WO-US008276.
XX
XX 21-MAR-2001; 2001US-0277340P.
XX
XX 19-JUL-2001; 2001US-0306171P.
XX
XX 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2003-029900/02.
XX N-PSDB; ABZ71450.
XX
XX New human secreted proteins and nucleic acids, useful for detecting,
XX preventing, diagnosing, prognosticating, treating and/or ameliorating
XX e.g. gastrointestinal diseases and disorders, or cancers.
XX
XX Claim 13; Page 1107; 1216pp; English.
XX
XX ABZ71130-ABZ71478 represent cDNAs corresponding to 178 human secreted
XX protein genes, and ABP00011-ABP00299 represent the proteins they encode.
XX ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The
XX invention also encompasses antibodies specific for the secreted proteins,
XX the use of the secreted proteins in drug screening, and recombinant
XX vectors and host cells comprising a nucleic acid of the invention. The
XX secreted proteins, nucleic acids encoding them, antibodies or antibody
XX fragments specific for the secreted proteins, and modulators of protein
XX activity are useful for diagnosing, treating, ameliorating or preventing
XX digestive disorders. Such conditions include disorders of the mouth,
XX oesophagus, stomach, small intestine, large intestine, liver, biliary
XX tract and pancreas, and include cancers of these organs and tissues. The
XX secreted proteins and their nucleic acids may also be used in the
XX treatment of immune disorders, inflammation, infection,
XX hyperproliferative disorders, and to promote wound healing. Nucleic acids
XX of the invention may be used for chromosome identification, chromosome
XX mapping, in gene therapy, for identifying individuals from minute
XX biological samples, as hybridisation probes, and as molecular weight
XX markers. The present sequence represents a human secreted protein of the
XX invention
XX
XX Sequence 63 AA;
XX
XX Query Match 90.9%; Score 30; DB 6; Length 63;
XX Best Local Similarity 80.0%; Pred. No. 2e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GYVMS 5
XX |||||
XX 45 GYVLS 49
XX
XX RESULT 12
XX ADC74531
XX ID ADC74531 standard; protein; 63 AA.
XX
XX AC ADC74531;
XX
XX 01-JAN-2004 (first entry)
XX
XX Human secreted protein - SEQ ID 1164.
XX
```

```
RESULT 11
ADB91793
ID ADB91793 standard; protein; 63 AA.
AC ADB91793;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human secreted protein #SEQ ID 739.
XX
XX Secreted protein; gene therapy; antidiabetic; diabetes; human.
XX
XX Homo sapiens.
XX WO2003004622-A2.
XX
XX 16-JAN-2003.
XX
XX 19-MAR-2002; 2002WO-US008124.
XX
XX 21-MAR-2001; 2001US-0277340P.
XX
XX 19-JUL-2001; 2001US-0306171P.
XX
XX 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2003-229407/22.
XX
XX Nucleic acid encoding a human secreted protein is useful in diagnosing or
XX treating diabetes or conditions related to diabetes.
XX
XX Claim 3; SEQ ID NO 739; 1537pp; English.
XX
XX The invention relates to isolated nucleic acid molecules ADB91065-
XX ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-
XX ADB91834. Also disclosed is a recombinant vector comprising a
XX polynucleotide of the invention, and a recombinant host cell comprising
XX the recombinant vector. The polypeptide of the invention is useful in
XX identifying a binding partner by contacting the polypeptide with a
XX binding partner, and determining whether the binding partner increases or
XX decreases activity of the polypeptide. The polypeptide, polynucleotide,
XX antibody or its fragment, agonist or antagonist are useful for preparing
XX a pharmaceutical composition for diagnosing or treating diabetes or
XX conditions related to diabetes. The present sequence is that of the human
XX immunoglobulin Fc portion used to generate fusion proteins, increasing
XX the stability of the fused protein as compared to the secreted protein
XX only. Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 63 AA;
XX
XX Query Match 90.9%; Score 30; DB 7; Length 63;
XX Best Local Similarity 80.0%; Pred. No. 2e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GYVMS 5
XX |||||
XX 45 GYVLS 49
XX
XX RESULT 12
XX ADC74531
XX ID ADC74531 standard; protein; 63 AA.
XX
XX AC ADC74531;
XX
XX 01-JAN-2004 (first entry)
XX
XX Human secreted protein - SEQ ID 1164.
XX
```

KW antianemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;  
 KW antididiabetic; immunosuppressive; dermatological; nephrotropic;  
 KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;  
 KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;  
 KW haemopoietic; haematologic; anaemia; autoimmune disorder;  
 KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;  
 KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;  
 KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;  
 KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;  
 KW human.

OS Homo sapiens.

XX WO2003038063-A2.

XX 08-MAY-2003.

XX 19-MAR-2002; 2002WO-US008277.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-430516/40.

XX N-PSDB; ADC73916.

XX New human secreted polypeptide for diagnosing, preventing or treating

XX hematoopoietic or hematologic disorders (e.g. anemia), autoimmune

XX disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or

XX atherosclerosis).

XX Claim 16; SEQ ID NO 1164; 2272pp; English.

XX The invention relates to a novel human secreted polypeptide comprising a

XX defined sequence given in the specification. The polypeptide, nucleic

XX acid molecule, antibody, agonist or antagonist of the invention may be

XX useful for preparing a composition for diagnosing or treating a

XX haemopoietic or haematologic disorder such as anaemia, autoimmune

XX disorders such as rheumatoid arthritis, inflammation, Grave's disease,

XX diabetes, systemic lupus erythematosus or glomerulonephritis.

XX neurodegenerative disorders including Parkinson's disease and Alzheimer's

XX disease, wounds and hyperproliferative disorders including

XX atherosclerosis or cancer, as well as bacterial, viral, fungal or

XX parasitic infections. The polypeptide may also be used during gene

XX therapy procedures and for identifying a binding partner by contacting

XX the polypeptide with a binding partner and determining whether the

XX binding partner increases or decreases the activity of the polypeptide.

XX The current sequence is that of the human secreted protein of the

XX invention.

XX Sequence 63 AA;

XX Query Match 90.9%; Score 30; DB 7; Length 63;

XX Best Local Similarity 80.0%; Pred. No. 2e+02;

XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DE Human secreted protein fragment encoded from gene 70.

XX Human; secreted protein; prevention; cancer; tumour; protein therapy;  
 KW gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder;  
 KW developmental abnormality; foetal deficiency; blood disorder; lymphoma;  
 KW leukemia; immune system disorder; autoimmune disease; hepatic disease;  
 KW renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS;  
 KW Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis;  
 KW arthritis; psoriasis; digestive; endocrine; infection.

XX Homo sapiens.

XX WO9909155-A1.

XX 25-FEB-1999.

XX 18-AUG-1998; 98WO-US017044.

XX 19-AUG-1997; 97US-0056368P.

XX 19-AUG-1997; 97US-0056369P.

XX 19-AUG-1997; 97US-0056535P.

XX 19-AUG-1997; 97US-0056555P.

XX 19-AUG-1997; 97US-0056558P.

XX 19-AUG-1997; 97US-0056628P.

XX 19-AUG-1997; 97US-0056629P.

XX 19-AUG-1997; 97US-0056726P.

XX 19-AUG-1997; 97US-0056728P.

XX 16-JUN-1998; 98US-0089510P.

XX 15-JUL-1998; 98US-0092956P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Young PE, Brewer LA, Ebner R, Olsen HS, Florence KA;

XX Rosen CA, Duan R, Moore RA, Shi Y, Lafleur DW, Florence C;

XX Soppet DR, Endress GA, Feng P, Komatsoulis GA;

XX WPI; 1999-190160/16.

XX N-PSDB; AAX37438.

XX New isolated human genes and the secreted polypeptides they encode -

XX useful for diagnosis and treatment of e.g. cancers, neurological

XX disorders, immune diseases, inflammation or blood disorders.

XX Claim 1b; Page 264; 280pp; English.

XX This invention describes novel isolated human secreted proteins and their

XX encoding nucleic acid sequences. The products of the invention are useful

XX for preventing, treating or ameliorating medical conditions e.g. by

XX protein or gene therapy. Also pathological conditions can be diagnosed by

XX determining the presence or amount of expression of the new polypeptides

XX in a sample or by determining the presence or absence of mutations in the

XX new polynucleotides. Specific uses are described for each of the 70

XX polynucleotides, based on which tissues they are most highly expressed

XX in, and include developing products for the diagnosis or treatment of

XX cancer, tumours, neurodegenerative disorders, developmental abnormalities

XX and foetal deficiencies, blood disorders, leukemias, diseases of the

XX immune system, autoimmune diseases, hepatic and renal diseases, lymphomas,

XX inflammation, allergies, asthma, sepsis, diabetes, Alzheimer's and

XX cognitive disorders, schizophrenia, osteoporosis, arthritis, psoriasis,  
 XX digestive/endocrine disorders, infections and AIDS. The human secreted  
 XX proteins of the invention are represented in AAY07744-Y07850 and the  
 XX encoding nucleic acids are represented in AAX37369-X37441

XX Sequence 64 AA;

XX Query Match 90.9%; Score 30; DB 2; Length 64;

XX Best Local Similarity 80.0%; Pred. No. 2e+02;

XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX 1 GYWNWS 5

XX 45 GYWLWS 49

XX 06-JUL-1999 (first entry)

XX 06-JUL-1999 (first entry)

XX 06-JUL-1999 (first entry)

XX 06-JUL-1999 (first entry)

XX 06-JUL-1999 (first entry)

RESULT 14  
 AAY35482  
 ID AAY35482 standard; protein; 181 AA.  
 XX  
 AC AAY35482;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 13-SEP-1999 (first entry)  
 XX  
 XX Chlamydia pneumoniae transmembrane protein sequence.  
 XX  
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
 KW neutralising epitope.  
 XX  
 OS Chlamydia pneumoniae.  
 XX  
 PN WO9927105-A2.  
 XX  
 PD 03-JUN-1999.  
 XX  
 PF 20-NOV-1998; 98WO-IB001890.  
 XX  
 PR 21-NOV-1997; 97FR-00014673.  
 PR 04-NOV-1998; 98US-0107078P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Griffais R;  
 XX  
 DR WPI; 1999-357842/30.  
 XX  
 PT Genome sequence of Chlamydia pneumoniae.  
 XX  
 PS Page 1244; Disclosure; 1912pp; English.  
 XX  
 CC AAY34584-Y35879 represent the proteins encoded by all the open reading  
 CC frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.  
 CC pneumoniae causes respiratory disease such as pneumonia and bronchitis.  
 CC and is thought to be a contributing factor in heart disease, sarcoidosis,  
 CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The  
 CC polypeptides encoded by the open reading frames of the C. pneumoniae  
 CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as  
 CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also  
 CC be used as immunogenic compositions, especially where the vector directs  
 CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17  
 CC -OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 181 AA;  
 Query Match 90.9%; Score 30; DB 2; Length 181;  
 Best Local Similarity 80.0%; Pred. No. 5.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYWS 5  
 DB 48 GYWS 52  
 RESULT 15  
 AAUL7327  
 ID AAUL7327 standard; protein; 210 AA.  
 XX  
 AC AAUL7327;  
 XX  
 DT 07-NOV-2001 (first entry)  
 DT  
 XX  
 DE Novel signal transduction pathway protein, Seq ID 892.  
 XX  
 KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;  
 KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;  
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;

organ transplant rejection; infection; hepatitis C; blood disorder;  
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;  
 KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;  
 KW reproductive system; gastrointestinal; liver disorder; AIDS;  
 XX acquired immune deficiency syndrome.  
 XX Homo sapiens.  
 OS  
 PN WO200154733-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 17-JAN-2001; 2001WO-US001312.  
 XX  
 PR 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.  
 PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217486P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225213P.  
 PR 14-AUG-2000; 2000US-0225214P.  
 PR 14-AUG-2000; 2000US-0225266P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225757P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 14-AUG-2000; 2000US-0225759P.  
 PR 18-AUG-2000; 2000US-0226279P.  
 PR 22-AUG-2000; 2000US-0226681P.  
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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465460/50.
DR N-PSDB; AAS27244.
XX
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX
XX Claim 1; SEQ ID NO 892; 880pp; English.
XX
XX The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders, in wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
CC AAU17683 represent novel signal transduction pathway protein, amino acid
CC sequences of the invention
XX
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Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYWMS 5
Db 68 GYWLS 72
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; APPLICANT: da Silva, Ana Claudia Raseira
; APPLICANT: Farah, Shaker Chuck
; APPLICANT: Quaggio, Ronaldo Bento
; APPLICANT: Reinach, Fernando de Castro
; APPLICANT: Ferro, Jesus Aparecido
; APPLICANT: De Oliveira, Julio Cezar Franco
; APPLICANT: De Laia, Marcelo Luiz
; APPLICANT: Setubal Joao C.
; APPLICANT: Furlan, Luiz Roberto
; TITLE OF INVENTION: Isolated Xanthomonas nucleic acid molecules, proteins encoded the
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: FAPESP 205.1 US
; CURRENT APPLICATION NUMBER: US/10/418,861B
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/374,620
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 57
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Xanthomonas
; FEATURE:
US-10-418-861B-57

Query Match      100.0%; Score 33; DB 15; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      6 GYWS 10

RESULT 3
US-10-437-963-178878
; Sequence 178878, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 178878
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(103)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT4530_76394C.1.pep
US-10-437-963-178878

Query Match      100.0%; Score 33; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      15 GYWS 19

RESULT 4
US-10-437-963-128079
; Sequence 128079, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128079
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(504)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30468C.1.pep
US-10-437-963-128079

Query Match      100.0%; Score 33; DB 16; Length 504;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      4 GYWS 8

RESULT 5
US-10-437-963-144813
; Sequence 144813, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 144813
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45593C.1.pep
US-10-437-963-144813

Query Match      100.0%; Score 33; DB 16; Length 721;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      15 GYWS 19

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Db 319 GYWMS 323

RESULT 6

US-10-144-929-162

; Sequence 162, Application US/10144929

; Publication No. US20030069405A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 70 Human Secreted Proteins

; FILE REFERENCE: P2014P1

; CURRENT APPLICATION NUMBER: US/10/144,929

; CURRENT FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: US/09/251,329

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: PCT/US98/17044

; PRIOR FILING DATE: 1998-08-18

; NUMBER OF SEQ ID NOS: 257

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 162

; LENGTH: 64

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (64)

; OTHER INFORMATION: Xaa equals stop translation

US-10-144-929-162

Query Match 90.9%; Score 30; DB 14; Length 64;

Best Local Similarity 80.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 45 GYWLS 49

RESULT 7

US-10-144-929-162

; Sequence 162, Application US/10144929

; Publication No. US20040014954A9

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 70 Human Secreted Proteins

; FILE REFERENCE: P2014P1

; CURRENT APPLICATION NUMBER: US/10/144,929

; CURRENT FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: US/09/251,329

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: PCT/US98/17044

; PRIOR FILING DATE: 1998-08-18

; NUMBER OF SEQ ID NOS: 257

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 162

; LENGTH: 64

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (64)

; OTHER INFORMATION: Xaa equals stop translation

US-10-144-929-162

Query Match 90.9%; Score 30; DB 15; Length 64;

Best Local Similarity 80.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 45 GYWLS 49

RESULT 8

US-10-424-599-231107

; Sequence 231107, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 231107

; LENGTH: 77

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_50710C.1.pep

US-10-424-599-231107

Query Match 90.9%; Score 30; DB 12; Length 77;

Best Local Similarity 80.0%; Pred. No. 6.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 36 GYWLS 40

RESULT 9

US-10-767-701-41902

; Sequence 41902, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 41902

; LENGTH: 88

; TYPE: PRT

; ORGANISM: Sorghum bicolor

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(88)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3478-024-P1-K1-P2.pep

US-10-767-701-41902

Query Match 90.9%; Score 30; DB 16; Length 88;

Best Local Similarity 80.0%; Pred. No. 7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 70 GYWLS 74

RESULT 10

US-10-767-701-53836

; Sequence 53836, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

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; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 53836
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 13586731.pep
US-10-767-701-53836

Query Match          90.9%; Score 30; DB 16; Length 95;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
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Db      16 GYWS 20

RESULT 11
US-10-424-599-178190
; Sequence 178190, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 178190
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131921C.1.pep
US-10-424-599-178190

Query Match          90.9%; Score 30; DB 12; Length 167;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
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Db      89 GYWS 93

RESULT 12
US-10-289-762-900
; Sequence 900, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 900
; LENGTH: 181
; TYPE: PRT
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; ORGANISM: Chlamydia pneumoniae
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...181
; OTHER INFORMATION: Xaa=unknown or other
US-10-289-762-900
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Query Match          90.9%; Score 30; DB 15; Length 181;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GYWS 5
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Db      48 GYWS 52
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RESULT 13
US-09-764-868-892
; Sequence 892, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 892
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-892
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Query Match          90.9%; Score 30; DB 9; Length 210;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GYWS 5
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Db      68 GYWS 72
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RESULT 14
US-10-424-599-210785
; Sequence 210785, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 210785
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3236C.1.pep
US-10-424-599-210785
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Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GYWS 5
      |||:|
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Db 109 GYWLS 113

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US-09-866-050A-393  
; Sequence 393, Application US/09866050A  
; Publication No. US20030040471A1  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James G.  
; APPLICANT: Kumble, Krishanand D.  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; FILE REFERENCE: 11000.1011c4U  
; CURRENT APPLICATION NUMBER: US/09/866,050A  
; CURRENT FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 725  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 393  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Rat  
US-09-866-050A-393

Query Match 90.9%; Score 30; DB 10; Length 242;  
Best Local Similarity 80.0%; Pred. NO. 1.7e-03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5

Db 224 GYWLS 228

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:00:45 ; Search time 8.47458 Seconds  
(without alignments)

30.459 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/2/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	466	4	US-09-489-039A-14325
2	30	90.9	43	2	US-08-488-161-39
3	30	90.9	43	3	US-09-273-685-39
4	30	90.9	43	5	PCT-US95-11934-39
5	30	90.9	181	4	US-09-198-452A-900
6	30	90.9	242	4	US-09-312-283C-393
7	30	90.9	243	4	US-09-134-001C-4114
8	30	90.9	334	4	US-09-134-000C-6029
9	30	90.9	383	4	US-09-252-991A-29457
10	30	90.9	396	4	US-09-252-991A-20263
11	30	90.9	408	4	US-09-107-532A-6992
12	30	90.9	420	4	US-09-907-794A-109
13	30	90.9	420	4	US-09-903-125A-109
14	30	90.9	420	4	US-09-902-775A-109
15	30	90.9	478	4	US-09-107-532A-6868
16	30	90.9	484	4	US-09-634-238-216
17	30	90.9	534	4	US-09-107-532A-6549
18	30	90.9	538	4	US-09-489-039A-8363
19	30	90.9	667	4	US-09-315-127-5
20	30	90.9	667	4	US-09-315-127-5
21	30	90.9	685	4	US-09-489-039A-12981
22	29	87.9	5	2	US-08-480-434-22
23	29	87.9	5	2	US-08-480-434-31
24	29	87.9	5	2	US-08-053-451B-22
25	29	87.9	5	2	US-08-053-451B-31
26	29	87.9	14	1	US-08-204-658B-11
27	29	87.9	14	1	US-08-470-702-11

Sequence 11, Appl  
Sequence 114, Appl  
Sequence 125, Appl  
Sequence 29, Appl  
Sequence 29, Appl  
Sequence 18, Appl  
Sequence 19, Appl  
Sequence 7742, Appl  
Sequence 19, Appl  
Sequence 32, Appl  
Sequence 4282, Appl  
Sequence 23328, A  
Sequence 6217, Appl  
Sequence 7475, Appl  
Sequence 8223, Appl  
Sequence 18697, A  
Sequence 23790, A

28 29 87.9 14 1 US-08-467-831-11  
29 87.9 20 2 US-08-053-451B-114  
30 29 87.9 119 2 US-08-053-451B-125  
31 29 87.9 121 2 US-08-480-434-29  
32 29 87.9 121 2 US-08-053-451B-39  
33 29 87.9 126 2 US-08-480-434-18  
34 29 87.9 126 2 US-08-480-434-19  
35 29 87.9 126 2 US-08-053-451B-18  
36 29 87.9 126 2 US-08-053-451B-19  
37 29 87.9 240 4 US-09-489-039A-7742  
38 29 87.9 252 4 US-09-431-887-32  
39 29 87.9 256 4 US-09-543-681A-4282  
40 29 87.9 499 4 US-09-252-991A-23328  
41 29 87.9 522 4 US-09-107-532A-6217  
42 29 87.9 526 4 US-09-328-352-7475  
43 29 87.9 526 4 US-09-489-039A-8223  
44 29 87.9 543 4 US-09-252-991A-18697  
45 29 87.9 563 4 US-09-252-991A-23790

#### ALIGNMENTS

RESULT 1  
US-09-489-039A-14325  
; Sequence 14325, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 14325  
; LENGTH: 466  
; TYPE: PRI  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-14325

Query Match 100.0%; Score 33; DB 4; Length 466;  
Best Local Similarity 100.0%; Pred. No. 28+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
Db 437 GYWS 441

RESULT 2  
US-08-488-161-39  
; Sequence 39, Application US/08488161  
; Patent No. 5885577  
; GENERAL INFORMATION:  
; APPLICANT: Alvarez, Vernon L.  
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From  
; TITLE OF INVENTION: Peptide Libraries  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/488,161  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 436  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Misrock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-176  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 39:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 43 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-488-161-39

Query Match 90.9%; Score 30; DB 2; Length 43;  
Best Local Similarity 80.0%; Pred. No. 68;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||:  
Db 6 GYWS 10

RESULT 3  
US-09-273-685-39  
; Sequence 39, Application US/09273685  
; Patent No. 6015561  
; GENERAL INFORMATION:  
; APPLICANT: Alvarez, Vernon L.  
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From  
; TITLE OF INVENTION: Peptide Libraries  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/273,685  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/488,161  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-176  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 43 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-09-273-685-39

Query Match 90.9%; Score 30; DB 3; Length 43;  
Best Local Similarity 80.0%; Pred. No. 68;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||:  
Db 6 GYWS 10

RESULT 4  
PCT-US95-11934-39  
; Sequence 39, Application PC/TUS9511934  
; GENERAL INFORMATION:  
; APPLICANT: Cytogen Corporation  
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From  
; TITLE OF INVENTION: Peptide Libraries  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/11934  
; FILING DATE: 20-SEP-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-196-228  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 43 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US95-11934-39

Query Match 90.9%; Score 30; DB 5; Length 43;  
Best Local Similarity 80.0%; Pred. No. 68;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||:  
Db 6 GYWS 10

RESULT 5  
US-09-198-452A-900  
; Sequence 900, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24



; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 900  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: 1...181  
; OTHER INFORMATION: Xaa=unknown or other  
US-09-198-452A-900

Query Match 90.9%; Score 30; DB 4; Length 181;  
Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
DB 48 GYWS 52

## RESULT 6

US-09-312-283C-393  
; Sequence 393, Application US/09312283C  
; Patent No. 6573095  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Marison, James G.  
; APPLICANT: Kumble, Krishanand D.  
; TITLE OF INVENTION: Compositions Isolated from Skin Cells  
; TITLE OF INVENTION: and Methods for Their Use  
; FILE REFERENCE: 11000.1011c2  
; CURRENT APPLICATION NUMBER: US/09/312,283C  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 425  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 393  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-312-283C-393

Query Match 90.9%; Score 30; DB 4; Length 242;  
Best Local Similarity 80.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
DB 224 GYWS 228

## RESULT 7

US-09-134-001C-4114  
; Sequence 4114, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4114  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis

## US-09-134-001C-4114

Query Match 90.9%; Score 30; DB 4; Length 243;  
Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
DB 52 GYWS 56

## RESULT 8

US-09-134-000C-6029  
; Sequence 6029, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6029  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-6029

Query Match 90.9%; Score 30; DB 4; Length 334;  
Best Local Similarity 80.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
DB 111 GYWS 115

## RESULT 9

US-09-252-991A-29457  
; Sequence 29457, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29457  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29457

Query Match 90.9%; Score 30; DB 4; Length 383;  
Best Local Similarity 80.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
DB 228 GYWS 232

## RESULT 10

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US-09-252-991A-20263
; Sequence 20263, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20263
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20263

Query Match          90.9%; Score 30; DB 4; Length 396;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      40 GYWS 44

RESULT 11
US-09-107-532A-6992
; Sequence 6992, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6992:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES

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; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...408
; SEQUENCE DESCRIPTION: SEQ ID NO: 6992:
US-09-107-532A-6992

Query Match          90.9%; Score 30; DB 4; Length 408;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      263 GYWT 267

RESULT 12
US-09-907-794A-109
; Sequence 109, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313

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; PRIOR FILING DATE: 1999-11-30  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ; PRIOR FILING DATE: 2000-01-05  
 ; NUMBER OF SEQ ID NOS: 423  
 ; SEQ ID NO 109  
 ; LENGTH: 420  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-907-794A-109

Query Match 90.9%; Score 30; DB 4; Length 420;  
 Best Local Similarity 80.0%; Pred. No. 5.8e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
 Db 402 GYWS 406

RESULT 13  
 US-09-905-125A-109  
 ; Sequence 109, Application US/09905125A  
 ; Patent No. 6664376  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genentech, Inc.  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, A.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kijavlin, Ivar J.  
 ; APPLICANT: Mather, Jennie P.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William, I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: 10466-14  
 ; CURRENT APPLICATION NUMBER: US/09/905,125A  
 ; CURRENT FILING DATE: 2001-07-12  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: 2000-02-22  
 ; PRIOR APPLICATION NUMBER: US 60/143,048  
 ; PRIOR FILING DATE: 1999-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/145,698  
 ; PRIOR FILING DATE: 1999-07-26  
 ; PRIOR APPLICATION NUMBER: US 60/146,222  
 ; PRIOR FILING DATE: 1999-07-28  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944  
 ; PRIOR FILING DATE: 1999-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089  
 ; PRIOR FILING DATE: 1999-10-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214  
 ; PRIOR FILING DATE: 1999-11-29  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: 1999-11-30  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ; PRIOR FILING DATE: 2000-01-05  
 ; NUMBER OF SEQ ID NOS: 423  
 ; SEQ ID NO 109  
 ; LENGTH: 420  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-905-125A-109

Query Match 90.9%; Score 30; DB 4; Length 420;  
 Best Local Similarity 80.0%; Pred. No. 5.8e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
 Db 402 GYWS 406

RESULT 14  
 US-09-902-775A-109  
 ; Sequence 109, Application US/09902775A  
 ; Patent No. 6686451  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genentech, Inc.  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, A.  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kijavlin, Ivar J.  
 ; APPLICANT: Mather, Jennie P.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William, I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: 10466-14  
 ; CURRENT APPLICATION NUMBER: US/09/905,125A  
 ; CURRENT FILING DATE: 2001-07-12  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: 2000-02-22  
 ; PRIOR APPLICATION NUMBER: US 60/143,048  
 ; PRIOR FILING DATE: 1999-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/145,698  
 ; PRIOR FILING DATE: 1999-07-26  
 ; PRIOR APPLICATION NUMBER: US 60/146,222  
 ; PRIOR FILING DATE: 1999-07-28  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594

FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902,775A  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 109  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-902-775A-109

Query Match 90.9%; Score 30; DB 4; Length 420;  
Best Local Similarity 80.0%; Pred. No. 5.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
Db 402 GYWS 406

## RESULT 15

US-09-107-532A-6868  
Sequence 6868, Application US/09107532A  
Patent No. 6583275

## GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
CORRESPONDENCE ADDRESS:  
ADDRESS: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354

## COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 6868:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 478 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...478  
SEQUENCE DESCRIPTION: SEQ ID NO: 6868:  
US-09-107-532A-6868

Query Match 90.9%; Score 30; DB 4; Length 478;  
Best Local Similarity 80.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
Db 98 GYWS 102

Search completed: September 30, 2004, 06:39:18  
Job time : 9.47458 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 20.6102 Seconds  
(without alignments)  
88.677 Million cell updates/sec

Title: US-09-674-716B-11  
Perfect score: 98  
Sequence: 1 EIRLKSDNYTHYAESVKG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	98	100.0	101	2	S26460		Ig heavy chain V r
2	98	100.0	115	2	S38714		Ig heavy chain V r
3	93	94.9	106	2	S24521		Ig heavy chain V r
4	93	94.9	115	1	AVMS06		Ig heavy chain V-I
5	91	92.9	113	1	AVMSAB		Ig heavy chain V-I
6	91	92.9	113	1	AVMS61		Ig heavy chain V-I
7	91	92.9	113	1	AVMS09		Ig heavy chain V-I
8	91	92.9	113	1	AVMSB7		Ig heavy chain V-I
9	91	92.9	115	1	AVMS82		Ig heavy chain V-I
10	89	90.8	115	2	A25803		Ig heavy chain V r
11	86	87.8	113	1	AVMS57		Ig heavy chain V-I
12	85	86.7	113	1	HVMSAM		Ig heavy chain V-I
13	75.5	77.0	111	1	MEMS76		Ig heavy chain pre
14	73	74.5	139	2	PC1213		Ig heavy chain V r
15	68	69.4	64	2	I77394		Ig heavy chain V-D
16	68	69.4	121	2	S09958		Ig heavy chain V r
17	67	68.4	100	2	S26462		Ig heavy chain V r
18	67	68.4	110	2	PH1091		Ig heavy chain V r
19	67	68.4	110	2	PH1092		Ig heavy chain V r
20	67	68.4	119	2	A27630		Ig heavy chain pre
21	67	68.4	121	2	A41940		Ig heavy chain V r
22	67	68.4	141	2	I32513		Ig heavy chain pre
23	66	67.3	125	2	S67945		Ig heavy chain pre
24	65	66.3	139	2	G29380		Ig heavy chain pre
25	64	65.3	110	2	PH1093		Ig heavy chain V r
26	63	64.3	220	2	S68211		Ig heavy chain (Ma
27	63	64.3	444	2	PC4436		monoclonal antibod
28	61	62.2	119	2	PH1293		Ig heavy chain pre
29	61	62.2	137	2	S42467		Ig heavy chain V r

ALIGNMENTS

RESULT 1

S26460

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S26460

R;Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26460

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-101 <KAV>

A:Cross-references: EMBL:X59106; NID:G51707; PIDN:CAA41832.1; PID:G51708

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 98; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLKSDNYTHYAESVKG 19

Db 32 EIRLKSDNYTHYAESVKG 50

RESULT 2

S38714

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jun-2000

C:Accession: S38714

R;Climanis, A. V.

submitted to the EMBL Data Library, November 1993

A:Reference number: S38713

A:Accession: S38714

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-115 <CIM>

A:Cross-references: EMBL:X76014; NID:G416092; PIDN:CAA53601.1; PID:G1334076

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-99/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 98; DB 2; Length 115;

Best Local Similarity 100.0%; Pred. No. 1.3e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLKSDNYTHYAESVKG 19

Db 49 EIRLKSDNYTHYAESVKG 67

## RESULT 3

S24521  
 IG heavy chain V region - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C/Accession: S24521  
 R/Kaartinen, M.  
 submitted to the EMBL Data Library, October 1991  
 A/Reference number: S24490  
 A/Accession: S24521  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-106 <KAA>  
 A/Cross-references: EMBL:X66664; NID:G51247; PIDN:CAA47226.1; PID:G51248  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:21-106/Domain: immunoglobulin homology <IMM>

Query Match 94.9%; Score 93; DB 2; Length 106;  
 Best Local Similarity 94.7%; Pred. No. 7.4e-08;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
 |||||:|||||  
 Db 56 EIRLKSNHYATHYAESVKG 74

## RESULT 4

AVMS06  
 IG heavy chain V-III region (J606) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996  
 C/Accession: C92811; A02072  
 R/Johnson, N.; Slankard, J.; Paul, L.; Hood, L.  
 J. Immunol. 128, 302-307, 1982  
 A/Title: The complete V domain amino acid sequences of two myeloma inulin-binding proteins  
 A/Reference number: A92811; MUID:82099361; PMID:6798111  
 A/Accession: C92811  
 A/Molecule type: protein  
 A/Residues: 1-115 <JOH>  
 C/Comment: This chain was isolated from a myeloma protein that binds inulin.  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:15-100/Domain: immunoglobulin homology <IMM>  
 F:22-98/Disulfide bonds: #status predicted

Query Match 94.9%; Score 93; DB 1; Length 115;  
 Best Local Similarity 94.7%; Pred. No. 8.1e-08;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
 |||||:|||||  
 Db 50 EIRLKSNHYATHYAESVKG 68

## RESULT 5

AVMSAB  
 IG heavy chain V-III region (A4) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 24-Apr-1984 #sequence\_revision 30-Jun-1993 #text\_change 31-Mar-1997  
 C/Accession: A93818; A02072  
 R/Vrana, M.; Rudikoff, S.; Potter, M.  
 Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978  
 A/Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.  
 A/Reference number: A93818; MUID:78158406; PMID:417344  
 A/Accession: A93818  
 A/Molecule type: protein  
 A/Residues: 1-113 <VRA>  
 C/Comment: This chain was isolated from a myeloma protein that binds inulin.  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 91; DB 1; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 1.7e-07;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 1.7e-07;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
 |||||:|||||  
 Db 50 EIRLKSNHYATHYAESVKG 68

## RESULT 6

AVMS61  
 IG heavy chain V-III region (U61) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996  
 C/Accession: B93818; A02072  
 R/Vrana, M.; Rudikoff, S.; Potter, M.  
 Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978  
 A/Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.  
 A/Reference number: A93818; MUID:78158406; PMID:417344  
 A/Accession: B93818  
 A/Molecule type: protein  
 A/Residues: 1-113 <VRA>  
 C/Comment: This chain was isolated from a myeloma protein that binds inulin.  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:15-100/Domain: immunoglobulin homology <IMM>  
 F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 1.7e-07;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
 |||||:|||||  
 Db 50 EIRLKSNHYATHYAESVKG 68

## RESULT 7

AVMS09  
 IG heavy chain V-III region (E109) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996  
 C/Accession: C93818; A02072  
 R/Vrana, M.; Rudikoff, S.; Potter, M.  
 Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978  
 A/Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.  
 A/Reference number: A93818; MUID:78158406; PMID:417344  
 A/Accession: C93818  
 A/Molecule type: protein  
 A/Residues: 1-113 <VRA>  
 C/Comment: This chain was isolated from a myeloma protein that binds inulin.  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:15-100/Domain: immunoglobulin homology <IMM>  
 F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 1.7e-07;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
 |||||:|||||  
 Db 50 EIRLKSNHYATHYAESVKG 68

## RESULT 8

AVMSB7  
 IG heavy chain V-III region (ABE-47N) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996  
 C/Accession: A90406; A02072

R;Vrana, M.; Rudikoff, S.; Potter, M.  
Biochemistry 16, 1170-1175, 1977

A;Title: Heavy-chain variable-region sequence from an inulin-binding myeloma protein.  
A;Reference number: A90400; MUID:77134726; PMID:402936

A;Accession: A90400

A;Molecule type: protein

A;Residues: 1-113 <VPA>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;

Best Local Similarity 94.7%; Pred. No. 1.7e-07;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19

Db 50 EIRKSHNYATHYAESVKG 68

RESULT 9

AVMS82

Ig heavy chain V-III region (W3082) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996

C;Accession: D92811; A02072

R;Johnson, N.; Slankard, J.; Paul, L.; Hood, L.

J. Immunol. 128, 302-307, 1982

A;Title: The complete V domain amino acid sequences of two myeloma inulin-binding proteins

A;Reference number: A92811; MUID:8209361; PMID:679811

A;Accession: D92811

A;Molecule type: protein

A;Residues: 1-115 <JOH>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 115;

Best Local Similarity 94.7%; Pred. No. 1.7e-07;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19

Db 50 EIRKSHNYATHYAESVKG 68

RESULT 10

A25803

Ig heavy chain V region (281.3) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 16-Aug-1996

C;Accession: A25803

R;Herbst, H.; Grutter, T.; Aebersold, R.; Braun, D.G.

Biol. Chem. Hoppe-Seyler 367, 843-851, 1986

A;Title: The complete amino-acid sequence of the variable domain of a monoclonal anti-s

A;Reference number: A25803; MUID:87076047; PMID:3539142

A;Accession: A25803

A;Molecule type: protein

A;Residues: 1-115 <HER>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 90.8%; Score 89; DB 2; Length 115;

Best Local Similarity 89.5%; Pred. No. 3.6e-07;

Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19

Db 50 EIRKSHNYATHYAESVKG 68

Db 50 QIRLASDNYATHYAESVKG 68

RESULT 11

AVMS57

Ig heavy chain V-III region (T957) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996

C;Accession: A92810; A02072

R;Rudikoff, S.; Potter, M.

J. Immunol. 127, 191-194, 1981

A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a ne

A;Reference number: A92810; MUID:81216632; PMID:6787122

A;Accession: A92810

A;Molecule type: protein

A;Residues: 1-113 <RUD>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 87.8%; Score 86; DB 1; Length 113;

Best Local Similarity 89.5%; Pred. No. 1.1e-06;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19

Db 50 EIRKSHNYATHYAESVKG 68

RESULT 12

HVMSAM

Ig heavy chain V region (AMPC1) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 31-Mar-1997

C;Accession: A02073

R;Rudikoff, S.; Potter, M.

J. Immunol. 127, 191-194, 1981

A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a ne

A;Reference number: A92810; MUID:81216632; PMID:6787122

A;Accession: A02073

A;Molecule type: protein

A;Residues: 1-113 <RUD>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 86.7%; Score 85; DB 1; Length 113;

Best Local Similarity 89.5%; Pred. No. 1.6e-06;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19

Db 50 EIRKSHNYATHYAESVKG 68

RESULT 13

HMMS76

Ig heavy chain V-III region (HPC76) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1980 #sequence\_revision 30-Sep-1980 #text\_change 31-Mar-1997

C;Accession: A02074

R;Bernard, O.; Gough, N.M.

Proc. Natl. Acad. Sci. U.S.A. 77, 3630-3634, 1980

A;Title: Nucleotide sequence of immunoglobulin heavy chain joining segments between trans

A;Reference number: A02074; MUID:81013337; PMID:6251474

A;Accession: A02074

A;Molecule type: mRNA

A;Residues: 1-111 <BER>

A;Note: the sequence was also determined from the differentiated gene

A:Note: the sequence of the first 197 residues of the C region was also determined and d  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:10-94/Domain: immunoglobulin homology <IMM>  
F:17-92/Disulfide bonds: #status predicted

Query Match 77.0%; Score 75.5; DB 1; Length 111;  
Best Local Similarity 89.5%; Pred. No. 5.3e-05;  
Matches 17; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 EIRLKSDNYATHYAESVKG 19  
Db 45 EIRLKS-GYATHYAESVKG 62

## RESULT 14

PC1213  
Ig heavy chain precursor V region (mAb H8) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Jul-1999  
C:Accession: PC1213  
R:Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim,  
Gene 121, 331-335, 1992  
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m  
A:Reference number: PC1213; MUID:93077049; PMID:1446832  
A:Accession: PC1213  
A:Molecule type: mRNA  
A:Residues: 1-139 <HON>  
A:Cross-references: GB:M98041; NID:G195092; PIDN:AAA38159.1; PID:G195093  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-139/Product: Ig heavy chain V region #status predicted <MAT>  
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 73; DB 2; Length 139;  
Best Local Similarity 73.7%; Pred. No. 0.00017;  
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
Db 69 EIRSKANNHATYAESVKG 87

## RESULT 15

I77394  
Ig heavy chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 23-Jul-1999  
C:Accession: I77394  
R:Owens, J.D.  
Mol. Cell. Biol. 11, 5660-5670, 1991  
A:Title: Non-homologous recombination/deletion at sites within the mouse JH-Cdelta locus  
A:Reference number: I57520; MUID:92017847; PMID:1922069  
A:Accession: I77394  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-64 <RES>  
A:Cross-references: GB:M64568; NID:G198472; PIDN:AAA39341.1; PID:G198473  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 69.4%; Score 68; DB 2; Length 64;  
Best Local Similarity 72.2%; Pred. No. 0.00047;  
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVKG 19  
Db 9 ITVKSDNYCANYAESVKG 26

Search completed: September 30, 2004, 06:00:37  
Job time : 20.6102 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 11.5932 Seconds  
(without alignments)  
85.337 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98  
Sequence: 1 BIRLSDNYATHAESVKG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	94.9	115	1 HV32 MOUSE	P01801 mus musculus
2	91	92.9	113	1 HV27 MOUSE	P01796 mus musculus
3	91	92.9	113	1 HV28 MOUSE	P01797 mus musculus
4	91	92.9	113	1 HV29 MOUSE	P01798 mus musculus
5	91	92.9	113	1 HV30 MOUSE	P01799 mus musculus
6	91	92.9	115	1 HV31 MOUSE	P01800 mus musculus
7	86	87.8	113	1 HV34 MOUSE	P01803 mus musculus
8	85	86.7	113	1 HV35 MOUSE	P01804 mus musculus
9	75.5	77.0	111	1 HV01 RAT	P01805 rattus norv
10	57	58.2	142	1 HV21 MOUSE	P01790 mus musculus
11	48	49.0	122	1 HV18 MOUSE	P01787 mus musculus
12	48	49.0	123	1 HV19 MOUSE	P01788 mus musculus
13	48	49.0	123	1 HV22 MOUSE	P01791 mus musculus
14	48	49.0	123	1 HV25 MOUSE	P01794 mus musculus
15	48	49.0	123	1 HV20 MOUSE	P01789 mus musculus
16	46	46.9	144	1 HV26 MOUSE	P01795 mus musculus
17	46	46.9	145	1 HUNE CLOAL	O96785 clegmia alb
18	45	45.9	485	1 HUNE CLOAL	P01792 mus musculus
19	44	44.9	123	1 HV23 MOUSE	O96785 clegmia alb
20	43	43.9	485	1 YS76 ANASP	O96785 clegmia alb
21	42	42.9	250	1 Y186 MYCGE	O96785 clegmia alb
22	42	42.9	595	1 VPI_BPCHP	O96785 clegmia alb
23	42	42.9	734	1 GLGE NITEU	O96785 clegmia alb
24	42	42.9	822	1 BPBA_PSEAE	O96785 clegmia alb
25	41.5	42.3	117	1 HV17 MOUSE	O96785 clegmia alb
26	41	41.8	123	1 HV24 MOUSE	O96785 clegmia alb
27	41	41.8	126	1 HV3K_HUMAN	O96785 clegmia alb
28	41	41.8	318	1 RLPA_TREPA	O96785 clegmia alb
29	41	41.8	385	1 HUNE_BOWMO	O96785 clegmia alb
30	41	41.8	664	1 DHSK_HUMAN	O96785 clegmia alb
31	41	41.8	665	1 DHSK_BOVIN	O96785 clegmia alb
32	41	41.8	705	1 CATE_RHIME	O96785 clegmia alb
33	41	41.8	868	1 N180_YEAST	O96785 clegmia alb

34 40.5 41.3 627 1 GLGB\_BACSU  
35 40 40.8 116 1 HV05\_CARAU  
36 40 40.8 136 1 HV16\_MOUSE  
37 40 40.8 216 1 CAT\_VIBAN  
38 40 40.8 381 1 GRK2\_ECOLI  
39 40 40.8 430 1 YJCF\_ECOLI  
40 40 40.8 439 1 SYE2\_HELPJ  
41 40 40.8 439 1 SYE2\_HELPJ  
42 40 40.8 500 1 MOO\_EACHD  
43 40 40.8 555 1 VGLF\_PIIHC  
44 40 40.8 564 1 YC62\_AQUAE  
45 40 40.8 647 1 ACSA\_XANCP

P39118 bacillus su  
P19181 carassius a  
P01783 mus musculu  
P49417 vibrio angu  
P3524 escherichia  
P32704 escherichia  
Q921j1 helicobacte  
Q25360 helicobacte  
Q829g7 bacillus ha  
P12605 human parai  
O87301 aquifex aeo  
Q89311 xanthomonas

## ALIGNMENTS

RESULT 1  
HV32\_MOUSE  
ID HV32\_MOUSE STANDARD; PRT; 115 AA.  
AC P01801;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-III region J606.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=8209361; PubMed=6798111;  
RA Johnson N., Sliankard J., Paul L., Hood L.;  
RT "The complete V domain amino acid sequences of two myeloma inulin-binding proteins.";  
RL J. Immunol. 128:302-307(1982).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; C92811; AVMS06.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 114  
FT DISULFID 22 98  
FT NON TER 115 115  
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;  
Query Match 94.9%; Score 93; DB 1; Length 115;  
Best Local Similarity 94.7%; Pred. No. 2e-08;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 BIRLSDNYATHAESVKG 19  
DQ 50 BIRLSDNYATHAESVKG 58  
RESULT 2  
HV27\_MOUSE  
ID HV27\_MOUSE STANDARD; PRT; 113 AA.  
AC P01796;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-III region A4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

```

RN SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RL proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC -!- BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93818; AVMSAB.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 >113
FT DISULFID 22 98
FT NON TER 113 113
FT SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;
SQ
Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
Db 50 EIRLSDNYATHYAESVKG 68

RESULT 3
HV28 MOUSE
ID HV28 MOUSE STANDARD; PRT; 113 AA.
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RL proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC -!- BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; B93818; AVMS61.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 >113
FT DISULFID 22 98
FT NON TER 113 113
FT SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;
SQ
Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
Db 50 EIRLSDNYATHYAESVKG 68

RESULT 4
HV29 MOUSE
ID HV29 MOUSE STANDARD; PRT; 113 AA.
AC P01798;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region E109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RL proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC -!- BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; C93818; AVMS09.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 >113
FT DISULFID 22 98
FT NON TER 113 113
FT SEQUENCE 113 AA; 12647 MW; EE50F2F20EDB129B CRC64;
SQ
Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
Db 50 EIRLSDNYATHYAESVKG 68

RESULT 5
HV30 MOUSE
ID HV30 MOUSE STANDARD; PRT; 113 AA.
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region ABE-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=77134726; PubMed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
RL protein.";
RL Biochemistry 16:1170-1175(1977).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC -!- BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90400; AVMSB7.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.

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DR PFAM: PF00047; Ig; 1.
DR SMART: SMO0406; IGV; 1.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76659C16C779845E CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 50 EIRKSHNYATHYAESVKG 68

RESULT 6
HV33_MOUSE
ID HV33_MOUSE STANDARD; PRT; 115 AA.
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
EX MEDLINE=8209361; PubMed=6798111;
RA Johnson N., Slackard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: P92811; AVMS82.
DR HSSP: P01810; 2FEJ.
DR InterPro: IPR007110; IG-LIKE.
DR InterPro: IPR003596; IGV.
DR PFAM: PF00047; Ig; 1.
DR SMART: SMO0406; IGV; 1.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 114 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Query Match 92.9%; Score 91; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 50 EIRKSHNYATHYAESVKG 68

RESULT 7
HV31_MOUSE
ID HV31_MOUSE STANDARD; PRT; 113 AA.
AC P01800;
DT 21-JUL-1986 (Rel. 01, Created)
DT 10-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region T957.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
EX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment."
J. Immunol. 127:191-194(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A92810; AVMS57.
DR HSSP: P01810; 2FEJ.
DR InterPro: IPR007110; IG-LIKE.
DR InterPro: IPR003596; IGV.
DR PFAM: PF00047; Ig; 1.
DR SMART: SMO0406; IGV; 1.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12732 MW; 26618F626B59859E CRC64;

Query Match 87.8%; Score 86; DB 1; Length 113;
Best Local Similarity 89.5%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 50 EIRKSHNYATHYAESVKG 68

RESULT 8
HV34_MOUSE
ID HV34_MOUSE STANDARD; PRT; 113 AA.
AC P01803;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region AMPC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
EX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment."
J. Immunol. 127:191-194(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02073; HVMSAM.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; IG-LIKE.
DR InterPro: IPR003596; IGV.
DR PFAM: PF00047; Ig; 1.
DR SMART: SMO0406; IGV; 1.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 13691 MW; 7A6D906AAA96659E CRC64;

Query Match 86.7%; Score 85; DB 1; Length 113;
Best Local Similarity 89.5%; Pred. No. 4.1e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19

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Db      50 EIRLKSHNYATHYAESVKG 68
|||||
RESULT 9
HV35 MOUSE
ID HV35 MOUSE STANDARD; PRT; 111 AA.
AC P01804;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region HPC76 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81013937; PubMed=6251474;
RA Bernard O., Gough N.M.;
RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
between translocated VH and mu constant regions genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
CC REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
DR PIR; A02074; MMSW76.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 110 IG-LIKE.
FT NON TER 111
FT SEQUENCE 111 AA; 12304 MW; 0EDE98EC7348056A CRC64;

Query Match 77.0%; Score 75.5; DB 1; Length 111;
Best Local Similarity 89.5%; Pred. No. 1.5e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 EIRLKSDNYATHYAESVKG 19
|||||
Db      45 EIRLKS-GYATHYAESVKG 62
|||||
RESULT 10
HV01 RAT
ID HV01 RAT STANDARD; PRT; 142 AA.
AC P01805;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region IR2 precursor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83064537; PubMed=6292865;
RA Hellman L., Pettersson U., Engstrom A., Karlsson T., Bennich H.;
RT "Structure and evolution of the heavy chain from rat immunoglobulin
B.";
RL Nucleic Acids Res. 10:6041-6049(1982).
CC -!- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING
IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
DR PIR; A02075; EVRTE2.
DR HSP; P01789; IMCP.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 142 IG HEAVY CHAIN V REGION IR2.
FT DOMAIN 20 133 IG-LIKE.
FT NON TER 142
SQ SEQUENCE 142 AA; 16024 MW; DE29E6CFE745DF3B CRC64;

Query Match 58.2%; Score 57; DB 1; Length 142;
Best Local Similarity 52.6%; Pred. NO. 0.023;
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
|||||
Db      69 EIRKANNYVAYGKSLKG 87
|||||
RESULT 11
HV21 MOUSE
ID HV21 MOUSE STANDARD; PRT; 122 AA.
AC P01790;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MS11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054880; PubMed=6776528;
RA Robinson E.A., Appella E.;
RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
(MOPC 511).";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORICHOLOINE.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 114 IG-LIKE.
FT NON TER 122
SQ SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 122;
Best Local Similarity 52.9%; Pred. NO. 0.59;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVKG 19.
|||||
Db      52 RNKANDYTYEYSASVKG 68
|||||
RESULT 12
HV18 MOUSE
ID HV18 MOUSE STANDARD; PRT; 123 AA.
AC P01787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81197602; PubMed=7231520;  
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;  
 RT "IGG antibodies to phosphorylcholine exhibit more diversity than  
 their IGM counterparts.";  
 RL Nature 291:29-34(1981).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 BINDS PHOSPHORYLCHOLINE.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; G93256; AVMS14.  
 DR HSP; P01789; 1MGP.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 FT DOMAIN 1 114  
 FT NON\_TER 123 123  
 SQ SEQUENCE 123 AA; 13807 MW; A7584FB098B7785D CRC64;  
 Query Match 49.0%; Score 48; DB 1; Length 123;  
 Best Local Similarity 52.9%; Pred.No. 0.59;  
 Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 RLKSDNYATHVAESVKG 19  
 DB 52 RNKANDYTTTYSASVKG 68

Search completed: September 30, 2004, 06:01:21  
 Job time : 12.5932 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 62.1525 Seconds  
(without alignments)  
96.454 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98  
Sequence: 1 EIRKSDNYATHVAESVKG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mmc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvrius.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	91.8	487	11	Q80Z17 mus musculus
2	68	69.4	64	11	Q61750 mus musculus
3	57	58.2	479	11	Q7TWK4
4	51	52.0	469	11	Q8R3V9 mus musculus
5	51	52.0	480	11	Q91XE1
6	49	50.0	361	2	Q9RBZ2 pseudomonas
7	47.5	48.5	754	11	Q8CGQ1 mus musculus
8	47	48.0	357	2	Q9RBZ3 pseudomonas
9	47	48.0	398	16	Q88ZK4 lactobacill
10	46	46.9	2910	10	Q9FND5
11	45.5	46.4	703	11	Q8COV3
12	45	45.9	121	4	Q9UL71
13	45	45.9	300	5	Q8ID86 plasmodium
14	45	45.9	422	5	Q8WR61 lymantria d
15	45	45.9	450	16	Q8U651 agrobacteri
16	44	44.9	253	16	Q8S516 streptococc

Q8dzt9 streptococc  
Q7vix9 haemophilus  
Q45962 clostridium  
Q7vrs2 candidatus  
Q8cux1 oceanobacil  
Q8dwn2 streptococc  
Q7wsg9 onion yello  
Q35037 archaeoglob  
Q85227 mycobacteri  
Q8tzk5 pyrococcus  
Q992f6 streptococc  
Q8k7b3 streptococc  
Q89d85 bradyrhizob  
Q89ydl bradyrhizob  
Q73837 synechocyst  
Q8YCK5 brucella me  
Q8fvg7 brucella su  
Q9xut8 caenorhabdi  
Q8ab59 bacteroides  
Q93nc6 myxococcus  
P82987 homo sapien  
Q9p219 xestia c-ni  
Q7xjg8 linaria vul  
Q7xjg9 linaria mar  
Q8a0q5 bacteroides  
Q84rb8 linaria can  
Q84rb7 linaria vul  
Q8pou7 streptococc

#### ALIGNMENTS

#### RESULT 1

Q80Z17 PRELIMINARY; PRT; 487 AA.  
ID Q80Z17  
AC Q80Z17;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RA Strausberg R;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC049143; AAH49143.1; -  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 3.  
DR SMART; SM00409; IG; 3.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 487 AA; 53019 MW; 31F2C893900A4D80 CRC64;

Query Match 91.8%; Score 90; DB 11; Length 487;

Best Local Similarity 89.5%; Pred.No. 2.4e-06; Indels 0; Gaps 0;

Matches 17; Conservative 2; Mismatches 0;

Qy 1 EIRKSDNYATHVAESVKG 19

Db 69 EIRLSNNYATHVAESVKG 87

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RA Straubeberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; EC055905; AAH55905.1; -.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 52209 MW; 532DED9D46D0AEEED CRC64;

Query Match 58.2%; Score 57; DB 11; Length 479;
Best Local Similarity 57.9%; Pred. No. 0.69;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0

QY 1 EIRLKSDNYATHYAESVKG 19
Db :||| ||| ||| ||| |||
69 QIRKNPYNYETYSVSKG 87

RESULT 4
Q8R3V9 PRELIMINARY; PRT; 469 AA.
ID Q8R3V9 AC Q8R3V9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straubeberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024405; AAH24405.1; -.
DR PIR; B45837; B45837.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein_KW
RP SEQUENCE 469 AA; 51976 MW; 534793F15D050457 CRC64;

Query Match 52.0%; Score 51; DB 11; Length 469;
Best Local Similarity 55.6%; Pred. No. 6.6;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVKG 19
Db :||| ||| ||| ||| |||
70 IIRKANGYTTYSVSKG 87

RESULT 5
Q91XEL PRELIMINARY; PRT; 480 AA.
ID Q91XEL AC Q91XEL;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;

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RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC010798; AAH0798.1; -  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 480 AA; 51936 MW; 20B9234E9F2B41ED CRC64;

Query Match 52.0%; Score 51; DB 11; Length 480;  
 Best Local Similarity 50.0%; Pred. No. 6.8;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 LKSDNYATHYAESVK 19  
 Db 69 ISNGYATHYPSMKG 84

RESULT 6  
 Q9RBZ2 PRELIMINARY; PRT; 361 AA.  
 AC Q9RBZ2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE IS870-like transposase.  
 OS Pseudomonas syringae (pv. glyciniae).  
 OG Plasmid p4180A.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=318;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PG4180;  
 RX MEDLINE=20015131; PubMed=10545263;  
 RA Alarcon-Chaidez F.J., Penaloza-Vazquez A., Ullrich M., Bender C.L.;  
 RT "Characterization of plasmids encoding the phytotoxin coronatine in  
 RT Pseudomonas syringae";  
 RL Plasmid 42:210-220(1999).  
 DR EMBL; AF170066; AAD50977.1; -  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 KW Plasmid.  
 SQ SEQUENCE 361 AA; 41448 MW; 0416AA0203BES427 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 361;  
 Best Local Similarity 52.6%; Pred. No. 11;  
 Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVK 19  
 Db 247 QLHLVDNYATHKPKVK 265

RESULT 7  
 Q8CGQ1 PRELIMINARY; PRT; 754 AA.  
 AC Q8CGQ1;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE ADAM6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ICR; TISSUE=Testis;

RA Choi I., Cho C.;  
 RT Cloning and Characterization of ADAM6.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY158689; AAN77878.1; -  
 DR PIR; PT0706; PT0706.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR006586; ADAM\_cysteine.  
 DR InterPro; IPR001762; Disintegrin.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR001590; Peptidase\_M12B.  
 DR InterPro; IPR002870; Peptidase\_M12B\_N.  
 DR Pfam; PF00200; disintegrin; 1.  
 DR Pfam; PF01562; pep\_M12B\_proep; 1.  
 DR Pfam; PF01421; Reptolysin; 1.  
 DR ProDom; PD000664; Disintegrin; 1.  
 DR SMART; SM00608; ACR; 1.  
 DR SMART; SM00050; DISIN; 1.  
 DR PROSITE; PS50215; ADAM\_MEPPO; 1.  
 DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 SQ SEQUENCE 754 AA; 85089 MW; AF97643DBF05F648 CRC64;

Query Match 48.5%; Score 47.5; DB 11; Length 754;  
 Best Local Similarity 64.7%; Pred. No. 43;  
 Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 3 RLKSDNYATHYAESVK 19  
 Db 204 RLSSKNYATHPA-AIKG 219

RESULT 8  
 Q9RBZ3 PRELIMINARY; PRT; 357 AA.  
 AC Q9RBZ3;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Transposase.  
 OS Pseudomonas syringae (pv. glyciniae).  
 OG Plasmid p4180A.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=318;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20015131; PubMed=10545263;  
 RA Alarcon-Chaidez F.J., Penaloza-Vazquez A., Ullrich M., Bender C.L.;  
 RT "Characterization of plasmids encoding the phytotoxin coronatine in  
 RT Pseudomonas syringae";  
 RL Plasmid 42:210-220(1999).  
 DR EMBL; AF169828; AAD50908.1; -  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0006310; P:DNA recombination; IEA.  
 DR InterPro; IPR001584; Rve.  
 DR Pfam; PF00665; rve; 1.  
 KW Plasmid.  
 SQ SEQUENCE 357 AA; 40339 MW; F21B4028AA5A9BD2 CRC64;

Query Match 48.0%; Score 47; DB 2; Length 357;  
 Best Local Similarity 58.8%; Pred. No. 22;  
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVK 18  
 Db 254 IHLIMVDNYATHKNDKVK 270

RESULT 9  
 Q88ZK4 PRELIMINARY; PRT; 398 AA.  
 ID Q88ZK4

Q882K4;  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Acetate kinase (EC 2.7.2.1).  
 GN ACK2 OR LP 0310.  
 OS Lactobacillus plantarum.  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OX NCBI\_TaxID=1590;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCIMB 8826 / WCFS1;  
 RX MEDLINE=22480296; PubMed=12566566;  
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,  
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,  
 RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,  
 RA Hofer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,  
 RA De Vos W.M., Siezen R.J.;  
 RL "Complete genome sequence of Lactobacillus plantarum WCFS1.";  
 RL EMBL: AL935252; CAB62963.1; -;  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0008776; F:acetate kinase activity; IEA.  
 DR GO: GO:0016740; F:transferase activity; IEA.  
 DR GO: GO:0008152; P:metabolism; IEA.  
 DR GO: GO:0016310; P:phosphorylation; IEA.  
 DR InterPro: IPR000890; Acetate.kin.  
 DR Pfam: PF00871; Acetate.kinase; 1.  
 DR PRINTS: PR00471; ACETATEKINASE.  
 DR PROSITE: PS01075; ACETATE\_KINASE\_1; 1.  
 DR PROSITE: PS01076; ACETATE\_KINASE\_2; 1.  
 KW Kinase; Transferase; Complete proteome.  
 SQ SEQUENCE 398 AA; 43848 MW; 93EE9243DD71C94A CRC64;

Query Match 48.08; Score 47; DB 16; Length 398;  
 Best Local Similarity 69.28; Pred. No. 25;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAE 15  
 |||||  
 DB 71 RLKSDNIVTHLSE 83

RESULT 10  
 Q9FND5  
 ID Q9FND5 PRELIMINARY; PRT; 2910 AA.  
 AC Q9FND5  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Similarity to heat shock protein.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RX MEDLINE=98069011; PubMed=9405937;  
 RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,  
 RA Tabata S.;  
 RL "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned P1 clones."  
 RL DNA Res. 4:291-300(1997).  
 DR EMBL: AB006702; BAB11602.1; -;  
 DR EMBL: AB017062; BAB11602.1; JOINED.  
 DR GO: GO:0003773; F:heat shock protein activity; IEA.  
 KW Heat shock.  
 SQ SEQUENCE 2910 AA; 325351 MW; A8475C3FE1427DF7 CRC64;

Query Match 46.9%; Score 46; DB 10; Length 2910;  
 Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LKSDNYATHYAESVK 18  
 |||||  
 DB 297 LKSDNYATHYAESVK 311

RESULT 11  
 Q8COV3  
 ID Q8COV3 PRELIMINARY; PRT; 703 AA.  
 AC Q8COV3  
 DT 01-MAR-2003 (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Similar to TWDC IV protein (Fragment).  
 GN 4930523C11RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL: AK029742; BAC26593.1; -;  
 DR MGI: 2444636; 4930523C11RIK.  
 DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.  
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro: IPR005886; ADAM\_cysteine.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR006209; EGF like.  
 DR InterPro: IPR001590; Peptidase\_M12B.  
 DR InterPro: IPR002870; Peptidase\_M12B\_N.  
 DR Pfam: PF00200; disintegrin; 1.  
 DR Pfam: PF01562; Pep\_M12B\_propep; 1.  
 DR Pfam: PF01421; Reprolysin; 1.  
 DR ProDom: PD000664; Disintegrin; 1.  
 DR SMART: SMO0608; ACR; 1.  
 DR SMART: SMO0050; DISTRIN; 1.  
 DR PROSITE: PS02115; ADAM\_MEPRO; 1.  
 DR PROSITE: PS02114; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS01186; EGF\_2; 1.  
 FT NON-TER 703  
 SQ SEQUENCE 703 AA; 79325 MW; 1D80313DAECF2F3E CRC64;

Query Match 46.4%; Score 45.5; DB 11; Length 703;  
 Best Local Similarity 58.8%; Pred. No. 85;  
 Matches 10; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 3 RLKSDNYATHYAESVK 19  
 |||||  
 DB 204 RLKSDNYATHYAE-AIK 219

RESULT 12  
 Q9UL71  
 ID Q9UL71 PRELIMINARY; PRT; 121 AA.  
 AC Q9UL71  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 28045CCFA5D50736 CRC64;

Query Match 45.9%; Score 45; DB 4; Length 121;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 LKSDNYATHYAEVKG 19
DB 51 ISGGGGSTYYADSVKG 66

RESULT 13
Q8ID86 PRELIMINARY; PRT; 300 AA.
ID Q8ID86
AC Q8ID86;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN MAL13P1.309
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844509; CAD52741.1; -.
DR GO; GO:0019904; F:protein domain specific binding; IEA.
DR InterPro; IPR000308; 14-3-3.
DR Pfam; PF00244; 14-3-3; 1.
DR PRINTS; PR00305; 1433ZETA.
DR ProDom; PD000600; 14-3-3; 1.
KW Hypothetical protein.
SQ SEQUENCE 300 AA; 35090 MW; B1B678EC606D2B63 CRC64;

Query Match 45.9%; Score 45; DB 5; Length 300;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAEVSK 18
DB 181 EKSMSYSYALHYANKMK 198

RESULT 14
Q8WR61 PRELIMINARY; PRT; 422 AA.
ID Q8WR61
AC Q8WR61;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hemolisin.

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OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE FROM N.A.
RA Denlinger D.L., Lee K.-Y., Horodyski F.M., Valaitis A.P.;
RT "Molecular characterization of the insect immune protein hemolin and
RT the high induction during embryonic diapause in the gypsy moth,
RT Lymantria dispar.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF453868; AAL49765.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR Immunoglobulin domain.
KW SEQUENCE 422 AA; 47234 MW; 0DC52EC4BF142617 CRC64;

Query Match 45.9%; Score 45; DB 5; Length 422;
Best Local Similarity 53.3%; Pred. No. 58;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAE 15
DB 42 EVRFKADNYSTALLE 56

RESULT 15
Q8U651 PRELIMINARY; PRT; 450 AA.
ID Q8U651
AC Q8U651;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nitrolioriacetate monooxygenase, component A.
GN ATU6084 OR AGR_PTI_161.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Gordon D.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liac L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294.2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorillo B., Hinkle G., Gattung S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmle K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294.2323-2328 (2001).
DR EMBL; AE009427; AAL46320.1; -.

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DR EMBL; AE007935; AAK91044.1; --  
DR PIR; AB3238; AB3238.  
DR GO; GO:004821; C:extrachromosomal DNA; IEA.  
DR GO; GO:0005840; C:ribosome; IEA.  
DR GO; GO:0004497; F:monooxygenase activity; IEA.  
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
DR GO; GO:0006412; P:protein biosynthesis; IEA.  
DR InterPro; IPR002103; Bac luciferase.  
DR InterPro; IPR001865; Ribosomal S2.  
DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; 1.  
KW Monooxygenase; Plasmid; Complete proteome.  
SQ SEQUENCE 450 AA; 50163 MW; D3ADB8261D68C026 CRC64;  
Query Match 45.9%; Score 45; DB 16; Length 450;  
Best Local Similarity 58.3%; Pred. No. 62;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 7 DNYATHYAESVK 18  
DB 57 DNYGQHFDTVK 68

Search completed: September 30, 2004, 05:59:36  
Job time : 65.3192 secs

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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 92.7458 Seconds  
(without alignments)  
57.883 Million cell updates/sec.

Title: US-09-674-716B-11

Perfect score: 98  
Sequence: 1 EIRLKSDNYATHAESVKG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_29Jan04.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	98	100.0	19	AAY32258 Light cha
2	98	100.0	123	ABO10742 Variable
3	98	100.0	123	ABR44686 Murine Mu
4	98	100.0	137	AAY32260 Mouse ant
5	98	100.0	286	AB50426 Antibody
6	98	100.0	444	AAY32263 Humanised
7	95	96.9	100	Aae06973 Mouse ger
8	95	95.9	299	AB50425 Mouse ant
9	93	94.9	115	ABR34018 BW 835 VH
10	93	94.9	116	AAY03869 SM3 heavy
11	93	94.9	119	AAW48958 Amino aci
12	93	94.9	119	ABR82775 Hybridoma
13	93	94.9	119	ABR82885 Hybridoma
14	93	94.9	120	AAW01589 Lead bind
15	93	94.9	122	AAY90812 2G3 hybri
16	93	94.9	142	AAW06212 MAB Br-3
17	93	94.9	142	AAW85059 Mouse Br-
18	93	94.9	142	ABU58893 Mouse ant
19	93	94.9	143	AAW0423 Br-3 Heav
20	93	94.9	255	AAU72870 P5-23 sin
21	93	94.9	256	AAU72866 P5-3 sing
22	93	94.9	503	AAU72874 3B10xP5-2
23	93	94.9	570	AAY39451 Antibody
24	91	92.9	19	AB35297 Murine PS
25	91	92.9	151	AAU76696 Mouse hea

26	91	92.9	151	4	AA335292	Aab35292 Murine PS
27	90	91.8	123	6	ABO10743	ABO10743 Consensus
28	90	91.8	123	6	ABR44687	ABR44687 Murine J4
29	88	89.8	160	2	AA370829	Aar70829 MAB 4197X
30	88	89.8	554	2	AA370827	Aar70827 Anti-cata
31	85	86.7	114	2	AA325410	Aar25410 Heavy cha
32	85	86.7	114	2	AA328748	Aar28748 Heavy cha
33	85	86.7	114	3	AAW01588	Aaw01588 Lead bind
34	80.5	82.1	119	3	AAW01588	Aaw01588 Lead bind
35	80	81.6	17	3	AB330033	AB330033 Scaffold
36	79	80.6	19	6	ABO10709	ABO10709 Murine J4
37	79	80.6	19	6	ABR44653	ABR44653 Murine J4
38	79	80.6	116	6	ABO10728	ABO10728 Variable
39	79	80.6	116	6	ABO10734	ABO10734 Consensus
40	79	80.6	116	6	ABO10726	ABO10726 Variable
41	79	80.6	116	6	ABO10733	ABO10733 Variable
42	79	80.6	116	6	ABR44672	ABR44672 Murine J4
43	79	80.6	116	6	ABR44670	ABR44670 Murine J4
44	79	80.6	116	6	ABR44678	ABR44678 Murine J4
45	79	80.6	116	6	ABR44677	ABR44677 Murine J4

## ALIGNMENTS

RESULT 1  
AAY32258  
ID AAY32258 standard; peptide; 19 AA.

XX AC AAY32258;  
XX  
DT 15-FEB-2000 (first entry)  
XX  
DE Light chain CDR H2 of mouse anti-CD23 MAB C11.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
KW monoclonal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;  
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
KW therapy.

XX Mus musculus.

XX WO9558679-A1.

PD 18-NOV-1999.

PF 07-MAY-1999; 99WO-GE001434.

XX 09-MAY-1998; 98GB-00009839.

(GLAX ) GLAXO GROUP LTD.

PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

DR WPI; 2000-053101/04.

DR N-PSDB; AA234743.

PT Cell receptor specific antibodies useful for treating e.g. arthritis,  
diabetes, multiple sclerosis and psoriasis.

XX Claim 1; Page 40; 81pp; English.

PS This sequence represents complementarity determining region 2 (CDR H2)  
of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11  
(see also AAY32263). The invention provides altered antibodies, such as  
chimeric or humanised antibodies, which comprise sufficient of the amino  
acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents

XX Sequence 19 AA;  
 SQ Query Match 100.0%; Score 98; DB 3; Length 19;  
 Best Local Similarity 100.0%; Pred. NO. 2.5e-09; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0;

QY 1 EIRLKSNDYATHYAESVKG 19  
 Db 1 EIRLKSNDYATHYAESVKG 19  
 |||||

RESULT 2  
 ABO10742  
 ID ABO10742 standard; protein; 123 AA.

AC ABO10742;

XX 20-AUG-2003 (first entry)

DE Variable region of murine antibody MuVHIIC.

XX Modified antibody; deimmunised antibody; anti-PSMA antibody;  
 KW prostate specific membrane antigen; immunogenic; CDR; murine;  
 KW complementarity determining region; J591, J415; J533; E99; mouse;  
 KW prostatic disorder; cancerous disorder; genitourinary inflammation;  
 KW prostatitis; benign enlargement; prostatic cancer; testicular cancer;  
 KW solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;  
 KW antiinflammatory; cytostatic; framework region; variable heavy chain;  
 KW variable light chain; VH; VL; variable region.

XX Mus musculus.

XX WO200298897-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-US017068.

XX 01-JUN-2001; 2001US-0295214P.

XX 20-SEP-2001; 2001US-0323585P.

XX 08-MAR-2002; 2002US-0362810P.

XX (CORR ) CORNELL RES FOUND INC.

XX Bander N, Carr FU, Hamilton A;

XX WPI; 2003-156839/15.

XX New modified anti-prostate specific membrane antigen (PSMA)  
 PT immunoglobulins, useful for treating or preventing a prostatic or  
 PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or  
 PT prostatic or testicular cancer.

XX Disclosure; Fig 7C; 254pp; English.

XX The present invention relates to modified (e.g. deimmunised) antibodies  
 CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA  
 CC antibodies are less immunogenic compared to the unmodified anti-PSMA  
 CC antibodies. The modified antibodies comprise complementarity determining  
 CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,

CC J533 or E99), and framework sequences that are less immunogenic in humans  
 CC (e.g. less antigenic than the murine frameworks in which a murine CDR  
 CC naturally occurs). The modified antibodies bind with PSMA, preferably  
 CC human PSMA, with high affinity and specificity. The anti-PSMA antibodies  
 CC are useful for treating or preventing a prostatic or cancerous disorder,  
 CC e.g. genitourinary inflammation, prostatitis, benign enlargement,  
 CC prostatic cancer or testicular cancer, or solid tumours, soft tissue  
 CC tumours or metastatic lesions, and its associated pain. The present  
 CC sequence represents a variable region from a murine antibody

XX Sequence 123 AA;

Query Match 100.0%; Score 98; DB 6; Length 123;

Best Local Similarity 100.0%; Pred. NO. 2.3e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDYATHYAESVKG 19

Db 50 EIRLKSNDYATHYAESVKG 68  
 |||||

RESULT 3

ABR44686

ID ABR44686 standard; protein; 123 AA.

XX ABR44686;

XX 25-JUL-2003 (first entry)

XX Murine MuVHIIC amino acid sequence SEQ ID NO:69.

XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;  
 KW prostate specific membrane antigen; antipsoriatic; antiarthritic;  
 KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;  
 KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;  
 KW neoplastic disorder.

XX Mus musculus.

XX WO2003024388-A2.

XX 27-MAR-2003.

XX 30-MAY-2002; 2002WO-US017204.

XX 20-SEP-2001; 2001US-0324100P.

XX 08-MAR-2002; 2002US-0362612P.

XX (CORR ) CORNELL RES FOUND INC.

XX Bander N;

XX WPI; 2003-313319/30.

XX Ablating/killing aberrant prostate specific membrane antigen-expressing  
 PT cells for treating skin disorders, by contacting the cell with an  
 PT antibody that binds to the extracellular domain of prostate specific  
 PT membrane antigen.

XX Disclosure; Page 37; 225pp; English.

XX The present invention describes a method (M1) for ablating or killing an  
 CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g.  
 CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a  
 CC vascular endothelial cell proximate to the cell, with an antibody (or its  
 CC antigen-binding fragment), which binds specifically to the extracellular  
 CC domain of PSMA in an amount sufficient to ablate or kill the cell. The  
 CC antibodies have antipsoriatic, antiarthritic, dermatological, cytostatic,  
 CC antiinflammatory and antiallergic activities, and can be used in  
 CC vaccines. M1 is useful for treating a skin disorder in a subject, by  
 CC administering to the subject, an amount of an antibody which binds  
 CC specifically to the extracellular domain of PSMA (the subject is a  
 CC mammal, preferably human and is having, or at risk of, a skin disorder).

CC The skin disorder is a dermal or an epidermal disorder, and is selected  
 CC from psoriasis (preferably chronic stationary psoriasis, psoriasis  
 CC vulgaris, eruptive (glutinate) psoriasis, psoriatic erythroderma,  
 CC generalised pustular psoriasis (Von Zumbusch), annular pustular  
 CC psoriasis, and localised pustular psoriasis), psoriatic arthritis,  
 CC exfoliative dermatitis, pityriasis rubra pilaris, pityriasis roseacea,  
 CC parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus,  
 CC ichthyosiform dermatosis, keratoderma, dermatosis, and prokeratosis,  
 CC preferably psoriasis. MI is useful for treating a skin disorder such as  
 CC an inflammatory or neoplastic disorder of the epidermis or dermis,  
 CC preferably an epidermal precancerous or cancerous lesion. MI is also  
 CC useful to treat or prevent disorders involving aberrant activity of PSMA-  
 CC expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837  
 CC and ABR44613 to ABR44733 represent sequences used in the exemplification  
 CC of the present invention

XX SQ Sequence 123 AA;

Query Match 100.0%; Score 98; DB 6; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-08;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
 |||||  
 DB 50 EIRLKSNDNYATHYAESVKG 68

RESULT 4

AAI32260  
 ID AAY32260 standard; protein; 137 AA.

XX AC AAY32260;

XX DT 15-FEB-2000 (first entry)

DE Mouse anti-CD23 Mab C11 heavy chain variable region.

XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;  
 XX monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.

XX OS Mus musculus.

XX FH Key Location/Qualifiers  
 FT Region 59..63 /note= "CDR H1"  
 FT Region 78..96 /note= "CDR H2"  
 FT Region 129..131 /note= "CDR H3"

XX PN WO958679-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001434.

XX PR 09-MAY-1998; 98GB-00009839.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX DR WPI; 2000-053101/04.

XX DR N-PSDB; AA234745.

XX

PT Cell receptor specific antibodies useful for treating e.g. arthritis,  
 XX diabetes, multiple sclerosis and psoriasis.

PS Claim 8; Fig 1; 81pp; English.

XX This sequence represents the heavy chain variable region (VH) of murine  
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides  
 CC altered antibodies, such as chimeric or humanised antibodies (see  
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions (see AAY32254-59) to render them capable of binding to the CD23  
 CC type II molecule expressed on haematopoietic cells. The antibodies are  
 CC used to block soluble CD23 formation in human therapy, for the treatment  
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents

XX SQ Sequence 137 AA;

Query Match 100.0%; Score 98; DB 3; Length 137;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
 |||||  
 DB 78 EIRLKSNDNYATHYAESVKG 96

RESULT 5

AAI50426  
 ID AAB50426 standard; protein; 286 AA.

XX AC AAB50426;

XX DT 13-MAR-2001 (first entry)

DE Antibody 33F12 catalytic fragment.

XX Antibody 33F12; ketone compound; antitumour; cytotoxic;  
 KW targeted drug delivery.

XX OS Unidentified.

XX PN WO200071556-A1.

XX PD 30-NOV-2000.

XX PF 24-MAY-2000; 2000WO-US014366.

XX PR 25-MAY-1999; 99US-00318661.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Shabat D, Rader C, List B, Lerner RA;

XX DR WPI; 2001-061339/07.

XX DR N-PSDB; AAC90472.

XX PT New ketone compounds containing active agents useful as carriers for e.g.  
 FT antitumor agents, antibiotics or fluorescent molecules.

XX PS Disclosure; Fig 10; 45pp; English.

XX The present sequence may be used in the activation of new ketone prodru  
 CC compounds containing active agents. The ketone derivatives are useful as  
 CC carriers for antitumor agents such as cytotoxic agents, where the  
 CC antitumor agent is a microtubule stabilising agent such as paclitaxel,

CC epothilone or its therapeutically active analogue or an anthracycline  
 CC antibiotic such as doxorubicin or its therapeutically active analogue.  
 CC The ketone derivatives are useful for targeted drug delivery. The  
 CC inactive molecules in the ketone compounds are converted to active  
 CC molecules by retro-Michael reaction. The antibody has bifunctional  
 CC activity and specifically immunoreacts with cell surface antigen of a  
 CC target cell. The active ingredients can be mixed effectively with  
 CC excipients as per desired amount along with the buffering agent to  
 CC enhance the effectiveness and activity of the compound  
 XX  
 XX

SQ Sequence 286 AA;

Query Match 100.0%; Score 98; DB 4; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-08;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
 |||||  
 Db 203 EIRLKSNDNYATHYAESVKG 221

RESULT 6  
 AAY32263  
 ID AAY32263 standard; protein; 444 AA.

AC AAY32263;

DT 15-FEB-2000 (first entry)

XX Humanised anti-CD23 Mab C11 heavy chain.

XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.

XX Homo sapiens.  
 OS Synthetic.

Key	Location/Qualifiers
FT Region	1..30 /note="framework region 1"
FT Region	31..35 /note="CDR 1"
FT Region	36..49 /note="framework region 2"
FT Region	50..68 /note="CDR 2"
FT Region	69..100 /note="framework region 3"
FT Region	101..103 /note="CDR 3"
FT Region	104..111 /note="framework region 4"
FT Region	112..444 /note="constant region"

XX WO9558679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX ) GLAXO GROUP LTD.

PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX N-PSDB; AAZ34748.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.

XX Claim 9; Fig 4; 81pp; English.

XX This amino acid sequence represents the heavy chain of humanised anti-  
 CC CD23 (FCERII) monoclonal antibody C11, composed of a human framework  
 CC (HSIGKVII) and the heavy chain complementarity determining regions (see  
 CC AAY32257-59) of murine antibody C11. The DNA was constructed by splice  
 CC overlap PCR. The invention provides altered antibodies, such as chimeric  
 CC or humanised antibodies, which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions to render them capable of binding to the CD23 type II molecule  
 CC expressed on haematopoietic cells. The antibodies are used to block  
 CC soluble CD23 formation in human therapy, for the treatment of arthritis,  
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,  
 CC diabetes, uveitis, dermatitis, psoriasis, uterine cancer, nephrotic syndrome,  
 CC glomerulonephritis, inflammatory bowel disease, ulcerative colitis,  
 CC Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents  
 XX

SQ Sequence 444 AA;

Query Match 100.0%; Score 98; DB 3; Length 444;

Best Local Similarity 100.0%; Pred. No. 1e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19

|||||

Db 50 EIRLKSNDNYATHYAESVKG 68

RESULT 7

AAE06973

ID AAE06973 standard; protein; 100 AA.

XX AAE06973;

DT 16-OCT-2001 (first entry)

XX Mouse germline heavy chain variable (VH) region, V(H)22.1.

XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; VH; heavy chain variable region.

XX Mus sp.

XX WO200157226-A1.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US003537.

XX 03-FEB-2000; 2000US-00497625.

XX (MILL-) MILLENNIUM PHARM INC.



PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
 DR WPI; 2001-489888/53.  
 XX  
 XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
 PT disorder in a patient, comprises a binding specificity for CCR2, and a  
 PT non-human antigen binding region and human immunoglobulin.  
 XX  
 XX Disclosure; Page 152-153; 183pp; English.  
 XX  
 CC The patent discloses a humanised antibody or its antigen-binding  
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
 CC comprising an antigen binding region of non-human origin and at least a  
 CC portion of an immunoglobulin of human origin. The humanised antibodies  
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They  
 CC are useful for inhibiting or treating HIV infection. The proteins of the  
 CC invention are useful for inhibiting leukocyte trafficking. For treating  
 CC CCR2-mediated disorders such as inflammatory disorder, autoimmune  
 CC disorders such as rheumatoid arthritis and multiple sclerosis,  
 CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They  
 CC are useful in therapy or diagnosis, and in the manufacture of a  
 CC medicament for treating CCR-2 mediated disease. They are also useful for  
 CC treating allergy, anaphylaxis, malignancy, chronic and acute  
 CC inflammation, histamine and IgE-mediated allergic reaction, shock,  
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
 CC associated with vascular intervention, including angioplasty and/or stent  
 CC placement in a mammal. Humanised antibodies are also useful for  
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated  
 CC with vascular intervention. The present sequence is mouse germline heavy  
 CC chain variable (VH) region, V(H)22.1  
 XX  
 XX Sequence 100 AA;  
 SQ

Query Match 96.9%; Score 95; DB 4; Length 100;  
 Best Local Similarity 94.7%; Pred. No. 5.6e-08;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19  
 |||||  
 DQ 50 QIRKSDNYATHYAESVKG 68  
 |||||

RESULT 8  
 AAB50425  
 ID AAB50425 standard; protein; 299 AA.  
 AC AAB50425;  
 XX  
 XX 13-MAR-2001 (first entry)  
 DE Mouse antibody 38C2 catalytic fragment.  
 XX  
 KW Mouse; antibody 38C2; ketone compound; antitumour; cytotoxic;  
 KW targeted drug delivery.  
 XX  
 OS Mus sp.  
 XX  
 XX WO200071556-A1.  
 PN  
 XX  
 XX 30-NOV-2000.  
 PD  
 XX  
 XX 24-MAY-2000; 2000WO-US014366.  
 PF  
 XX  
 XX 25-MAY-1999; 99US-00318661.  
 PR  
 XX  
 XX (SCRI ) SCRIPPS RES INST.  
 PA  
 XX  
 XX Barbas CF, Shabat D, Rader C, List B, Lerner RA;  
 PI WPI; 2001-061339/07.  
 DR N-PSDB; AAC90471.  
 DR

XX New ketone compounds containing active agents useful as carriers for e.g.  
 PT antitumor agents, antibiotics or fluorescent molecules.  
 PT  
 XX Disclosure; Fig 9; 45pp; English.  
 XX  
 XX The present sequence may be used in the activation of new ketone prodnug  
 CC compounds containing active agents. The ketone derivatives are useful as  
 CC carriers for antitumour agents such as cytotoxic agents, where the  
 CC antitumour agent is a microtubule stabilising agent such as paclitaxel,  
 CC epothilone or its therapeutically active analogue or an anthracycline  
 CC antibiotic such as doxorubicin or its therapeutically active analogue.  
 CC The ketone derivatives are useful for targeted drug delivery. The  
 CC inactive molecules in the ketone compounds are converted to active  
 CC molecules by retro-Michael reaction. The antibody has bifunctional  
 CC activity and specifically immunoreacts with cell surface antigen of a  
 CC target cell. The active ingredients can be mixed effectively with  
 CC excipients as per desired amount along with the buffering agent to  
 CC enhance the effectiveness and activity of the compound  
 XX  
 XX Sequence 299 AA;  
 SQ

Query Match 96.9%; Score 95; DB 4; Length 299;  
 Best Local Similarity 94.7%; Pred. No. 2.1e-07;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19  
 |||||  
 DQ 205 EIRKSDNYATHYAESVKG 223  
 |||||

RESULT 9  
 AAR34018  
 ID AAR34018 standard; protein; 115 AA.  
 XX  
 AC AAR34018;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 02-AUG-1993 (first entry)  
 XX  
 XX BW 835 VH.  
 DE  
 XX Monoclonal antibody; MAB; hybridoma; lung; adenocarcinoma; mammary;  
 KW ovary; prostate; polymorphic epithelial mucin; PEM.  
 KW  
 OS Synthetic.  
 XX  
 XX DE4133791-A1.  
 PN  
 XX  
 XX 15-APR-1993.  
 PD  
 XX  
 XX 11-OCT-1991; 91DE-04133791.  
 PF  
 XX  
 XX 11-OCT-1991; 91DE-04133791.  
 PR  
 XX  
 XX (BEHW ) BEHRINGERWERKE AG.  
 PA  
 XX  
 XX Bosslet K, Pfeleiderer P, Seemann G;  
 PI WPI; 1993-127068/16.  
 DR N-PSDB; AAQ40046.  
 DR  
 XX  
 XX New monoclonal antibody BW835 specific for tumour antigens - useful for  
 PT diagnosis and treatment of tumours affecting the breasts, ovaries,  
 PT prostate and lungs.  
 XX  
 XX Disclosure; Fig 1a; 24pp; German.  
 PS  
 XX Monoclonal antibody BW 835 is produced by hybridoma cell line BW 835. The  
 CC antibody strongly reacts with lung adenocarcinomas and human mammary-  
 CC ovary- and prostate carcinomas. It additionally reacts with polymorphic  
 CC epithelial mucin (PEM) but does not react with normal human tissue.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC

```

XX SQ Sequence 115 AA;
Query Match 94.9%; Score 93; DB 2; Length 115;
Best Local Similarity 94.7%; Pred. No. 1.4e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
Db 46 EIRLKSNVATHYAESVKG 64

RESULT 10
AAV03869
ID RAY03869 standard; protein; 116 AA.
XX AC AAY03869;
XX DT 16-JUN-1999 (first entry)
XX DE SM3 heavy chain variable region.
XX KW SM3 antibody; epitope; mimic; crystal; tumour; MUC1 epitope; allergy;
XX KW immune response; arthritis; multiple sclerosis; asthma; diabetes;
XX KW inflammatory disorder; transplant rejection; graft versus host disease.
XX OS Unidentified.
XX PN WO9910379-AL.
XX PD 04-MAR-1999.
XX PF 24-AUG-1998; 98WO-GB002542.
XX PR 22-AUG-1997; 97GB-00017946.
XX PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX PI Freemont PS, Snary D, Sternberg MJE, Bates PA, Dokurno P;
XX DR WPI; 1999-204650/17.
XX DR N-PSDB; AAX31971.
XX PT New SM3 antibody crystal structures - used to develop agents for treating
XX PT e.g. tumors, autoimmune disorders, allergies, inflammatory disorders or
XX PT transplant rejection.
XX PS Disclosure; Page 279-280; 316pp; English.
XX CC The invention relates to a process for preparing a crystal using cadmium.
XX CC Structure factors or structural coordinates obtained from the crystal of
XX CC SM3 antibody bound to an epitope can be used to design mimics of the
XX CC antibody or the epitope. The crystals comprise at least an epitope
XX CC binding fragment of the SM3 antibody bound to a peptide recognised by the
XX CC epitope binding site of SM3. The products and methods can be used to
XX CC develop agents for the detection of tumour cells and for therapy against
XX CC tumours. MUC1 epitope mimics can also be used to prevent or decrease an
XX CC immune response, e.g. in the therapy of diseases caused by autoimmune
XX CC responses (such as arthritis, multiple sclerosis, asthma or diabetes),
XX CC allergies, inflammatory disorders or transplant rejections such as graft
XX CC versus host disease. The present sequence represents the amino acid
XX CC sequence of a heavy chain variable region of SM3 antibody
XX SQ Sequence 116 AA;
Query Match 94.9%; Score 93; DB 2; Length 116;
Best Local Similarity 94.7%; Pred. No. 1.4e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
Db 50 EIRLKSNVATHYAESVKG 68

RESULT 11
AAW46958
ID AAW46958 standard; protein; 119 AA.
XX AC AAW46958;
XX DT 06-JUL-1998 (first entry)
XX DE Amino acid sequence of a synthetic branched mucin type glycolipid.
XX KW Branched mucin type glycolipid; V region; heavy chain; antibody;
XX KW cancer treatment; diagnosis.
XX OS Synthetic.
XX PN JPI0084963-A.
XX PD 07-APR-1998.
XX PF 12-SEP-1996; 96JP-00241725.
XX PR 12-SEP-1996; 96JP-00241725.
XX PA (TOYJ ) TOSOH CORP.
XX DR WPI; 1998-254850/24.
XX DR N-PSDB; AAV22331.
XX PT Recognising branched mucin type synthetic glycolipid - using gene
XX PT fragment of an antibody, useful in cancer treatment and diagnosis.
XX PS Disclosure; Page 4-5; 6pp; Japanese.
XX CC The present sequence represents a branched mucin type synthetic
XX CC glycolipid. A gene fragment encoding the V region of the heavy chain of
XX CC an antibody recognising the present protein is claimed. The antibody gene
XX CC fragment is useful for the development of cancer treatments and
XX CC diagnosing agents
XX SQ Sequence 119 AA;
Query Match 94.9%; Score 93; DB 2; Length 119;
Best Local Similarity 94.7%; Pred. No. 1.5e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
Db 50 EIRLKSNVATHYAESVKG 68

RESULT 12
ABR82775
ID ABR82775 standard; protein; 119 AA.
XX AC ABR82775;
XX DT 18-DEC-2003 (first entry)
XX DE Hybridoma HB22-23 anti-CD22 MAB heavy chain Vh-D-Jh junction sequence.
XX KW CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-23.
XX OS Homo sapiens.
XX PN WO2003072036-A2.
XX PD 04-SEP-2003.
XX PF 20-FEB-2003; 2003WO-US005323.
XX PR 21-FEB-2002; 2002US-0359419P.
XX PR 21-OCT-2002; 2002US-0420472P.

```

XX (UYDU-) UNIV DUKE  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Tedder T, Tuscano J;  
XX  
DR WPI; 2003-712652/67.  
DR N-PSDB; ACF36425.  
XX  
XX Treating a human patient diagnosed with a B-cell malignancy by  
PT administering a blocking anti-CD22 monoclonal antibody binding to the  
PT first two Ig-like domains of native human CD22 (hCD22).  
XX  
XX Claim 31; Fig 14; 72pp; English.  
XX  
XX The invention relates to treating a human patient diagnosed with a B-cell  
CC malignancy. The method involves (a) administering to the human patient a  
CC blocking anti-CD22 monoclonal antibody binding to the first two Ig-like  
CC domains, or to an epitope within the first two Ig-like domains of native  
CC human CD22 (hCD22) (ABR82771) and (b) monitoring the response of the  
CC malignancy to the treatment. The method is useful for treating a human  
CC patient diagnosed with a B-cell malignancy comprising Hodgkin's lymphoma,  
CC Burkitt's lymphoma, multiple myeloma, chronic lymphocytic leukemia, hairy  
CC cell leukemia or polymphocytic leukemia. The present sequence represents  
CC the amino acid sequence for heavy chain Vh-D-Jh junction for anti-CD22  
CC antibody from hybridoma HB22-23  
XX  
XX Sequence 119 AA;  
CC  
CC Query Match 94.9%; Score 93; DB 7; Length 119;  
CC Best Local Similarity 94.7%; Pred. No. 1.5e-07;  
CC Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 EIRLKSNDNYATHYAESVKG 19  
XX |||||:|||||||  
XX Db 50 EIRLKSNNYATHYAESVKG 68  
XX  
XX  
XX RESULT 13  
XX ABR82885  
XX ID ABR82885 standard; protein; 119 AA.  
XX AC ABR82885;  
XX  
XX DT 18-DEC-2003 (first entry)  
XX  
XX DE Hybridoma HB22-23 anti-CD22 MAb heavy chain (VH) fragment.  
XX  
XX CD22; autoimmune disease; anti-CD22 antibody; immunosuppressive;  
XX cytostatic; nephrotropic; dermatological; antiinflammatory; anti-ulcer;  
XX antirheumatic; antiarthritic; antipsoriatic; thyromimetic; antianemic;  
XX antidiabetic; antiallergic; gene therapy; HB22-23.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO2003072736-A2.  
XX  
XX PD 04-SEP-2003.  
XX  
XX PF 21-FEB-2003; 2003WO-US005549.  
XX  
XX PR 21-FEB-2002; 2002US-0359419P.  
XX PR 21-OCT-2002; 2002US-0420472P.  
XX  
XX PA (UYDU-) UNIV DUKE.  
XX  
XX PI Tedder TF;  
XX  
XX DR WPI; 2003-721765/68.  
XX DR N-PSDB; ACF36493.  
XX  
XX Treating an autoimmune disease or a B-cell malignancy in a human patient  
PT comprises administering an amount of an anti-CD22 monoclonal antibody to

PT the patient and monitoring the response of the disease to the treatment.  
XX  
XX Claim 1; Fig 14; 69pp; English.  
XX  
XX The invention relates to treating a human patient diagnosed with an  
CC autoimmune disease. The method involves administering to the patient an  
CC amount of a blocking anti-CD22 monoclonal antibody and monitoring the  
CC response of the autoimmune disease to the treatment. The method is useful  
CC in treating autoimmune diseases (e.g. glomerulonephritis, systemic lupus  
CC erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis,  
CC Hashimoto's thyroiditis, autoimmune haemolytic anemias, diabetes or  
CC allergies) or B-cell malignancies (e.g. lymphomas or leukemias). The  
CC present sequence represents the amino acid sequence for heavy chain Vh-D-  
CC Jh junction for anti-CD22 antibody from hybridoma HB22-23  
XX  
XX Sequence 119 AA;  
CC  
CC Query Match 94.9%; Score 93; DB 7; Length 119;  
CC Best Local Similarity 94.7%; Pred. No. 1.5e-07;  
CC Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 EIRLKSNDNYATHYAESVKG 19  
XX |||||:|||||||  
XX Db 50 EIRLKSNNYATHYAESVKG 68  
XX  
XX  
XX RESULT 14  
XX AAW01589  
XX ID AAW01589 standard; protein; 120 AA.  
XX AC AAW01589;  
XX  
XX DT 22-AUG-1997 (first entry)  
XX  
XX DE Lead binding MAb 4E8 heavy chain variable region.  
XX  
XX KM Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;  
XX KW pharmaceutical; health care; skin treatment; pesticide; herbicide;  
XX heavy metal.  
XX  
XX OS Mus musculus.  
XX  
XX PN WO9639518-A1.  
XX  
XX PD 12-DEC-1996.  
XX  
XX PF 05-JUN-1996; 96WO-US009258.  
XX  
XX PR 05-JUN-1995; 95US-00462798.  
XX PR 10-OCT-1995; 95US-00541373.  
XX  
XX PA (BION-) BIONEERASKA INC.  
XX  
XX PI Wylie DE, Lopez O, Murray PJ;  
XX  
XX DR WPI; 1997-043140/04.  
XX DR N-PSDB; AAT58263.  
XX  
XX PT DNA encoding heavy metal binding polypeptide sequences - used for  
XX detecting, removing, adding or neutralising heavy metals, such as lead  
XX cations.  
XX  
XX PS Claim 12; Page 81; 125pp; English.  
XX  
XX CC The present sequence represents the heavy chain variable region for  
XX monoclonal antibody (MAb) 4E8, which immunoreacts with a lead cation. The  
XX sequence was derived from RNA isolated from mouse hybridoma cells. The  
XX protein can be used for binding heavy metals, such as lead cations. It  
XX can be used for detecting, removing, adding or neutralising the heavy  
XX metals in biological and inanimate systems. It can be used in e.g.  
XX aqueous liquid systems, in biological or environmental systems or in such  
XX compositions as perfumes, cosmetics, pharmaceuticals, health care  
XX products, skin treatment products, pesticides, herbicides, solvents used

CC in the production of semi-conductor and integrated circuit components and  
CC production materials for electronic components. The products can provide  
CC for applications involving minute amounts of specific heavy metals  
XX  
SQ Sequence 120 AA;

Query Match 94.9%; Score 93; DB 2; Length 120;  
Best Local Similarity 94.7%; Pred. NO. 1.5e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIRLSDNYATHYAESVKG 19  
DB 50 EIRLSDNYATHYAESVKG 68

RESULT 15  
AAY90812  
ID AAY90812 standard; protein; 122 AA.  
XX  
AC AAY90812;  
XX  
DT 29-AUG-2000 (first entry)  
XX  
DE 2G3 hybridoma VH domain SEQ ID NO:2.  
XX  
KW Antigen binding site; immunoglobulin; cancer antigen; immunological;  
KW antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;  
KW specific binding assay; affinity purification; drug targeting;  
KW toxin targeting; imaging; genetic; therapeutic.  
XX  
OS Homo sapiens.  
XX  
PN US6054561-A.  
XX  
PD 25-APR-2000.  
XX  
PE 07-JUN-1995; 95US-00483749.  
XX  
PR 08-FEB-1984; 84US-00577976.  
PR 11-JAN-1985; 85US-00690750.  
PR 21-MAR-1986; 86US-00842476.  
PR 08-MAY-1988; 88US-00190778.  
PR 11-AUG-1994; 94US-00288981.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Ring DB;  
XX  
DR WPI; 2000-338508/29.  
DR N-PSDB; AAA38896.  
XX  
PT Monoclonal antibody capable of binding to human breast cancer antigen  
PT useful for affinity purification, drug or toxin targeting, imaging, and  
PT treating cancer.  
XX  
PS Disclosure; Fig 1; 57pp; English.  
XX  
CC The present invention describes a monoclonal antibody (Mab) (I) that  
CC binds to a human breast cancer antigen that is also bound by Mab 454C11  
CC and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also  
CC described is a hybridoma that produces (I). (I) is useful in specific  
CC binding assays, affinity purification, drug or toxin targeting, imaging,  
CC and genetic or immunological therapeutics for various cancers. The  
CC present sequence represents a VH domain derived from a 2G3 hybridoma,  
CC which is used in the exemplification of the present invention  
XX  
SQ Sequence 122 AA;

Query Match 94.9%; Score 93; DB 3; Length 122;  
Best Local Similarity 94.7%; Pred. NO. 1.5e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIRLSDNYATHYAESVKG 19

Db 50 EIRLSDNYATHYAESVKG 68  
Search completed: September 30, 2004, 06:06:22  
Job time : 94.7458 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:01:30 ; Search time 318.814 Seconds  
(without alignments)  
19.178 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLKSDNYATHAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	123	14	US-10-160-506-69
2	98	100.0	123	16	US-10-449-379-69
3	98	100.0	123	16	US-10-688-015-69
4	98	100.0	285	9	US-09-883-758-4
5	95	96.9	100	9	US-09-840-459-36
6	95	96.9	100	16	US-10-766-773-36
7	95	96.9	100	16	US-10-766-610-36
8	95	96.9	100	16	US-10-733-563-36
9	95	96.9	298	9	US-09-883-758-2
10	93	94.9	119	12	US-10-372-481-15
11	93	94.9	119	15	US-10-371-797-15
12	93	94.9	255	12	US-10-239-656-69
13	93	94.9	256	12	US-10-239-656-61
14	93	94.9	503	12	US-10-239-656-77
15	91	92.9	151	9	US-09-564-329A-15

16	91	92.9	151	9	US-09-855-153-15	Sequence 15, Appl
17	91	92.9	151	9	US-09-854-811-15	Sequence 15, Appl
18	91	92.9	151	9	US-09-934-773-15	Sequence 15, Appl
19	91	92.9	151	9	US-09-963-620-15	Sequence 15, Appl
20	91	92.9	151	10	US-09-855-632-15	Sequence 15, Appl
21	91	92.9	151	14	US-10-225-784-15	Sequence 15, Appl
22	91	92.9	151	14	US-10-224-720-15	Sequence 15, Appl
23	91	92.9	151	14	US-10-225-779-15	Sequence 15, Appl
24	91	92.9	151	15	US-10-374-381-15	Sequence 15, Appl
25	91	92.9	151	15	US-10-446-542-15	Sequence 15, Appl
26	90	91.8	123	14	US-10-160-506-70	Sequence 70, Appl
27	90	91.8	123	16	US-10-449-379-70	Sequence 70, Appl
28	90	91.8	123	16	US-10-688-015-70	Sequence 70, Appl
29	85	86.7	114	14	US-10-422-049-11	Sequence 11, Appl
30	85	86.7	114	14	US-10-422-049-12	Sequence 12, Appl
31	82	83.7	117	14	US-10-277-471A-7	Sequence 7, Appl
32	82	83.7	262	14	US-10-277-471A-5	Sequence 5, Appl
33	79	80.6	19	14	US-10-160-506-30	Sequence 30, Appl
34	79	80.6	19	16	US-10-449-379-30	Sequence 30, Appl
35	79	80.6	19	16	US-10-688-015-30	Sequence 30, Appl
36	79	80.6	116	14	US-10-160-506-47	Sequence 47, Appl
37	79	80.6	116	14	US-10-160-506-49	Sequence 49, Appl
38	79	80.6	116	14	US-10-160-506-60	Sequence 60, Appl
39	79	80.6	116	14	US-10-160-506-61	Sequence 61, Appl
40	79	80.6	116	16	US-10-449-379-47	Sequence 47, Appl
41	79	80.6	116	16	US-10-449-379-49	Sequence 49, Appl
42	79	80.6	116	16	US-10-449-379-60	Sequence 60, Appl
43	79	80.6	116	16	US-10-449-379-61	Sequence 61, Appl
44	79	80.6	116	16	US-10-688-015-47	Sequence 47, Appl
45	79	80.6	116	16	US-10-688-015-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1  
US-10-160-506-69  
; Sequence 69, Application US/10160506  
; Publication No. US20030161832A1  
; GENERAL INFORMATION:  
; APPLICANT: Bander, Neil H.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING  
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR  
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN  
; FILE REFERENCE: 10448-162001  
; CURRENT APPLICATION NUMBER: US/10/160,506  
; CURRENT FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/324,100  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/362,612  
; PRIOR FILING DATE: 2002-03-08  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-160-506-69

Query Match 100.0%; Score 98; DB 14; Length 123;  
Best Local Similarity 100.0%; Pred No. 9,3e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLKSDNYATHAESVKG 19  
|||||  
Db 50 EIRLKSDNYATHAESVKG 68

RESULT 2  
US-10-449-379-69  
; Sequence 69, Application US/10449379  
; Publication No. US20040120958A1  
; GENERAL INFORMATION:

; APPLICANT: Bander, Neil H.  
; TITLE OF INVENTION: MEMBRANE ANTIBODIES TO PROSTATE-SPECIFIC  
; FILE REFERENCE: 10448-163002  
; CURRENT APPLICATION NUMBER: US/10/449,379  
; PRIOR FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: 10/160,505  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/323,585  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/362,810  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/295,214  
; PRIOR FILING DATE: 2001-06-01  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-449-379-69

Query Match 100.0%; Score 98; DB 16; Length 123;  
Best Local Similarity 100.0%; Pred. No. 9.3e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19  
Db 50 EIRKSDNYATHYAESVKG 69

RESULT 3  
US-10-688-015-69  
; Sequence 62, Application US/10688015  
; Publication No. US20040136998A1  
; GENERAL INFORMATION:  
; APPLICANT: Bander, Neil H.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING  
; FILE REFERENCE: 10448-196001  
; CURRENT APPLICATION NUMBER: US/10/688,015  
; PRIOR FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/422,396  
; PRIOR FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-688-015-69

Query Match 100.0%; Score 98; DB 16; Length 123;  
Best Local Similarity 100.0%; Pred. No. 9.3e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19  
Db 50 EIRKSDNYATHYAESVKG 69

RESULT 4  
US-09-883-758-4  
; Sequence 4, Application US/09883758  
; Patent No. US20020058804A1  
; GENERAL INFORMATION:  
; APPLICANT: Barbas III, Carlos F.  
; APPLICANT: Shabat, Doron  
; APPLICANT: Rader, Christoph  
; APPLICANT: List, Benjamin  
; APPLICANT: Leiner, Richard A.  
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES

; FILE REFERENCE: PLF0011S  
; CURRENT APPLICATION NUMBER: US/09/883,758  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US/09/318,661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 285  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
; OTHER INFORMATION: residue sequence of catalytic fragment  
US-09-883-758-4

Query Match 100.0%; Score 98; DB 9; Length 285;  
Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19  
Db 203 EIRKSDNYATHYAESVKG 221

RESULT 5  
US-09-840-459-36  
; Sequence 36, Application US/09840459  
; Patent No. US20020150576A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 36  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-840-459-36

Query Match 96.9%; Score 95; DB 9; Length 100;  
Best Local Similarity 94.7%; Pred. No. 2.2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19  
Db 50 EIRKSDNYATHYAESVKG 68

RESULT 6  
US-10-766-773-36  
; Sequence 36, Application US/10766773  
; Publication No. US20040126851A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-028  
CURRENT APPLICATION NUMBER: US/10/766,773  
CURRENT FILING DATE: 2004-01-27  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 36  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-766-773-36

Query Match 96.9%; Score 95; DB 16; Length 100;  
Best Local Similarity 94.7%; Pred. No. 2.2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
:|||||  
Db 50 QIRLKSDNYATHYAESVKG 68

RESULT 7  
US-10-766-610-36  
Sequence 36, Application US/10766610  
Publication No. US20040132980A1  
GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-029  
CURRENT APPLICATION NUMBER: US/10/766,610  
CURRENT FILING DATE: 2004-01-27  
PRIOR APPLICATION NUMBER: 09/840,459  
PRIOR FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 36  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-766-610-36

Query Match 96.9%; Score 95; DB 16; Length 100;  
Best Local Similarity 94.7%; Pred. No. 2.2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
:|||||  
Db 50 QIRLKSDNYATHYAESVKG 68

RESULT 8  
US-10-733-563-36  
Sequence 36, Application US/10733563  
Publication No. US20040151721A1  
GENERAL INFORMATION:  
APPLICANT: O'Keefe, Theresa  
APPLICANT: Ponath, Paul  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREOF  
FILE REFERENCE: 10448-213001  
CURRENT APPLICATION NUMBER: US/10/733,563  
CURRENT FILING DATE: 2003-12-10  
PRIOR APPLICATION NUMBER: US 10/272,899  
PRIOR FILING DATE: 2002-10-17  
PRIOR APPLICATION NUMBER: US 60/392,364  
PRIOR FILING DATE: 2002-06-26  
PRIOR APPLICATION NUMBER: US 60/350,166  
PRIOR FILING DATE: 2001-10-19  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 36  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-733-563-36

Query Match 96.9%; Score 95; DB 16; Length 100;  
Best Local Similarity 94.7%; Pred. No. 2.2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
:|||||  
Db 50 QIRLKSDNYATHYAESVKG 68

RESULT 9  
US-09-883-758-2  
Sequence 2, Application US/09883758  
Patent No. US20020058804A1  
GENERAL INFORMATION:  
APPLICANT: Barbas III, Carlos F.  
APPLICANT: Shabat, Doron  
APPLICANT: Rader, Christoph  
APPLICANT: List, Benjamin  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
FILE REFERENCE: PLF00115  
CURRENT APPLICATION NUMBER: US/09/883,758  
CURRENT FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: US/09/318,661  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-883-758-2

Query Match 96.9%; Score 95; DB 9; Length 298;  
Best Local Similarity 94.7%; Pred. No. 7.2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
:|||||  
Db 205 EIRLKSDNYATHYAESVKG 223

RESULT 10  
US-10-372-481-15  
Sequence 15, Application US/10372481

; Publication No. US20030202975A1

; GENERAL INFORMATION:

; APPLICANT: Tedder, Thomas F.

; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES

; FILE REFERENCE: 5405.306

; CURRENT APPLICATION NUMBER: US/10/372,481

; PRIOR FILING DATE: 2003-02-21

; PRIOR APPLICATION NUMBER: PCT/US03/05549

; PRIOR FILING DATE: 2003-02-21

; PRIOR APPLICATION NUMBER: US 60/420,472

; PRIOR FILING DATE: 2002-10-21

; PRIOR APPLICATION NUMBER: US 60/359,419

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 15

; LENGTH: 119

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-372-481-15

Query Match 94.9%; Score 93; DB 12; Length 119;

Best Local Similarity 94.7%; Pred. No. 5.6e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19

|||||:|||||

Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 11

US-10-371-797-15

; Sequence 15, Application US/10371797

; Publication No. US20040001828A1

; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

; APPLICANT: TUSCANO, Joseph

; APPLICANT: TEDDER, Thomas

; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22

; TITLE OF INVENTION: ANTIBODIES

; FILE REFERENCE: 39754-0951

; CURRENT APPLICATION NUMBER: US/10/371,797

; PRIOR FILING DATE: 2003-02-21

; PRIOR APPLICATION NUMBER: US 60/420,472

; PRIOR FILING DATE: 2002-10-21

; PRIOR APPLICATION NUMBER: US 60/359,419

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 119

; TYPE: PRT

; ORGANISM: homo sapiens

; US-10-371-797-15

Query Match 94.9%; Score 93; DB 15; Length 119;

Best Local Similarity 94.7%; Pred. No. 5.6e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19

|||||:|||||

Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 12

US-10-239-656-69

; Sequence 69, Application US/10239656

; Publication No. US20040038339A1

; GENERAL INFORMATION:

; APPLICANT: KUFER, PETER

; APPLICANT: RIETHMULLER, GERT

; APPLICANT: LUTTERBUSE, RALF

; APPLICANT: BORSCHERT, KATRIN

; APPLICANT: KISCHEL, ROMAN

; APPLICANT: MAYER, MONIKA

; APPLICANT: HOFMEISTER, ROBERT

; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE

; FILE REFERENCE: 029976/0106

; CURRENT APPLICATION NUMBER: US/10/239,656

; PRIOR FILING DATE: 2003-03-06

; PRIOR APPLICATION NUMBER: PCT/EP01/03414

; PRIOR FILING DATE: 2001-03-26

; PRIOR APPLICATION NUMBER: EP 00106467.4

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 92

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 69

; LENGTH: 255

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-11 single

; OTHER INFORMATION: Chain Fv

; US-10-239-656-69

Query Match 94.9%; Score 93; DB 12; Length 255;

Best Local Similarity 94.7%; Pred. No. 1.3e-06;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19

|||||:|||||

Db 51 EIRLKSNNYATHYAESVKG 69

RESULT 13

US-10-239-656-61

; Sequence 61, Application US/10239656

; Publication No. US20040038339A1

; GENERAL INFORMATION:

; APPLICANT: KUFER, PETER

; APPLICANT: RIETHMULLER, GERT

; APPLICANT: LUTTERBUSE, RALF

; APPLICANT: BORSCHERT, KATRIN

; APPLICANT: KISCHEL, ROMAN

; APPLICANT: MAYER, MONIKA

; APPLICANT: HOFMEISTER, ROBERT

; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE

; FILE REFERENCE: 029976/0106

; CURRENT APPLICATION NUMBER: US/10/239,656

; PRIOR FILING DATE: 2003-03-06

; PRIOR APPLICATION NUMBER: PCT/EP01/03414

; PRIOR FILING DATE: 2001-03-26

; PRIOR APPLICATION NUMBER: EP 00106467.4

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 92

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 61

; LENGTH: 256

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-2 single

; OTHER INFORMATION: Chain Fv

; US-10-239-656-61

Query Match 94.9%; Score 93; DB 12; Length 256;

Best Local Similarity 94.7%; Pred. No. 1.3e-06;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19

|||||:|||||

Db 51 EIRLKSNNYATHYAESVKG 69



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RESULT 14
US-10-239-656-77
; Sequence 77, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFWEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; TITLE OF INVENTION: TO AN EPIOTOPE OF THE NKG2D RECEPTOR COMPLEX
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 77
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 3B10xP5-
; OTHER INFORMATION: 2 bispecific single chain Fv
US-10-239-656-77

Query Match          94.9%; Score 93; DB 12; Length 503;
Best Local Similarity 94.7%; Pred. No. 2.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLXSDNYATHYAESVKG 19
Db 298 EIRLKSNNYATHYAESVKG 316
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RESULT 15
US-09-564-329A-15
; Sequence 15, Application US/09564329A
; Patent No. US20010055751A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
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; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-15

Query Match          92.9%; Score 91; DB 9; Length 151;
Best Local Similarity 89.5%; Pred. No. 1.5e-06;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLXSDNYATHYAESVKG 19
Db 69 EIRLRSNNYATHYAESVKG 87
|||||:|||||

Search completed: September 30, 2004, 06:54:53
Job time : 319.814 secs
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Blank sheet

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:00:45 ; Search time 32.2034 Seconds  
(without alignments)  
30.459 Million cell updates/sec

Title: US-09-674-716B-11  
Perfect score: 98  
Sequence: 1 EIRKSDNVATHYAESVKG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	285	3	US-09-318-661-4
2	98	100.0	285	4	US-09-883-758-4
3	95	96.9	298	3	US-09-318-661-2
4	95	96.9	298	4	US-09-883-758-2
5	93	94.9	115	1	US-08-468-661-1
6	93	94.9	115	1	US-08-468-272A-1
7	93	94.9	115	1	US-08-478-857-1
8	93	94.9	115	2	US-08-471-771-1
9	93	94.9	115	3	US-09-130-783-1
10	93	94.9	120	3	US-08-767-128-28
11	93	94.9	122	3	US-08-483-749A-2
12	91	92.9	151	4	US-09-564-329A-15
13	85	86.7	114	3	US-08-483-749A-10
14	80.5	82.1	119	3	US-08-767-128-26
15	74	75.5	119	1	US-08-192-102-5
16	74	75.5	119	2	US-08-324-799-5
17	74	75.5	119	1	US-08-192-861A-5
18	74	75.5	119	3	US-09-133-119-5
19	74	75.5	119	3	US-08-192-093A-5
20	72	73.5	119	1	US-08-442-542-45
21	72	73.5	119	3	US-08-765-469-45
22	71	72.4	227	1	US-08-681-432-2
23	68	69.4	19	3	US-08-737-085A-4
24	68	69.4	19	3	US-09-246-258-4
25	68	69.4	19	3	US-09-532-106-4
26	68	69.4	19	4	US-09-839-666-4
27	68	69.4	27	2	US-08-737-085A-21

ALIGNMENTS

RESULT 1  
US-09-318-661-4  
; Sequence 4, Application US/09318661  
; Patent No. 6286488  
; GENERAL INFORMATION:  
; APPLICANT: Barbas III, Carlos F.  
; APPLICANT: Shabat, Doron  
; APPLICANT: Rader, Christoph  
; APPLICANT: List, Benjamin  
; APPLICANT: Lerner, Richard A.  
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
; FILE REFERENCE: PLF00115  
; CURRENT APPLICATION NUMBER: US/09/318,661  
; CURRENT FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 285  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
; OTHER INFORMATION: residue sequence of catalytic fragment  
US-09-318-661-4

Query Match 100.0%; Score 98; DB 3; Length 285;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNVATHYAESVKG 19  
Db 203 EIRKSDNVATHYAESVKG 221

RESULT 2  
US-09-883-758-4  
; Sequence 4, Application US/09883758  
; Patent No. 6677435  
; GENERAL INFORMATION:  
; APPLICANT: Barbas III, Carlos F.  
; APPLICANT: Shabat, Doron  
; APPLICANT: Rader, Christoph  
; APPLICANT: List, Benjamin  
; APPLICANT: Lerner, Richard A.  
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
; FILE REFERENCE: PLF00115  
; CURRENT APPLICATION NUMBER: US/09/883,758  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US/09/318,661  
; PRIOR FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 285  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
OTHER INFORMATION: residue sequence of catalytic fragment  
US-09-883-758-4

Query Match 100.0%; Score 98; DB 4; Length 285;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHAESVKG 19  
|||||:|||||:|||||:|||||  
Db 203 EIRLSDNYATHAESVKG 221

## RESULT 3

US-09-318-661-2  
Sequence 2, Application US/09318661  
Patent No. 6268488

GENERAL INFORMATION:  
APPLICANT: Barbas III, Carlos F.  
APPLICANT: Shabat, Doron  
APPLICANT: Rader, Christoph  
APPLICANT: List, Benjamin  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
FILE REFERENCE: PLF00115  
CURRENT APPLICATION NUMBER: US/09/318,661  
CURRENT FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-318-661-2

Query Match 96.9%; Score 95; DB 3; Length 298;  
Best Local Similarity 94.7%; Pred. No. 1.2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHAESVKG 19  
|||||:|||||:|||||:|||||  
Db 205 EIRLSDNYATHAESVKG 223

## RESULT 4

US-09-883-758-2  
Sequence 2, Application US/09883758  
Patent No. 6677435

GENERAL INFORMATION:  
APPLICANT: Barbas III, Carlos F.  
APPLICANT: Shabat, Doron  
APPLICANT: Rader, Christoph  
APPLICANT: List, Benjamin  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
FILE REFERENCE: PLF00115  
CURRENT APPLICATION NUMBER: US/09/883,758  
CURRENT FILING DATE: 2001-05-18  
PRIOR APPLICATION NUMBER: US/09/318,661  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Mus musculus

## US-09-883-758-2

Query Match 96.9%; Score 95; DB 4; Length 298;  
Best Local Similarity 94.7%; Pred. No. 1.2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHAESVKG 19  
|||||:|||||:|||||:|||||  
Db 205 EIRLSDNYATHAESVKG 223

## RESULT 5

US-08-468-661-1  
Sequence 1, Application US/08468661  
Patent No. 5639621

GENERAL INFORMATION:  
APPLICANT: Boslet, Klaus  
APPLICANT: Pfeiderer, Peter  
APPLICANT: Seeman, Gerhard  
TITLE OF INVENTION: Monoclonal Antibodies Against  
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the  
TITLE OF INVENTION: Preparation Thereof and the Use Thereof  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,661  
FILING DATE: 06-JUNE-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/957,827  
FILING DATE: 08-OCT-1992  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 35,694  
REFERENCE/DOCKET NUMBER: 05552-1227-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-468-661-1

Query Match 94.9%; Score 93; DB 1; Length 115;  
Best Local Similarity 94.7%; Pred. No. 8.7e-08;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHAESVKG 19  
|||||:|||||:|||||:|||||  
Db 46 EIRLSDNYATHAESVKG 64

## RESULT 6

US-08-466-272A-1  
Sequence 1, Application US/08466272A  
Patent No. 5674994

GENERAL INFORMATION:

```
/ APPLICANT: Bosslet, Klaus
/ APPLICANT: Pfeleiderer, Peter
/ APPLICANT: Seeman, Gerhard
/ TITLE OF INVENTION: Monoclonal Antibodies Against
/ TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the Preparation
/ TITLE OF INVENTION: Thereof and the Use Thereof
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESS: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,272A
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/957,827
/ FILING DATE: 08-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 02481-1227-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 115 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: Peptide
/ US-08-466-272A-1

Query Match 94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 8.7e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 46 EIRKSNNYATHYAESVKG 64

RESULT 7
US-08-478-857-1
/ Sequence 1, Application US/08478857
/ Patent No. 5695758
/ GENERAL INFORMATION:
/ APPLICANT: Bosslet, Klaus
/ APPLICANT: Pfeleiderer, Peter
/ APPLICANT: Seeman, Gerhard
/ TITLE OF INVENTION: Monoclonal Antibodies Against
/ TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the Preparation
/ TITLE OF INVENTION: Thereof and the Use Thereof
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESS: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM: disk
/ MEDIUM TYPE: Floppy disk
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/478,857
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/957,827
/ FILING DATE: 08-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 02481-1227-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 115 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-478-857-1

Query Match 94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 8.7e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 46 EIRKSNNYATHYAESVKG 64

RESULT 8
US-08-471-771-1
/ Sequence 1, Application US/08471771
/ Patent No. 5837824
/ GENERAL INFORMATION:
/ APPLICANT: Bosslet, Klaus
/ APPLICANT: Pfeleiderer, Peter
/ APPLICANT: Seeman, Gerhard
/ TITLE OF INVENTION: Monoclonal Antibodies Against
/ TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
/ TITLE OF INVENTION: Preparation Thereof and the Use Thereof
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESS: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/471,771
/ FILING DATE: 06-JUNE-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/957,827
/ FILING DATE: 08-OCT-1992
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Forman, David S.
/ REGISTRATION NUMBER: 33,694
/ REFERENCE/DOCKET NUMBER: 05552-1227-01000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
```

TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 115 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-471-771-1

Query Match 94.9%; Score 93; DB 2; Length 115;  
 Best Local Similarity 94.7%; Pred. No. 8.7e-08;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19  
 |||||:|||||  
 Db 46 EIRLKSNNYATHYAESVKG 64

## RESULT 9

US-09-130-783-1

; Sequence 1, Application US/09130783  
 ; Patent No. 6030797  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bosslet, Klaus  
 ; APPLICANT: Pfeleiderer, Peter  
 ; APPLICANT: Seeman, Gerhard  
 ; TITLE OF INVENTION: Monoclonal Antibodies Against  
 ; Tumor-Associated Antigens, Processes for the  
 ; TITLE OF INVENTION: Preparation Thereof and the Use Thereof  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 ; ADDRESSEE: Dunner  
 ; STREET: 1300 I Street, N.W., Suite 700  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005-3315  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/130,783  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/471,771  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Forman, David S.  
 ; REGISTRATION NUMBER: 33,694  
 ; REFERENCE/DOCKET NUMBER: 05552-1227-01000  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-408-4000  
 ; TELEFAX: 202-408-4400  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 115 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-09-130-783-1

Query Match 94.9%; Score 93; DB 3; Length 115;  
 Best Local Similarity 94.7%; Pred. No. 8.7e-08;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19  
 |||||:|||||  
 Db 46 EIRLKSNNYATHYAESVKG 64

RESULT 10  
 US-08-767-128-28  
 ; Sequence 28, Application US/08767128  
 ; Patent No. 611079  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WYLIE, DWANE E.  
 ; APPLICANT: LOPEZ, OSVALDO  
 ; APPLICANT: MURRAY, PETER JOSEPH  
 ; APPLICANT: GOEBEL, PETER  
 ; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
 ; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE  
 ; NUMBER OF SEQUENCES: 46  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
 ; STREET: 3100 No. 611079west Center, 90 South Seventh St  
 ; CITY: Minneapolis  
 ; STATE: MN  
 ; COUNTRY: USA  
 ; ZIP: 55402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/767,128  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE: 04-DEC-1996  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US96/09258  
 ; FILING DATE: 05-JUN-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/541,373  
 ; FILING DATE: 10-OCT-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/462,798  
 ; FILING DATE: 05-JUN-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Carter, Charles G.  
 ; REGISTRATION NUMBER: 35,093  
 ; REFERENCE/DOCKET NUMBER: 8648.49USF1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 612/371-5278  
 ; TELEFAX: 612/332-9081  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 28:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 120 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: internal  
 ; ORIGINAL SOURCE:  
 ; US-08-767-128-28

Query Match 94.9%; Score 93; DB 3; Length 120;  
 Best Local Similarity 94.7%; Pred. No. 9.1e-08;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19  
 |||||:|||||  
 Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 11  
US-08-483-749A-2  
; Sequence 2, Application US/08483749A  
; Patent No. 6054561  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
; CITY: EMERYVILLE  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,749A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL B.  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0508.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-749A-2  
Query Match 94.9%; Score 93; DB 3; Length 122;  
Best Local Similarity 94.7%; Pred. No. 9.2e-08;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EIRLKSNDNYATHYAESVKG 19  
|||:|||||  
DB 50 EIRLKSNNYATHYAESVKG 68  
|||:|||||  
RESULT 12  
US-09-564-329A-15  
; Sequence 15, Application US/09564329A  
; Patent No. 6541212  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 30435.54US14  
; CURRENT APPLICATION NUMBER: US/09/564,329A  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/359,326  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/113,230  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/120,536  
; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: 60/124,658  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/038,261  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 09/203,939  
; PRIOR FILING DATE: 1998-12-02  
; PRIOR APPLICATION NUMBER: 09/251,835  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 09/308,503  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: SCID Mice  
US-09-564-329A-15  
Query Match 92.9%; Score 91; DB 4; Length 151;  
Best Local Similarity 89.5%; Pred. No. 2.5e-07;  
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EIRLKSNDNYATHYAESVKG 19  
|||:|||||  
DB 69 EIRLRSNYATHYAESVKG 87  
|||:|||||  
RESULT 13  
US-08-483-749A-10  
; Sequence 10, Application US/08483749A  
; Patent No. 6054561  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
; CITY: EMERYVILLE  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,749A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL B.  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0508.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-749A-10  
Query Match 86.7%; Score 85; DB 3; Length 114;  
Best Local Similarity 84.2%; Pred. No. 1.7e-06;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EIRLKSNDNYATHYAESVKG 19  
|||:|||||

Db 50 EIKLSNNYPHYAESVKG 68

## RESULT 14

US-08-767-128-26  
; Sequence 26, Application US/08767128  
; Patent No. 6111079  
; GENERAL INFORMATION:  
; APPLICANT: WYLIE, DWANE E.  
; APPLICANT: LOPEZ, OSVALDO  
; APPLICANT: MURRAY, PETER JOSEPH  
; APPLICANT: GOBEL, PETER  
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
; NUCLEOTIDES CODING THEREFORE  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. 6111079west Center, 90 South Seventh St  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/767,128  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 04-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/09258  
; FILING DATE: 05-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/541,373  
; FILING DATE: 10-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/462,798  
; FILING DATE: 05-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.49USF1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/371-5278  
; TELEFAX: 612/332-3081  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-08-767-128-26

Query Match 82.1%; Score 80.5; DB 3; Length 119;  
Best Local Similarity 89.5%; Pred. No. 9.4e-06;  
Matches 17; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 EIRKSDNYATHYAESVKG 19  
Db 50 EVRLKS-NYATHYAESVKG 67

## RESULT 15

US-08-192-102-5  
; Sequence 5, Application US/08192102  
; Patent No. 5656272  
; GENERAL INFORMATION:  
; APPLICANT: Le, Junning  
; APPLICANT: Vilcek, Jan  
; APPLICANT: Daddona, Peter E.  
; APPLICANT: Chrayeb, John  
; APPLICANT: Knight, David M.  
; APPLICANT: Siegel, Scott A.  
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING  
; NUCLEOTIDES CODING THEREFORE  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/192,102  
; FILING DATE: 04-FEB-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/192,093  
; FILING DATE: 04-FEB-1994  
; APPLICATION NUMBER: US 08/013,413  
; FILING DATE: 02-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/010,406  
; FILING DATE: 29-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,852  
; FILING DATE: 11-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/853,606  
; FILING DATE: 18-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/670,827  
; FILING DATE: 18-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: NYU93-01M3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-192-102-5

Query Match 75.5%; Score 74; DB 1; Length 119;  
Best Local Similarity 84.2%; Pred. No. 0.00011;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19  
Db 50 EIRSKINSATHYAESVKG 68

Search completed: September 30, 2004, 06:38:20



us-09-674-716b-11.open.rai

Thu Sep 30 13:18:30 2004

Job time : 34.2034 secs

Blank sheet

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 3.25424 Seconds  
(without alignments)  
88.677 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : FID 78:\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	18	2 S43834	DNA topoisomerase
2	16	100.0	21	2 D48518	PEB1 5'-region hyp
3	16	100.0	23	1 S20453	pyrroloquinoline q
4	16	100.0	25	2 F84056	hypothetical prote
5	16	100.0	30	2 A26188	lipocortin I - pig
6	16	100.0	30	2 A46892	nitrobenzene nitro
7	16	100.0	31	2 H82818	hypothetical prote
8	16	100.0	32	2 PQ0413	nonstructural prot
9	16	100.0	33	2 PQ0416	RNA-directed RNA p
10	16	100.0	33	2 A95119	hypothetical prote
11	16	100.0	33	2 H32096	hypothetical prote
12	16	100.0	33	2 S36466	hypothetical prote
13	16	100.0	35	2 P80363	protein-tyrosine-p
14	16	100.0	35	2 P80364	protein-tyrosine-p
15	16	100.0	36	2 D87544	hypothetical prote
16	16	100.0	37	2 C70186	hypothetical prote
17	16	100.0	37	2 G95919	probable transposa
18	16	100.0	38	2 S34302	Ig heavy chain v r
19	16	100.0	38	2 B39803	proline-rich phosph
20	16	100.0	39	2 D82085	hypothetical prote
21	16	100.0	39	2 A96026	probable transposa
22	16	100.0	40	2 A23098	larvicidal toxin -
23	16	100.0	43	1 ZBPT9	gene 55.4 protein
24	16	100.0	43	2 B37505	hypothetical prote
25	16	100.0	45	2 C34669	calmodulin-related
26	16	100.0	45	2 H3816	hypothetical prote
27	16	100.0	46	2 B82461	hypothetical prote
28	16	100.0	47	2 PC4133	hypothetical 47 pr
29	16	100.0	48	2 C95060	hypothetical prote

30	16	100.0	48	2 T07316	hypothetical prote
31	16	100.0	50	2 AB0367	hypothetical prote
32	16	100.0	51	2 S00576	hypothetical prote
33	16	100.0	52	2 A71002	hypothetical prote
34	16	100.0	52	2 PN0481	cell division cycl
35	16	100.0	52	2 S15922	hypothetical prote
36	16	100.0	52	2 C82621	hypothetical prote
37	16	100.0	52	2 AF0293	hypothetical prote
38	16	100.0	53	2 A82862	hypothetical prote
39	16	100.0	53	2 H98094	hypothetical prote
40	16	100.0	54	2 S22937	sex-determining pr
41	16	100.0	54	2 S22946	SOX-11 protein - A
42	16	100.0	54	2 I50028	Sry-related sequen
43	16	100.0	54	2 I50029	Sry-related sequen
44	16	100.0	54	2 I50190	Sry-related sequen
45	16	100.0	54	2 I50191	Sry-related sequen

ALIGNMENTS

RESULT 1

S43834  
DNA topoisomerase (EC 5.99.1.2) - Klebsiella sp. (ATCC 15380) (fragment)  
C/Species: Klebsiella sp.  
A/Variety: ATCC 15380  
C/Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 07-May-1999  
C/Accession: S43834  
R/Lynch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wilkinson, A.J.  
Biochem. J. 299, 129-136, 1994  
A/Title: Characterization of the CysB protein of Klebsiella aerogenes: direct evidence th  
A/Reference number: S43834; MUID:94220019; PMID:8166630  
A/Accession: S43834  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-18 <LYN>  
A/Experimental source: ATCC 15380  
C/Genetics:  
A/Gene: topI  
C/Function:  
A/Description: catalyzes ATP-independent transient breakage of DNA phosphodiester bonds  
rejoining; this reaction will lead to the conversion of one topological isomer of DNA to  
C/Superfamily: bacterial type I DNA topoisomerase  
C/Keywords: DNA binding; DNA replication; isomerase; zinc finger

RESULT 2

D48518  
PEB1 5'-region hypothetical protein A - Campylobacter jejuni (fragment)  
C/Species: Campylobacter jejuni  
C/Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 19-May-1995  
C/Accession: D48518  
R/Pei, Z.; Blaser, M.J.  
J. Biol. Chem. 268, 18717-18725, 1993  
A/Title: PEB1, the major cell-binding factor of Campylobacter jejuni, is a homolog of the  
A/Reference number: A48518; MUID:93366784; PMID:8360165  
A/Accession: D48518  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-21 <PEI>  
A/Cross-references: GB:I13662

Query Match 100.0%; Score 16; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Feb-1997
C/Accession: A26188
R/De, B.K.; Misono, K.S.; Lukas, T.J.; Mroczkowski, B.; Cohen, S.
J. Biol. Chem. 261, 13784-13792, 1986
A/Title: A calcium-dependent 35-kilodalton substrate for epidermal growth factor receptor:
A/Reference number: A26188; MUID:87008618; PMID:3020049
A/Accession: A26188
A/Molecule type: protein
A/Residues: 1-30 <DEB>
C/Superfamily: annexin I; annexin repeat homology
C/Keywords: phosphoprotein

Query Match 100.0%; Score 16; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 1 FID 3

RESULT 6
A44682
nitrobenzene nitroreductase (BC 1.-.-.-) - Pseudomonas pseudoalcaligenes (fragment)
C/Species: Pseudomonas pseudoalcaligenes
C/Date: 28-Feb-1995 #sequence_revision 03-Mar-1995 #text_change 21-Mar-1996
C/Accession: A44682
R/Somerville, C.C.
submitted to the Protein Sequence Database, February 1995
A/Description: Purification and characterization of nitrobenzene nitroreductase from Pse.
A/Reference number: A44682
A/Accession: A44682
A/Status: Preliminary
A/Molecule type: protein
A/Residues: 1-30 <SOM>
A/Experimental source: strain JS45
C/Keywords: oxidoreductase

Query Match 100.0%; Score 16; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 5 FID 7

RESULT 7
H82818
hypothetical protein XF0341 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: H82818
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: H82818
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-31 <SIM>
A/Cross-references: GB:AE003896; GB:AE003849; NID:g9105157; PIDN:AAF03151.1; GSPDB:GN001:
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

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---

```

QY 1 FID 3
Db 17 FID 19

RESULT 3
S20453
pyrroloquinoline quinone precursor pqQA - Klebsiella pneumoniae
C/Species: Klebsiella pneumoniae
C/Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C/Accession: S20453; S21838
R/Meulenbergh, J.J.M.; Sellink, E.; Riegman, N.H.; Postma, P.W.
Mol. Gen. Genet. 232, 284-294, 1992
A/Title: Nucleotide sequence and structure of the Klebsiella pneumoniae pqQ operon.
A/Reference number: S20453; MUID:92212293; PMID:1313537
A/Accession: S20453
A/Molecule type: DNA
A/Residues: 1-23 <MEU>
A/Cross-references: EMBL:X58778; NID:G43903; PIDN:CAA41579.1; PID:G43905
R/Velterop, J.S.; Sellink, E.; Meulenbergh, J.J.; David, I.; Postma, P.W.
J. Bacteriol. 177, 5088-5098, 1995
A/Title: Synthesis of pyrroloquinoline quinone in vivo and in vitro and detection of an
A/Reference number: A69181; MUID:95394815; PMID:7665488
A/Contents: annotation
C/Genetics:
A/Gene: pqQA
C/Superfamily: pyrroloquinoline quinone precursor pqQA
C/Keywords: quinoprotein
F15-19/Product: pyrroloquinoline quinone #status predicted <MAT>
F15-19/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 100.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 7 FID 9

RESULT 4
F84066
hypothetical protein BH3334 [imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C/Accession: F84066
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: F84066
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-25 <STO>
A/Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BA07053.1; GSPDB:GN00
A/Experimental source: strain C-125
C/Genetics:
A/Gene: BH3334

Query Match 100.0%; Score 16; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 13 FID 15

RESULT 5
A26188
lipocortin I - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)

```

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A;References: A59328  
A;Content: annotation  
C;Genetics:  
A;Gene: XF0341

Query Match 100.0%; Score 16; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
|||  
Db 16 FID 18

## RESULT 8

P00413  
nonstructural protein NS1 - influenza A virus (strain A/Hebei/24/89 [H1N2]) (fragment)  
C;Species: influenza A virus  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: P00413  
R;Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerom  
J. Gen. Virol. 73, 1329-1337, 1992  
A;Title: Origin and evolutionary characteristics of antigenic reassortant influenza A (H  
A;Reference number: P00408; MUID:92300326; PMID:1607856  
A;Accession: P00413  
A;Molecule type: Genomic RNA  
A;Residues: 1-32 <LIA>  
C;Genetics:  
A;Map position: segment 8  
A;Superfamily: influenza virus nonstructural protein NS1  
C;Keywords: nonstructural protein

Query Match 100.0%; Score 16; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
|||  
Db 10 FID 12

## RESULT 9

P00416  
RNA-directed RNA polymerase (EC 2.7.7.48) 3 - influenza A virus (strain A/Yamagata/120/8  
N;Alternate names: P2 protein; PA protein  
C;Species: influenza A virus  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: P00416  
R;Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerom  
J. Gen. Virol. 73, 1329-1337, 1992  
A;Title: Origin and evolutionary characteristics of antigenic reassortant influenza A (H  
A;Reference number: P00408; MUID:92300326; PMID:1607856  
A;Accession: P00416  
A;Molecule type: Genomic RNA  
A;Residues: 1-33 <LIA>  
C;Genetics:  
A;Map position: segment 3  
A;Superfamily: influenza virus RNA-directed RNA polymerase 3  
C;Keywords: nucleotidyltransferase

Query Match 100.0%; Score 16; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
|||  
Db 11 FID 13

## RESULT 10

A95119  
hypothetical protein SP1031 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001  
C;Accession: A95119  
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: A95119  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-33 <KUR>  
A;Cross-references: GB:AE005672; PIDN:AAK75146.1; PID:gi4972505; GSPDB:GN00164; TIGR:SP48  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP1031

Query Match 100.0%; Score 16; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
|||  
Db 22 FID 24

## RESULT 11

H82096  
hypothetical protein VC2284 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C;Accession: H82096  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
Chadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, P.  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: H82096

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-33 <HEI>  
A;Cross-references: GB:AE003852; GB:AE004299; GB:AE03852; NID:g9656835; PIDN:AAF95428.1; GSPDB:GN0012  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC2284  
A;Map position: 1

Query Match 100.0%; Score 16; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
|||  
Db 19 FID 21

## RESULT 12

S33646  
Hypothetical protein 2 - pin mould (Absidia glauca) plasmid PSSP15 (fragment)  
C;Species: Absidia glauca  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Dec-1993  
C;Accession: S33646  
R;Haefliger, J.; Woestemeyer, J.; Weigel, C.T.  
submitted to the EMBL Data Library, June 1992  
A;Description: Complete nucleotide sequence of the papD9 extrachromosomal DNA element of  
A;Reference number: S33645  
A;Accession: S33646  
A;Molecule type: DNA

A;Residues: 1-33 <HAE>  
 A;Cross-references: EMBL:M94861  
 C;Genetics:  
 A;Genome: plasmid

Query Match 100.0%; Score 16; DB 2; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 Db 22 FID 24

## RESULT 13

PS0363  
 protein-tyrosine-phosphatase (EC 3.1.3.48) (clone PTP5) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 20-Mar-1998  
 C;Accession: PS0363  
 R;den Hertog, J.; Fals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.  
 Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992  
 A;Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase  
 A;Reference number: JH0609; MUID:92272714; PMID:1590786  
 A;Accession: PS0363  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-35 <DEN>  
 A;Experimental source: embryonal carcinoma cell, P19 cell  
 C;Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat  
 A;Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 100.0%; Score 16; DB 2; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 Db 6 FID 8

## RESULT 14

PS0364  
 protein-tyrosine-phosphatase (EC 3.1.3.48) (clone PTP31) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 20-Mar-1998  
 C;Accession: PS0364  
 R;den Hertog, J.; Fals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.  
 Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992  
 A;Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase  
 A;Reference number: JH0609; MUID:92272714; PMID:1590786  
 A;Accession: PS0364  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-35 <DEN>  
 A;Experimental source: embryonal carcinoma cell, P19 cell  
 C;Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat  
 A;Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 100.0%; Score 16; DB 2; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 Db 6 FID 8

## RESULT 15

DB87544  
 hypothetical protein CC2381 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus  
 C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
 C;Accession: D87544  
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.H.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonitskii, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A;Title: Complete Genome Sequence of Caulobacter crescentus.  
 A;Reference number: A87249; MUID:21173698; PMID:11259647  
 A;Accession: D87544  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-36 <STO>  
 A;Cross-references: GB:AE005673; NID:gl3423914; PIDN:AAK24352.1; GSPDB:GN00148  
 C;Genetics:  
 A;Gene: CC2381

Query Match 100.0%; Score 16; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 Db 28 FID 30

Search completed: September 30, 2004, 06:00:39  
 Job time : 5.25424 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 1.83051 Seconds  
(without alignments)  
85.337 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16  
Sequence: 1 FID 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	16	100.0	16	1	FIBA_RABIT	P14461 oryctolagus
2	16	100.0	18	1	TOPI_KLEAE	P46155 klebsiella
3	16	100.0	23	1	PQA_ENTIT	P59726 enterobacte
4	16	100.0	23	1	PQA_KLEPN	P27503 klebsiella
5	16	100.0	24	1	HMT_LINRE	P23543 lingula ree
6	16	100.0	32	1	RS19_YEREN	Q56847 yersinia en
7	16	100.0	36	1	SK2_CENLM	P59848 centruloide
8	16	100.0	37	1	Y62_BOREU	O51635 borrelia bu
9	16	100.0	43	1	Y44D_EPT4	P07080 bacterioph
10	16	100.0	52	1	YORV_FT1	P19306 thermoprote
11	16	100.0	54	1	AWA2_ALLMT	P40642 alligator m
12	16	100.0	54	1	AWA3_ALLMT	P40643 alligator m
13	16	100.0	54	1	CH01_CHICK	P40665 gallus gall
14	16	100.0	54	1	CH02_CHICK	P40666 gallus gall
15	16	100.0	54	1	CH03_CHICK	P40667 gallus gall
16	16	100.0	54	1	CH04_CHICK	P40668 gallus gall
17	16	100.0	54	1	CH07_CHICK	P40669 gallus gall
18	16	100.0	54	1	CH31_CHICK	P40670 gallus gall
19	16	100.0	54	1	DM23_DROME	P40658 drosophila
20	16	100.0	54	1	DM36_DROME	P40660 drosophila
21	16	100.0	54	1	DM63_DROME	P40662 drosophila
22	16	100.0	54	1	DM63_DROME	P40663 drosophila
23	16	100.0	54	1	DM64_DROME	P40664 drosophila
24	16	100.0	56	1	SOX1_PLEWA	P37839 pleurodeles
25	16	100.0	57	1	ANDP_DROME	O16825 drosophila
26	16	100.0	57	1	ANDP_DROME	P21663 drosophila
27	16	100.0	57	1	ANDP_DROS	Q8wsv2 drosophila
28	16	100.0	58	1	Y016_METUA	Q60322 methanococ
29	16	100.0	60	1	ANDP_DROS1	Q8wsv4 drosophila
30	16	100.0	60	1	Y02B_EPT4	P39232 bacterioph
31	16	100.0	62	1	Y12D_EPT4	P39496 bacterioph
32	16	100.0	63	1	YEBW_ECOLI	P76275 escherichia
33	16	100.0	66	1	COPP_HELPFJ	Q9zm70 helicobacte

34	16	100.0	66	1	COPP_HELPFJ	Q48271 helicobacte
35	16	100.0	66	1	SM64_HUMAN	Q9nrt5 homo sapien
36	16	100.0	67	1	VG10_SPVIR	P15901 spiroplasma
37	16	100.0	67	1	Y023_RICCN	Q92jp4 rickettsia
38	16	100.0	69	1	ACP_RHOSH	P12784 rhodobacter
39	16	100.0	70	1	Y06C_BPT4	P13308 bacterioph
40	16	100.0	71	1	RECA_STRGC	P49986 streptococ
41	16	100.0	72	1	YA94_ARCFU	Q29171 archaeoglob
42	16	100.0	72	1	YVGB_VACCC	P20566 vaccinia vi
43	16	100.0	73	1	RR18_GUITH	O78488 guillardia
44	16	100.0	73	1	RS19_YERPS	P11256 yersinia ps
45	16	100.0	73	1	YPO4_NPVLD	P30326 lymantria d

#### ALIGNMENTS

RESULT 1  
FIBA\_RABIT STANDARD; PRT; 16 AA.  
AC P14461;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).  
GN FGA.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RA Blomback B., Blomback M., Grondahl N.J.;  
RT "Studies on fibrinopeptides from mammals.";  
RL Acta Chem. Scand. 19:1789-1791(1965).  
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.  
KW Blood coagulation; Plasma.  
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.  
FT NON TER 16 16  
SQ SEQUENCE 16 AA; 1651 MW; 49623279EA55EB6 CRC64;  
Query Match 100.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
DB 8 FID 10

RESULT 2  
TOPI\_KLEAE STANDARD; PRT; 18 AA.  
AC P46155;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE DNA topoisomerase I (BC 5.99.1.2) (Omega-protein) (Relaxing enzyme)  
DE (Unwinding enzyme) (Swivelase) (Fragment).  
GN TOPA.  
OS Klebsiella aerogenes.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=28451;  
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 418 / ATCC 15380;
RA MEDLINE=9420019; PubMed=8166630;
RX Lynch A.S., Tyrell R., Smerdon S.J., Briggs G.S., Wilkinson A.J.;
RT "Characterization of the CysB protein of Klebsiella aerogenes: direct
RT evidence that N-acetylsuccinylserine rather than O-acetylsuccinylserine serves as the
RT inducer of the cysteine regulon.";
RL Biochem. J. 299:129-136(1994).
CC -!- FUNCTION: The reaction catalyzed by topoisomerases leads to the
CC conversion of one topological isomer of DNA to another.
CC -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
CC DNA, followed by passage and rejoining.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA
CC backbone bond, it simultaneously forms a protein-DNA link, in
CC which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus
CC at one end of the enzyme-severed DNA strand.
CC -!- SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase
CC family.
CC
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CC
CC EMBL; X78729; -; NOT_ANNOTATED_CDS.
CC HSSP; P06612; LYUA.
CC InterPro; IPR000380; DNA topoisomerase.
CC PROSITE; PS00396; TOPOISOMERASE I PROK; PARTIAL.
CC Isomerase; Topoisomerase; DNA-binding.
CC NON_TER 1
CC SEQUENCE 18 AA; 2043 MW; 8C1C81238FF0EFA4 CRC64;
CC
CC Query Match 100.0%; Score 16; DB 1; Length 18;
CC Best Local Similarity 100.0%; Pred. No. 1.9e+02;
CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 FID 3
CC Db 8 FID 10
CC
CC RESULT 3
CC PQQA_ENTIT STANDARD; PRT; 23 AA.
CC ID PQQA_ENTIT
CC AC P59726;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Coenzyme PQQ synthesis protein A (Pyrroloquinoline quinone
CC biosynthesis protein A).
CC GN PQQA.
CC OS Enterobacter intermedius.
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC OC Enterobacteriaceae; Enterobacter.
CC OX NCBI_TaxID=61648;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Kim C.H., Han S.H., Kim K.Y., Cho B.H., Kim Y.H., Gu B.S., Kim Y.C.;
CC RT "Cloning and expression of pyrroloquinoline (PQQ) genes from a
CC phosphate-solubilizing bacterium Enterobacter intermedius.";
CC RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ)
CC biosynthesis. Probably provides the glutamate and tyrosine
CC residues that are cross-linked and modified to form the coenzyme
CC (By similarity).
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
CC -!- SIMILARITY: Belongs to the pqqa family.
CC
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CC
CC EMBL; AY216883; AAP34378.1; -
CC DR HAMAP; MF_00656; -; 1.
CC KW PQQ biosynthesis; PQQ.
CC FT CROSSLINK 15 19 Pyrroloquinoline quinone (Glu-Tyr)
CC FT (Probable).
CC SQ SEQUENCE 23 AA; 2764 MW; ACCB321460871C5D CRC64;
CC
CC Query Match 100.0%; Score 16; DB 1; Length 23;
CC Best Local Similarity 100.0%; Pred. No. 2.4e+02;
CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 FID 3
CC Db 7 FID 9
CC
CC RESULT 4
CC PQQA_KLEPN STANDARD; PRT; 23 AA.
CC ID PQQA_KLEPN
CC AC P27503;
CC DT 01-AUG-1992 (Rel. 23, Created)
CC DT 01-AUG-1992 (Rel. 23, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Coenzyme PQQ synthesis protein A (Pyrroloquinoline quinone
CC biosynthesis protein A).
CC GN PQQA.
CC OS Klebsiella pneumoniae.
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC OC Enterobacteriaceae; Klebsiella.
CC OX NCBI_TaxID=573;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=NCTC 418;
CC RX MEDLINE=92212293; PubMed=1313537;
CC RA Meulenbergh J.J.W., Sellink E., Rieganman N.H., Postma P.W.;
CC RT "Nucleotide sequence and structure of the Klebsiella pneumoniae pqq
CC operon.";
CC RT Mol. Gen. Genet. 232:284-294 (1992).
CC RN [2]
CC RP FUNCTION.
CC RC STRAIN=NCTC 418;
CC RX MEDLINE=95394815; PubMed=7665488;
CC RA Veiterop J.S., Sellink E., Meulenbergh J.J., David S., Bulder I.,
CC RA Postma P.W.;
CC RT "Synthesis of pyrroloquinoline quinone in vivo and in vitro and
CC detection of an intermediate in the biosynthetic pathway.";
CC RL J. Bacteriol. 177:5088-5098(1995).
CC -!- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ)
CC biosynthesis. Probably provides the glutamate and tyrosine
CC residues that are cross-linked and modified to form the coenzyme.
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
CC -!- SIMILARITY: Belongs to the pqqa family.
CC
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CC
CC EMBL; X59778; CAA41579.1; -
CC DR PIR; S20453; S20453.
CC DR HAMAP; MF_00656; -; 1.
CC KW PQQ biosynthesis; PQQ.
CC FT CROSSLINK 15 19 Pyrroloquinoline quinone (Glu-Tyr)
CC

```



```

FT SEQUENCE 23 AA; 2764 MW; ACCB321460871C5D CRC64; (Probable).
SQ
Query Match 100.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 7 FID 9

RESULT 5
HEMT LINE
ID HEMT LINE STANDARD; PRT; 24 AA.
AC P23543;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hemerythrin alpha chain (Fragment).
OS Lingula reevii.
OC Eukaryota; Metazoa; Brachiopoda; Linguliformea; Lingulata; Lingulida;
OC Linguloidae; Lingulidae; Lingula.
OX NCBI_TaxID=7575;
RN [1]
SEQUENCE.
RP MEDLINE=91369922; PubMed=1892823;
RA Zhang J.-H., Kurtz D.M. Jr.;
RT "Two distinct subunits of hemerythrin from the brachiopod Lingula
RL Biochemistry 30:9121-9124(1991).
CC reevii: an apparent requirement for cooperativity in O2 binding.";
CC -!- FUNCTION: Hemerythrin is a respiratory protein in blood cells of
CC certain marine worms. The oxygen-binding site in each chain
CC contains two iron atoms.
CC -!- SUBUNIT: Octamer composed of two types of chains: alpha and beta.
CC -!- SIMILARITY: Belongs to the hemerythrin family.
DR InterPro: IPR002053; Hemerythrin.
DR Pfam: PF01814; Hemerythrin; 1.
DR PROSITE; PS00550; HEMERYTHRINS; PARTIAL.
KW Oxygen transport; Metal-binding; Iron.
FT METAL 24 24 IRON 1 (BY SIMILARITY).
FT NON TER 24 24
SQ SEQUENCE 24 AA; 2825 MW; 28675F45462C44BB CRC64;

Query Match 100.0%; Score 16; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 19 FID 21

RESULT 6
RS19 YEREN
ID RS19 YEREN STANDARD; PRT; 32 AA.
AC Q56847;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPSS.
OS Versinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=630;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=6471/76 / Serotype O:3;
RC MEDLINE=96382736; PubMed=8790600;
RA Mertz A.K.H., Daser A., Skurnik M., Wiesmuller K., Braun J., Appel H.,
RA Batsford S., Wu P., Distler A., Sieper J.;
RT "The evolutionarily conserved ribosomal protein L23 and the cationic

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RT urease beta-subunit of Versinia enterocolitica O:3 belong to the
RT immunodominant antigens in Versinia-triggered reactive arthritis:
RL Mol. Med. 1:44-55(1994).
CC -!- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
CC to the 16S ribosomal RNA (By similarity).
CC -!- SIMILARITY: Belongs to the S19P family of ribosomal proteins.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U11251; AAC43514.1; -
DR HAMAP; MF_00531; -; 1
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; 1.
DR ProDom; PD001012; Ribosomal_S19; 1.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON TER 32 32
SQ SEQUENCE 32 AA; 3659 MW; E534F701330F0338 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 10 FID 12

RESULT 7
SCK2 CENLM
ID -SCK2 CENLM STANDARD; PRT; 36 AA.
AC P59848;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hongotoxin 2 (HGTX2) (Fragment).
OS Centruroides limbatus (Scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=244936;
RN [1]
SEQUENCE.
RP MEDLINE=98112806; PubMed=9446567;
RA Koschak A., Bugianesi R.M., Mitterdorfer J., Kaczorowski G.J.,
RA Garcia M.L., Knaus H.-G.;
RT "Subunit composition of brain voltage-gated potassium channels
RT determined by hongotoxin-1, a novel peptide derived from Centruroides
RL limbatus venom.";
RL J. Biol. Chem. 273:2639-2644(1998).
CC -!- FUNCTION: Potent selective inhibitor of Kv1 voltage-gated
CC potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the short scorpion toxin family. Potassium
CC channel inhibitor subfamily.
DR PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
KW Toxin; Neurotoxin; Ionic channel inhibitor;
KW Potassium channel inhibitor.
FT NON TER 36 36
SQ SEQUENCE 36 AA; 3946 MW; A9D585FC06312E16 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3

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Db      ||||
        2 FID 4
RESULT 8
Y692 BORBU
ID Y692 BORBU STANDARD; PRT; 37 AA.
AC Q51635;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein BB0692.
GN BB0692.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Hanson M.,
RA Peterson J., Kervlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uitterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586 (1997).
CC -----
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CC -----
CC EMBL; AE001170; AAC67054.1; -.
DR PIR; C70186; C70186.
DR TIGR; BB0692; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 37 AA; 4589 MW; 5FA1F9470EDB51E2 CRC64;
Query Match 100.0%; Score 16; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FID 3
Db ||||
20 FID 22
RESULT 9
Y04D BPT4
ID Y04D BPT4 STANDARD; PRT; 43 AA.
AC P07080;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 5.1 kDa protein in Gp55-nrdG intergenic region.
GN Y04D OR 55.4.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C;
RX MEDLINE=87203398; PubMed=3575111;
Tomaschewski J., Rueger W.;

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RT "Nucleotide sequence and primary structures of gene products coded
RT for by the T4 genome between map positions 48.266 kb and 39.166 kb.";
RL Nucleic Acids Res. 15:3632-3633 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22514363; PubMed=12626685;
RT Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
RT "Bacteriophage T4 genome.";
RL Microbiol. Mol. Biol. Rev. 67:86-156 (2003).
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CC -----
CC EMBL; Y00122; CAA68317.1; -.
DR EMBL; AF158101; AAD42495.1; -.
DR PIR; C30292; ZDBPT9.
KW Hypothetical protein.
SQ SEQUENCE 43 AA; 5146 MW; 9549CB24D73F8D0C CRC64;
Query Match 100.0%; Score 16; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FID 3
Db ||||
34 FID 36
RESULT 10
YORV TTV1
ID YORV TTV1 STANDARD; PRT; 52 AA.
AC P19306;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hypothetical 5.9 kDa protein.
OS Thermoproteus tenax virus 1 (strain KRA1) (TTV1).
OC Viruses; dsDNA viruses, no RNA stage; Lipothirixviridae;
OC Lipothirixvirus.
OX NCBI_TaxID=10480;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90245666; PubMed=2336394;
RA Neumann H., Zillig W.;
RT "Nucleotide sequence of the viral protein TPX of the TTV1 variant
RT VT3.";
RL Nucleic Acids Res. 18:2171-2171 (1990).
CC -----
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CC -----
CC EMBL; X14855; CAA33003.1; -.
DR EMBL; X14717; CAA32839.1; -.
DR PIR; S15922; S15922.
KW Hypothetical protein.
SQ SEQUENCE 52 AA; 5903 MW; 6293C63C4CCEDE2B CRC64;
Query Match 100.0%; Score 16; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FID 3
Db ||||

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Db      16 FID 18

RESULT 11
AMA2_ALLMI
ID AMA2_ALLMI STANDARD; PRT; 54 AA.
AC P40642;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE SRY-related protein AMA2 (Fragment).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93184703; PubMed=8443573;
RA Coriati A.M., Mueller U., Harry J.L., Uwanogho D., Sharpe P.T.;
RT "PCR amplification of SRY-related gene sequences reveals evolutionary
RT conservation of the SRY-box motif."
RL PCR Methods Appl. 2:218-222(1993).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 1 HMG box domain.
CC
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CC
CC EMBL; M86319; AAA48532.1; -.
CC PIR; I50029; I50029.
CC HSSP; Q05066; 1HRY.
CC InterPro; IPR000910; HMG_12_box.
CC Pfam; PF00505; HMG_box; 1.
CC SMART; SM00398; HMG; 1.
CC PROSITE; PS0118; HMG_BOX_2; 1.
CC DNA-binding; Nuclear protein.
KW NON_TER 1
FT DNA_BIND <1 51 HMG BOX.
FT NON_TER 54 54
FT SEQUENCE 54 AA; 6535 MW; 1677E5076E9B7564 CRC64;
SQ
Query Match 100.0%; Score 16; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FID 3
Db 32 FID 34

RESULT 13
CH01_CHICK
ID CH01_CHICK STANDARD; PRT; 54 AA.
AC P40665;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE SRY-related protein CH1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RX MEDLINE=93184703; PubMed=8443573;
RA Coriati A.M., Mueller U., Harry J.L., Uwanogho D., Sharpe P.T.;
RT "PCR amplification of SRY-related gene sequences reveals evolutionary
RT conservation of the SRY-box motif."
RL PCR Methods Appl. 2:218-222(1993).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 1 HMG box domain.
CC
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CC
CC EMBL; M86320; AAA48676.1; -.
CC PIR; I50190; I50190.
CC HSSP; Q05066; 1HRY.
CC InterPro; IPR000910; HMG_12_box.
CC Pfam; PF00505; HMG_box; 1.
CC SMART; SM00398; HMG; 1.
CC PROSITE; PS0118; HMG_BOX_2; 1.

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KW DNA-binding; Nuclear protein.
FT NON TER 1 1
FT DNA_BIND <1 >54 HMG BOX.
FT NON TER 54 54
SQ SEQUENCE 54 AA; 6574 MW; A5B915076E95957D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 32 FID 34

RESULT 14
CH02_CHICK STANDARD; PRT; 54 AA.
AC P40666;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE SRY-related protein CH2 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93184703; PubMed=8443573;
RA Coriat A.M.; Mueller U.; Harry J.L.; Uwanogho D.; Sharpe P.T.;
RT "PCR amplification of SRY-related gene sequences reveals evolutionary
conservation of the SRY-box motif.";
RL PCR Methods Appl. 2:218-222(1993).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: Contains 1 HMG box domain.
CC
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CC
CC EMBL; M86322; AAA48678.1; -.
CC HSP; Q05066; IHRV.
CC InterPro: IPR000910; HMG_12_box.
CC Pfam; PF00505; HMG_box; 1.
CC SMART; SM00398; HMG; 1.
CC PROSITE; PS50118; HMG_BOX_2; 1.
CC DNA-binding; Nuclear protein.
FT NON TER 1 >54 HMG BOX.
FT DNA_BIND <1 >54
FT NON TER 54 54
SQ SEQUENCE 54 AA; 6489 MW; 1677E4B8EE59FD54 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 32 FID 34

Search completed: September 30, 2004, 06:01:23
Job time : 3.83051 secs

KW DNA-binding; Nuclear protein.
FT NON TER 1 1
FT DNA_BIND <1 >54 HMG BOX.
FT NON TER 54 54
SQ SEQUENCE 54 AA; 6574 MW; A5B915076E95957D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 32 FID 34

RESULT 15
CH03_CHICK STANDARD; PRT; 54 AA.
AC P40667;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE SRY-related protein CH3 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93184703; PubMed=8443573;
RA Coriat A.M.; Mueller U.; Harry J.L.; Uwanogho D.; Sharpe P.T.;
RT "PCR amplification of SRY-related gene sequences reveals evolutionary
conservation of the SRY-box motif.";
RL PCR Methods Appl. 2:218-222(1993).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: Contains 1 HMG box domain.
CC
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CC
CC EMBL; M86321; AAA48678.1; -.
CC FIR; I50191; I50191.
CC HSP; Q05066; IHRV.
CC InterPro: IPR000910; HMG_12_box.
CC Pfam; PF00505; HMG_box; 1.
CC SMART; SM00398; HMG; 1.
CC PROSITE; PS50118; HMG_BOX_2; 1.
CC DNA-binding; Nuclear protein.
FT NON TER 1 >54 HMG BOX.
FT DNA_BIND <1 >54
FT NON TER 54 54
SQ SEQUENCE 54 AA; 6523 MW; 1672A007A5A8EC54 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 32 FID 34

RESULT 15
CH03_CHICK STANDARD; PRT; 54 AA.
AC P40667;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE SRY-related protein CH3 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93184703; PubMed=8443573;
RA Coriat A.M.; Mueller U.; Harry J.L.; Uwanogho D.; Sharpe P.T.;
RT "PCR amplification of SRY-related gene sequences reveals evolutionary
conservation of the SRY-box motif.";
RL PCR Methods Appl. 2:218-222(1993).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: Contains 1 HMG box domain.
CC
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CC
CC EMBL; M86322; AAA48681.1; -.
CC HSP; Q05066; IHRV.
CC InterPro: IPR000910; HMG_12_box.
CC Pfam; PF00505; HMG_box; 1.
CC SMART; SM00398; HMG; 1.
CC PROSITE; PS50118; HMG_BOX_2; 1.
CC DNA-binding; Nuclear protein.
FT NON TER 1 >54 HMG BOX.
FT DNA_BIND <1 >54
FT NON TER 54 54
SQ SEQUENCE 54 AA; 6489 MW; 1677E4B8EE59FD54 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 32 FID 34

Search completed: September 30, 2004, 06:01:23
Job time : 3.83051 secs

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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 9.81356 Seconds  
(without alignments)  
96.454 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP\_TREMBL\_25.\*

2: SP\_Archaea.\*

3: SP\_Bacteria.\*

4: SP\_Fungi.\*

5: SP\_Human.\*

6: SP\_Invertebrate.\*

7: SP\_Mammal.\*

8: SP\_MHC.\*

9: SP\_Organelle.\*

10: SP\_Phage.\*

11: SP\_Plant.\*

12: SP\_Rodent.\*

13: SP\_Virus.\*

14: SP\_Vertebrate.\*

15: SP\_Unclassified.\*

16: SP\_Rv.\*

17: SP\_Bacteriophage.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	15	2 Q9KIV5	Q9Kiv5 anabaena sp
2	16	100.0	15	2 Q9R4K0	Q9r4k0 nocardia. n
3	16	100.0	20	15 Q95485	Q95485 avian leuko
4	16	100.0	24	2 Q92630	Q92630 streptococc
5	16	100.0	24	2 Q9R2R0	Q9r2r0 streptococc
6	16	100.0	24	11 Q8CGM9	Q8cgm9 mus musculu
7	16	100.0	25	16 Q9K7M7	Q9k7m7 bacillus ha
8	16	100.0	28	2 Q8KS87	Q8ks87 escherichia
9	16	100.0	29	16 Q8CLJ9	Q8clj9 versinia pe
10	16	100.0	29	16 Q87L17	Q87l17 vibrio para
11	16	100.0	30	4 Q9NRCS	Q9nrcs homo sapien
12	16	100.0	30	16 Q8INQ6	Q8inq6 bacillus an
13	16	100.0	31	2 Q9S0E6	Q9s0e6 borrelia bu
14	16	100.0	31	16 Q9PGG1	Q9pgg1 xylella fas
15	16	100.0	31	16 Q8KGF6	Q8kgf6 chlorobium
16	16	100.0	31	16 Q8EIW8	Q8eiw8 shewanella

17	16	100.0	32	2 Q50110	Q50110 mycobacteri
18	16	100.0	32	16 Q87IK8	Q87ik8 vibrio para
19	16	100.0	33	10 Q9S7Y3	Q9s7y3 picea abies
20	16	100.0	33	16 Q9KPS8	Q9kps8 vibrio chol
21	16	100.0	33	16 Q97R10	Q97r10 streptococc
22	16	100.0	34	3 Q00062	Q00062 absidia gla
23	16	100.0	34	16 Q8FXD9	Q8fxd9 brucella su
24	16	100.0	34	16 Q8FA7	Q8fa7 leptospira
25	16	100.0	34	16 Q8EFC4	Q8efc4 shewanella
26	16	100.0	35	2 Q939H2	Q939h2 pseudomonas
27	16	100.0	35	2 P95513	P95513 pasteurella
28	16	100.0	35	16 Q98NE6	Q98ne6 rhizobium l
29	16	100.0	35	16 Q8FOE7	Q8foe7 leptospira
30	16	100.0	36	16 Q9ASR6	Q9asr6 caulobacter
31	16	100.0	37	10 Q9SMC9	Q9smc9 lycopersico
32	16	100.0	37	16 Q92VS6	Q92vs6 rhizobium m
33	16	100.0	37	16 Q8F3C0	Q8f3c0 leptospira
34	16	100.0	37	16 Q8EZA2	Q8eza2 leptospira
35	16	100.0	38	5 Q7Z149	Q7z149 caenorhabdi
36	16	100.0	38	11 Q9ES99	Q9es99 rattus norv
37	16	100.0	38	16 Q8DYH6	Q8dyh6 streptococc
38	16	100.0	38	16 Q87LD2	Q87ld2 vibrio para
39	16	100.0	39	2 Q7WTL7	Q7wtl7 bacillus ce
40	16	100.0	39	16 Q9KPJ5	Q9kps5 vibrio chol
41	16	100.0	39	16 Q92TN5	Q92tn5 rhizobium m
42	16	100.0	40	2 Q8KSF6	Q8ksf6 mycobacteri
43	16	100.0	40	5 Q8MN47	Q8mn47 dictyosteli
44	16	100.0	40	8 Q8HBW1	Q8hbw1 arabidopsis
45	16	100.0	40	8 Q8HBW0	Q8hbw0 arabidopsis

ALIGNMENTS

RESULT 1

Q9KIV5 PRELIMINARY; PRT; 15 AA.

AC Q9KIV5; 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Putative deoxyribose-phosphate aldolase (Fragment).  
OS Anabaena sp. (strain PCC 7120).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
CX NCBI\_TaxID=103690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PC7120;  
RA Matveyev A.V., Young K.T., Elhai J.;  
RT "DNA methyltransferases with unusual structural properties from the  
cytobacterium Anabaena PCC7120.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF220508; AAF75233.1; -.  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1608 MW; 1B1307FDA6850099 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3

Db 13 FID 15

RESULT 2

Q9R4K0 PRELIMINARY; PRT; 15 AA.

AC Q9R4K0; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Nitric oxide synthase (EC 4.14.23.-) (Fragment).

OS Nocardia.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Nocardiaceae.  
 OX NCBI\_TaxID=1817;  
 RN [1]  
 RN SEQUENCE.  
 RP MEDLINE=95394819; PubMed=7545152;  
 RX Chen Y., Rosazza J.P.;  
 RA "Purification and characterization of nitric oxide synthase (NOSVoc)  
 RT from a Nocardia species.";  
 RL J. Bacteriol. 177:5122-5128(1995).  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1818 MW; 2BD5B859DE288B77 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 Db 13 FID 15

RESULT 3  
 Q85485  
 ID Q85485 PRELIMINARY; PRT; 20 AA.  
 AC Q85485;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Gag-erbB fusion protein (Fragment).  
 OS Avian leukosis virus.  
 OC Viruses; Retroviridae; Retroviridae; Alpharetrovirus.  
 OX NCBI\_TaxID=11864;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=RAV1;  
 RC MEDLINE=88230605; PubMed=2897475;  
 RX Raines M.A., Mailhe N.J., Moscovici C., Crittenden L., Kung H.-J.;  
 RA "Mechanism of c-erbB transduction: Newly released transducing viruses  
 RT retain poly(A) tracts of erbB transcripts and encode C-terminally  
 RT intact erbB proteins";  
 RL J. Virol. 62:2437-2443(1988).  
 DR EXBL; M19970; AAA42586.1; -;  
 DR InterPro; IPR009030; Grow\_fac\_recep.  
 FT NON\_TER 1 1  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2167 MW; 2A4EFD2E3A709011 CRC64;

Query Match 100.0%; Score 16; DB 15; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 Db 11 FID 13

RESULT 4  
 Q9Z630  
 ID Q9Z630 PRELIMINARY; PRT; 24 AA.  
 AC Q9Z630;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Capsular polysaccharide B (Fragment).  
 GN CPBB.  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1313;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=99287847; PubMed=10348877;  
 RA Morona J.K., Morona R., Paton J.C.;  
 RT "Analysis of the 5' portion of the type 19A capsule locus identifies  
 RT two classes of cpsC, cpsD, and cpsE genes in Streptococcus  
 RT pneumoniae.";  
 RL J. Bacteriol. 181:3599-3605(1999).  
 DR EXBL; AF106135; AAD17981.1; -;  
 FT NON\_TER 1 1  
 FT NON\_TER 24 24  
 SQ SEQUENCE 24 AA; 2834 MW; ED047715CF82D83B CRC64;

Query Match 100.0%; Score 16; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 Db 11 FID 13

RESULT 5  
 Q9R2R0  
 ID Q9R2R0 PRELIMINARY; PRT; 24 AA.  
 AC Q9R2R0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Capsular polysaccharide B (Fragment).  
 GN CPBB.  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=99287847; PubMed=10348877;  
 RA Morona J.K., Morona R., Paton J.C.;  
 RT "Analysis of the 5' portion of the type 19A capsule locus identifies  
 RT two classes of cpsC, cpsD, and cpsE genes in Streptococcus  
 RT pneumoniae.";  
 RL J. Bacteriol. 181:3599-3605(1999).  
 DR EXBL; AF106134; AAD17979.1; -;  
 DR EXBL; AF106132; AAD17975.1; -;  
 DR EXBL; AF106133; AAD17977.1; -;  
 FT NON\_TER 1 1  
 FT NON\_TER 24 24  
 SQ SEQUENCE 24 AA; 2820 MW; ED047715CF90483B CRC64;

Query Match 100.0%; Score 16; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 Db 11 FID 13

RESULT 6  
 Q8CGM9  
 ID Q8CGM9 PRELIMINARY; PRT; 24 AA.  
 AC Q8CGM9;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Retinoblastoma-binding protein 1 (Fragment).  
 GN RBP1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=129X1/SVD;  
 RA Binda O., Branton P.E.;

RT "Mus musculus 129x1/SvJ Partial RBSP1 Genomic Sequence.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY163235; AAN84616.1; -;  
 FT NON\_TER 1 1  
 FT NON\_TER 24 24  
 SQ SEQUENCE 24 AA; 2685 MW; BF6991AC3DS2BC4E CRC64;

Query Match 100.0%; Score 16; DB 11; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 ||||  
 Db 20 FID 22

RESULT 7  
 Q9K7M7 PRELIMINARY; PRT; 25 AA.

AC Q9K7M7;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein BH3334.

OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OC NCBI\_TaxID=86665;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C-125 / JCM 9153;

RA MEDLINE=20512582; PubMed=11058132;

RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,

RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,

RA Horikoshi K.;

RT "Complete genome sequence of the alkaliphilic bacterium Bacillus

RT halodurans and genomic sequence comparison with Bacillus subtilis.";

RL Nucleic Acids Res. 28:4317-4331(2000).

DR EMBL; AP001518; BAB07053.1; -;

DR PIR; F84066; F84066.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 25 AA; 2986 MW; OC31EA93BE976875 CRC64;

Query Match 100.0%; Score 16; DB 16; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 ||||  
 Db 13 FID 15

RESULT 8  
 Q8KS87 PRELIMINARY; PRT; 28 AA.

AC Q8KS87;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Putative oxidoreductase Fe-S subunit (Fragment).

GN B1589.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI\_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ECOR-9;

RA MEDLINE=22053230; PubMed=12057959;

RA Sandt C.H., Hopper J.E., Hill C.W.;

RT "Activation of Prophage e1b Genes for Immunoglobulin-Binding Proteins

RT by Genes from the IbrAB Genetic Island of Escherichia coli ECOR-9.";

RL J. Bacteriol. 184:3640-3648(2002).

DR EMBL; AF520223; AAM53254.1; -;  
 FT NON\_TER 28 28  
 SQ SEQUENCE 28 AA; 3185 MW; A2F42416487ED57B CRC64;

Query Match 100.0%; Score 16; DB 2; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 ||||  
 Db 8 FID 10

RESULT 9  
 Q8CLJ9 PRELIMINARY; PRT; 29 AA.

AC Q8CLJ9;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical.

GN Y1162.

OS Versinia pestis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Versinia.

OX NCBI\_TaxID=632;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=KIMS / Biovar Mediaevalis;

RA MEDLINE=22137863; PubMed=12142430;

RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,

RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,

RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

RA Perry R.D.;

RT "Genome sequence of Versinia pestis KIM.";

RL J. Bacteriol. 184:4601-4611(2002).

DR EMBL; AE013720; AAM84740.1; -;

KW Hypothetical protein.

SQ SEQUENCE 29 AA; 3489 MW; A300F9DE223524E CRC64;

Query Match 100.0%; Score 16; DB 16; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 ||||  
 Db 11 FID 13

RESULT 10  
 Q87L17 PRELIMINARY; PRT; 29 AA.

AC Q87L17;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein.

GN VP2800.

OS Vibrio parahaemolyticus.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI\_TaxID=670;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RMD 2210633 / Serotype O3:K6;

RA MEDLINE=22508454; PubMed=12620739;

RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

RT distinct from that of V. cholerae.";

RL Lancet 361:743-749(2003).

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DR EMBL; AF005082; BAC61063.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 29 AA; 3534 MW; B1263708FB2189DB CRC64;

Query Match 100.0%; Score 16; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 9 FID 11

RESULT 11
Q9NRCS PRELIMINARY; PRT; 30 AA.
ID Q9NRCS5
AC Q9NRCS5
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE ATP7B (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu Z.Y., Wang N., Murong S.X.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF234621; AAF89169.1; -.
FT NON_TER 1
FT NON_TER 30
SQ SEQUENCE 30 AA; 3451 MW; 90ED003AF2D173FB CRC64;

Query Match 100.0%; Score 16; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 19 FID 21

RESULT 12
Q81NQ6 PRELIMINARY; PRT; 30 AA.
ID Q81NQ6
AC Q81NQ6;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN B3122
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Remond C., Thwaitte J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AE017033; AAP26932.1; -.

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DR TIGR; BA3122; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 30 AA; 3565 MW; 8614AD8904A34084 CRC64;

Query Match 100.0%; Score 16; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 11 FID 13

RESULT 13
Q9S0E6 PRELIMINARY; PRT; 31 AA.
ID Q9S0E6
AC Q9S0E6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN BBR30
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RA Fraser C.M., Castjens S., Huang W.M., Sutton G.G., Lathigra R.,
RA White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt R.,
RA Palmer N., Haft D., Rosa P., Stevenson B.;
RT "A bacterial genome in flux: The twelve linear and nine circular
RT extrachromosomal DNAs in an infectious isolate of the Lyme disease
RT spirochete Borrelia burgdorferi."
RL Mol. Microbiol. 0:0-0(1999).
DR EMBL; AE001577; AAF07528.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; plasmid.
SQ SEQUENCE 31 AA; 3761 MW; E9D77A1F04A6FF3B CRC64;

Query Match 100.0%; Score 16; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 5 FID 7

RESULT 14
Q9PGG1 PRELIMINARY; PRT; 31 AA.
ID Q9PGG1
AC Q9PGG1;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein Xf0341.
GN XF0341.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OX Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvares R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo L.E.A., Camargo A.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.F., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

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Db 12 FID 14  
Search completed: September 30, 2004, 05:59:39  
Job time : 12.9802 secs

RA Praga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,  
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
RA Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
RA Krieger J.E., Kuranai E.Z., Laigret P., Lambais M.R., Leite L.C.C.,  
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.B.,  
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
RA Feixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,  
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,  
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,  
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,  
RA "The genome sequence of the plant pathogen Xylella fastidiosa."  
RL Nature 406:151-159(2000).  
DR EMBL; AEO03886; AAF83151.1; -.  
DR PIR; H82818; H82818.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 31 AA; 3827 MW; E955F867670E7382 CRC64;

Query Match 100.0%; Score 16; DB 16; Length 31;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FID 3  
Db 16 FID 18

RESULT 15  
Q8KGF6 PRELIMINARY; PRT; 31 AA.  
AC Q8KGF6  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein CT0012.  
GN CT0012.  
OS Chlorobium tepidum.  
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
OC Chlorobium.  
OX NCBI\_TaxID=1097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TLS / ATCC 49652 / DSM 12025;  
RX MEDLINE=22103685; Pubmed=12093901;  
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,  
RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,  
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,  
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,  
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,  
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,  
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;  
RA "The complete genome sequence of Chlorobium tepidum TLS, a  
RT photosynthetic, anaerobic, green-sulfur bacterium."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).  
DR EMBL; AE012781; AAW71260.1; -.  
DR TIGR; CT0012; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 31 AA; 3608 MW; 353F138B1A882EDF CRC64;

Query Match 100.0%; Score 16; DB 16; Length 31;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FID 3  
Db 16 FID 18

Blank Sheet

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 14.6441 Seconds  
(without alignments)  
57.883 Million cell updates/sec

Title: US-09-674-716B-13  
Perfect score: 16  
Sequence: 1 FID 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A Genesep 29Jan04:\*
- 1: genesep1980s:\*
  - 2: genesep1990s:\*
  - 3: genesep2000s:\*
  - 4: genesep2001s:\*
  - 5: genesep2002s:\*
  - 6: genesep2003as:\*
  - 7: genesep2003bs:\*
  - 8: genesep2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	3	AAY32259	Light chain CDR H3 of mouse anti-CD23 Mab C11.
2	16	100.0	3	AAP94794	Peripheral
3	16	100.0	5	AAM55773	Immunisat
4	16	100.0	5	AAM55773	Immunisat
5	16	100.0	5	AAM55773	Immunisat
6	16	100.0	6	AAR29321	Endotheli
7	16	100.0	6	AAR29321	Endotheli
8	16	100.0	6	AAR29321	Endotheli
9	16	100.0	6	AAR29321	Endotheli
10	16	100.0	7	AAB06594	Claudin-6
11	16	100.0	7	AAB06594	Claudin-6
12	16	100.0	7	AAB06594	Claudin-6
13	16	100.0	7	AAB06594	Claudin-6
14	16	100.0	8	AAB06597	Claudin-6
15	16	100.0	8	AAB06597	Claudin-6
16	16	100.0	8	AAB06597	Claudin-6
17	16	100.0	8	AAB06597	Claudin-6
18	16	100.0	8	AAB06597	Claudin-6
19	16	100.0	8	AAB06597	Claudin-6
20	16	100.0	8	AAB06597	Claudin-6
21	16	100.0	8	AAB06597	Claudin-6
22	16	100.0	8	AAB06597	Claudin-6
23	16	100.0	8	AAB06597	Claudin-6
24	16	100.0	8	AAB06597	Claudin-6
25	16	100.0	8	AAB06597	Claudin-6

26	16	100.0	9	3	AAB06780	Claudin-6
27	16	100.0	9	3	AAB06780	Claudin-6
28	16	100.0	9	3	AAB06780	Claudin-6
29	16	100.0	9	3	AAB06780	Claudin-6
30	16	100.0	9	3	AAB06780	Claudin-6
31	16	100.0	9	3	AAB06780	Claudin-6
32	16	100.0	9	3	AAB06780	Claudin-6
33	16	100.0	9	3	AAB06780	Claudin-6
34	16	100.0	9	3	AAB06780	Claudin-6
35	16	100.0	9	3	AAB06780	Claudin-6
36	16	100.0	9	3	AAB06780	Claudin-6
37	16	100.0	9	3	AAB06780	Claudin-6
38	16	100.0	9	3	AAB06780	Claudin-6
39	16	100.0	9	3	AAB06780	Claudin-6
40	16	100.0	9	3	AAB06780	Claudin-6
41	16	100.0	9	3	AAB06780	Claudin-6
42	16	100.0	9	3	AAB06780	Claudin-6
43	16	100.0	9	3	AAB06780	Claudin-6
44	16	100.0	9	3	AAB06780	Claudin-6
45	16	100.0	9	3	AAB06780	Claudin-6

ALIGNMENTS

RESULT 1  
RAY32259  
ID AAY32259 standard; peptide; 3 AA.  
XX  
AC AAY32259;  
XX  
DT 15-FEB-2000 (first entry)  
XX  
DE Light chain CDR H3 of mouse anti-CD23 Mab C11.  
XX  
KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;  
KW monoclonal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;  
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW Sjogren's syndrome; allergy; rhinitis; eczema; insulinitis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
KW therapy.  
XX  
OS Mus musculus.  
XX  
PN WO9958679-A1.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-GB001434.  
XX  
PR 09-MAY-1998; 98GB-00009839.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
XX  
DR WPI: 2000-053101/04.  
XX  
DR N-PSDB; AAZ34744.  
XX  
PT Cell receptor specific antibodies useful for treating e.g. arthritis,  
XX  
PT diabetes, multiple sclerosis and psoriasis.  
XX  
PS Claim 1; Page 40; 81pp; English.  
XX  
CC This sequence represents complementarity determining region 3 (CDR H3)  
XX  
CC of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11  
XX  
CC (see also AAY32259). The invention provides altered antibodies, such as  
XX  
CC chimeric or humanised antibodies, which comprise sufficient of the amino  
XX  
CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC ashmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type I diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents  
 XX

SQ Sequence 3 AA;

Query Match 100.0%; Score 16; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
 |||  
 Db 1 FID 3

#### RESULT 2

AAAP94794  
 ID AAP94794 standard; protein; 5 AA.

XX

AC AAP94794;

XX

DT 25-MAR-2003 (revised)

DT 09-JUL-1990 (first entry)

XX Peripheral nervous system myelin protein, proteolipid protein, a PNS CNS  
 DE myelin component and acetyl choline receptor epitope associated motif.

XX Autoantigen; MBP; myelin basic protein; transplantation antigen;

KW myasthenia gravis; myasthenics; Transplantation antigen.  
 XX

OS Synthetic.

XX

XX EP304279-A.

XX

PD 22-FEB-1989.

XX

PF 17-AUG-1988; 88EP-00307608.

XX

PR 17-AUG-1987; 87US-00086694.

XX

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

XX

PI Steinman L, Zamvil S;

XX

DR WPI; 1989-055696/08.

XX

XX Oligopeptide and polypeptide compns. - based on the amino acid sequence

PT of an immunogen and used for modulating the immune system.

XX

PS Disclosure; Page; 7pp; English.

XX

XX Sequences will normally be part of 9 to 15 AA sequence, excluded as

CC motifs for immunisation but useful in tolerisation. (Updated on 25-MAR-

CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)

CC (Updated on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 16; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
 |||

Db 3 FID 5

#### RESULT 3

AAW55773  
 ID AAW55773 standard; peptide; 5 AA.

XX

AC AAW55773;

XX

DT 25-MAR-2003 (revised)

DT 08-JUL-1998 (first entry)

XX

DE Immunisation motif associated with AChR 4.

XX

KW Myelin basic protein; immunity; immune response; neurological; T-cell;

KW human; immunogen; B-cell; transplantation antigen; immunomodulator.

XX

OS Unidentified.

XX

PN EP805162-A1.

XX

PD 05-NOV-1997.

XX

PF 17-AUG-1988; 97EP-00106788.

XX

PR 17-AUG-1987; 87US-00086694.

PR 17-AUG-1988; 88EP-00307608.

XX

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

XX

PI Steinman L, Zamvil S;

XX

DR WPI; 1998-034664/04.

XX

PT Polypeptide comprising human myelin basic protein fragment - useful as

PT immuno modulator.

XX

PS Disclosure; Page 8; 8pp; English.

XX

CC The present sequence represents an immunisation motif normally excluded,

CC but which may be used with advantage for tolerisation by itself or in

CC conjunction with other epitope sequences from the present invention. The

CC present invention describes a polypeptide comprising a human myelin basic

CC protein (hMBP) fragment including P89-101 of hMBP, excluding native hMBP.

CC The term P89-101 is not defined but may be intended to mean amino acids

CC 89-101 of hMBP. The polypeptide can be used for tolerising a mammalian

CC host immune system comprising B and T cells to an immunogen of interest,

CC wherein said immunogen is restricted by a transplantation antigen of said

CC host. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-

CC 2003 to correct PR field.)

XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 16; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3

|||

Db 3 FID 5

#### RESULT 4

AAU86974  
 ID AAU86974 standard; peptide; 5 AA.

XX

AC AAU86974;

XX

DT 21-MAY-2002 (first entry)

XX

DE Estradiol mimotope peptide #22.

XX

KW Estradiol; mimotope; estrone-3-glucuronide; steroid detection;

immunosuppressive; neuroprotective.  
Homo sapiens.  
US2002076412-A1.  
20-JUN-2002.  
07-JUN-1995; 95US-00484409.  
17-AUG-1987; 87US-00086694.  
12-JUL-1989; 89US-00379500.  
01-MAY-1990; 90US-00517245.  
01-MAY-1991; 91WO-US0002991.  
30-APR-1992; 92US-00877444.  
21-MAY-1993; 93US-0006325.  
22-SEP-1993; 93US-00125407.  
(STEI/) STEINMAN L.  
(ZAMV) ZAMVIL S.  
Steinman L, Zamvil S;  
WPI; 2002-598709/64.  
Modulating or tolerizing the immune system, useful for treating multiple sclerosis, by administering a peptide derived from human myelin binding protein.  
Disclosure; Page 15; 21pp; English.  
This invention describes a novel method for modulating or tolerizing the immune system, and for treating multiple sclerosis comprising administering a peptide derived from MBP (human myelin basic protein). The peptide induces an autoimmune response (T cell) to a self-antigen (or part of it), and binds to an MHC (major histocompatibility complex) antigen of a host susceptible to autoimmune diseases, i.e. competes with binding to MBP and inhibit proliferation of MBP-reactive cells. The peptide has immunosuppressive and neuroprotective activity. This sequence represents a peptide derived from the human MBP protein which can be used for tolerization  
Sequence 5 AA;  
Query Match 100.0%; Score 16; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FID 3  
Db 3 FID 5  
RESULT 6  
AAR29321  
ID AAR29321 standard; peptide; 6 AA.  
XX AAR29321;  
AC  
XX 25-MAR-2003 (revised)  
DT 13-APR-1993 (first entry)  
XX Endothelin antagonist peptide.  
DE  
XX Hypertension; myocardial infarction; congestive heart failure;  
KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;  
KW acute renal failure; pre-eclampsia; diabetes; metabolic; endocrinological;  
KW neurological disorders.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1  
FT

immunoassay; phage display; immunogen.  
Synthetic.  
WO200212270-A1.  
14-FEB-2002.  
26-JUL-2001; 2001WO-EP008705.  
03-AUG-2000; 2000EP-00306613.  
(UNIL ) UNILEVER PLC.  
(UNIL ) UNILEVER NV.  
(UNIL ) HINDUSTAN LEVER LTD.  
Badley RA, Berry MJ, Williams SC;  
WPI; 2002-241729/29.  
Peptide mimotope capable of binding specifically to antibody specific to estradiol, useful for assaying presence and/or amount of estradiol, especially estrone-3-glucuronide in sample.  
Claim 3; Page 22; 57pp; English.  
The invention relates to a purified peptide mimotope capable of binding specifically to an antibody specific to estradiol. Also included are a solid support having immobilised (releasably or non-releasably) peptide mimotopes, an immunoassay test device for the detection of estradiol in the sample, comprising the mimotopes and an antibody capable of binding specifically to the mimotopes to generate a detectable signal and an isolated nucleic acid encoding the peptide mimotopes. The mimotope is useful for assaying the presence and/or amount of estradiol preferably estrone-3-glucuronide in a sample which is urine or serum sample to be tested and is also utilised in an immunoassay test device, and further can be used as immunogens. The mimotope be used to construct new, or improve the performance of old, immunoassay test formats and devices. They can, for example, be utilised essentially to tune the signal in conventional displacement assays for the detection of estradiol. The mimotope can be bound directly to certain assay surfaces which are otherwise non-compatible with estradiol on such surfaces needing to be bound to the surface by complexing with another - often proteinaceous - molecule. The mimotope is capable of being bound to the antigen-binding site of an antibody in a selective fashion in the presence of excess quantities of other undesired materials, and tightly enough (i.e. with high enough affinity) that when used in an immunoassay, it provides a useful result). The present sequence is a peptide mimotopes of the invention  
Sequence 5 AA;  
Query Match 100.0%; Score 16; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FID 3  
Db 3 FID 5  
RESULT 5  
ABB84336  
ID ABB84336 standard; peptide; 5 AA.  
XX ABB84336;  
AC  
XX 17-OCT-2002 (first entry)  
DT  
XX Human MBP protein derived peptide SEQ ID 36.  
DE  
XX MBP; myelin basic protein; human; tolerance; immune system;  
KW multiple sclerosis; autoimmune response; autoimmune disease;  
KW

FT XX WO9220706-A1. /note= "Ac-D-Phe"

FN XX 26-NOV-1992.

PD XX 24-APR-1992; 92WO-US003408.

PF XX 16-MAY-1991; 91US-00701274.

PR XX 18-DEC-1991; 91US-00809746.

XX (WARN ) WARNER LAMBERT CO.

XX Cody WL, Depue P, Doherty AM, Taylor MD;

PI WPI; 1992-415706/50.

DR New peptide(s) used as endothelin antagonists - for treating

XX hypertension, metabolic and endocrine disorders, heart failure, diabetes,

PT asthma, neurological disorders, etc.

PT Claim 5; Page 86; 116pp; English.

PS The peptide is an endothelin antagonist useful in controlling

CC hypertension, myocardial infarction, congestive heart failure, endotoxemic

CC shock, subarachnoid haemorrhage, asthma, arrhythmias, acute renal

CC failure, preclampsia, diabetes and metabolic, endocrinological and

CC neurological disorders. Administration is oral parenteral or by

CC inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/ day. It may be

CC prepared by conventional peptide synthesis. (Updated on 25-MAR-2003 to

CC correct PN field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 16; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. NO. 1.4e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3

Db 1 FID 3

RESULT 7

AA069115

ID AAR69115 standard; peptide; 6 AA.

XX AAR69115;

AC 25-MAR-2003 (revised)

DT 05-MAR-1995 (first entry)

XX Endothelin C-terminal peptide analog, useful as antagonist.

DE Endothelin; ET-1; receptor; antagonist.

XX Synthetic.

OS Key Location/Qualifiers

FT Misc-difference 1 /note= "Ac-D-Phe"

FT WO9414843-A1.

PN 07-JUL-1994.

XX 17-DEC-1993; 93WO-US012377.

PF 21-DEC-1992; 92US-00995480.

XX (WARN ) WARNER LAMBERT CO.

PA Cody WL, Depue P, Doherty AM, He JX, Taylor MD;

PI

XX WPI; 1994-234617/28.

DR New hexa-peptide derivs. inhibiting endothelin - for treatment of e.g.

XX renal failure, hypertension, asthma, restenosis, angina, cancer etc.

PT Claim 5; Page 112; 146pp; English.

PS Novel antagonists of endothelin are claimed which are C-terminal

XX hexapeptides and analogs of ET-1. The first (N-terminal) amino acid of

CC the new peptides has D-configuration. The peptides are claimed

CC generically. The present peptide is a specifically claimed example of the

CC generic compounds. The peptides are useful for treating hypertension,

CC metabolic and endocrine disorders, congestive heart failure, myocardial

CC infarction, endotoxic shock, subarachnoid haemorrhage, arrhythmia,

CC asthma, acute and chronic renal failure, preclampsia, diabetes,

CC neurological disorders, pulmonary hypertension, ischaemic disease,

CC ischaemic bowel disease, gastric mucosal damage, Raynaud's disease,

CC restenosis, percutaneous transluminal coronary angioplasty, angina and

CC cancer. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 16; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. NO. 1.4e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3

Db 1 FID 3

RESULT 8

AAW31469

ID AAW31469 standard; protein; 6 AA.

XX AAW31469;

AC 04-AUG-1998 (first entry)

DT Transcriptional activator peptide fragment LSI32.

XX Activating sequence; Gal4; transcriptional activator; RNA polymerase;

DE Protein-protein interaction; gene therapy; therapeutic; holoenzyme;

KW Gall; DNA binding domain.

XX Synthetic.

OS WO9744447-A2.

PN 27-NOV-1997.

PD 02-MAY-1997; 97WO-US007338.

PF 03-MAY-1996; 96US-0017016P.

PR 01-MAY-1997; 97US-00017016.

XX (HARD ) HARVARD COLLEGE.

PA Ptashne M, Lu X, Wu Y;

XX WPI; 1998-018502/02.

DR N-PSDB; AAV02567.

XX New transcriptional activator containing DNA binding domain bound to

PT peptide - useful for controlling gene expression, especially in gene

PT therapy, and in protein-protein interaction assays, does not inhibit

PT other transcription activators.

XX Example 1; Page 26; 55pp; English.

PS AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076 are

XX fragments used in an assay to determine novel transcriptional activators.

CC

CC The method involves the production of transcriptional activators  
CC comprising of a DNA-binding group and a 6-25 amino acid peptide that is  
CC covalently bonded to the DNA binding group and does not represent a  
CC fragment of a natural transcription activator. Protein-protein  
CC interactions are identified in the assay by fusing a DNA-binding domain  
CC to a library of DNA fragments and introducing this and a fusion of target  
CC protein and a polypeptide containing a region of Gal4 which interacts  
CC with Galp1p into a cell containing Galp1p and identifying members of the  
CC library that interact with the target from activation of transcription.  
CC Such constructs are used to activate transcription in a cell, e.g. for  
CC controlling gene activity, particularly in gene therapy (e.g. recognizing  
CC a site close to a selected therapeutic gene). Transcription can be  
CC activated without blocking other transcriptional activators. They  
CC probably act by interacting with a component of the RNA polymerase II  
CC holoenzyme. Gal1, the strongest known yeast activator, which provides a  
CC more sensitive assay allowing detection of even weak protein-protein  
CC interactions. Such activators do not create toxicity problems even when  
CC overexpressed  
XX  
SQ Sequence 6 AA;  
  
Query Match 100.0%; Score 16; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FID 3  
DB 1 FID 3  
  
RESULT 9  
AAB06774  
ID AAB06774 standard; peptide; 7 AA.  
AC AAB06774;  
XX  
DT 28-SEP-2000 (first entry)  
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 345.  
XX  
KW Claudin-6 modulating agent; claudin-9 modulating agent;  
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;  
KW inflammatory disease; cancer; graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA001029.  
XX  
PR 03-NOV-1998; 98US-00185908.  
PR 30-MAR-1999; 99US-00282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX WPI; 2000-365610/31.  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin.  
XX  
PS Claim 73; Page 103; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins  
CC are cadherins, which are membrane glycoproteins involved in cell  
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,  
CC and these peptides can be used to modulate these levels, and thus treat  
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound

CC healing and implant adhesion. In addition, they can also be used to  
CC facilitate drug delivery to the desired target site. The present sequence  
CC has a cyclic conformation  
XX  
SQ Sequence 7 AA;  
  
Query Match 100.0%; Score 16; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FID 3  
DB 5 FID 7  
  
RESULT 10  
AAB06594  
ID AAB06594 standard; peptide; 7 AA.  
XX  
AC AAB06594;  
XX  
DT 28-SEP-2000 (first entry)  
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 227.  
XX  
KW Claudin-3 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA001029.  
XX  
PR 03-NOV-1998; 98US-00185908.  
PR 30-MAR-1999; 99US-00282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX WPI; 2000-365610/31.  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin.  
XX  
PS Claim 55; Page 99; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation  
XX  
SQ Sequence 7 AA;  
  
Query Match 100.0%; Score 16; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FID 3  
DB 5 FID 7

RESULT 11  
 AAB06656  
 ID AAB06656 standard; peptide; 7 AA.  
 AC AAB06656;  
 XX  
 DT 28-SEP-2000 (first entry)  
 XX  
 DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 174.  
 XX  
 KW Claudin-4 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.  
 XX  
 OS Mammalia.  
 XX  
 PN WO200026360-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 03-NOV-1999; 99WO-CA001029.  
 XX  
 PR 03-NOV-1998; 98US-00185908.  
 PR 30-MAR-1999; 99US-00282029.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 PI Blaschuck OW, Symonds JM, Gour BJ;  
 XX  
 DR WPI; 2000-365610/31.  
 XX  
 PT Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin.  
 XX  
 PS Claim 61; Page 101; 121pp; English.  
 XX  
 CC The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation  
 XX  
 SQ Sequence 7 AA;  
 XX  
 Query Match 100.0%; Score 16; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FID 3  
 DB 5 FID 7  
 XX  
 RESULT 12  
 ABU96533  
 ID ABU96533 standard; peptide; 7 AA.  
 AC ABU96533;  
 XX  
 DT 28-JUL-2003 (first entry)  
 XX  
 DE Human cytochrome P450 polypeptide 2C8 wild type peptide #6.  
 XX  
 KW Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;  
 KW cancer; cardiovascular disease; cytostatic; cardiovascular; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2000299099-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 31-MAY-2002; 2002WO-EP006000.  
 PR 01-JUN-2001; 2001EP-00112899.  
 XX  
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
 XX  
 PI Penger A, Sprenger R, Brinkmann U;  
 XX  
 DR WPI; 2003-167344/16.  
 XX  
 PT New polymorphic variants of the gene encoding Cytochrome P450 polypeptide  
 PT 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.  
 PT arachidonic acid metabolism, cancer or cardiovascular diseases.  
 XX  
 PS Disclosure; Page 58; 178pp; English.  
 XX  
 CC The invention describes a new polynucleotide comprises a polynucleotide:  
 CC (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined  
 CC in the specification; (b) encoding any of seven polypeptides having 7  
 CC amino acids, or a polypeptide with 3 amino acids; (c) capable of  
 CC hybridising to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)  
 CC encoding a molecular CYP2C8 variant polypeptide or its fragment. The  
 CC polynucleotide, gene, vector, polypeptide or antibody is useful for  
 CC diagnosing or treating a disease, for preparing a diagnostic composition  
 CC for diagnosing a disease, or for preparing a pharmaceutical composition  
 CC for treating a disease. This disease includes arachidonic acid  
 CC metabolism, cancer or cardiovascular diseases. This is the amino acid  
 CC sequence of a human cytochrome P450 polypeptide 2C8 (CYP2C8) wild type  
 CC peptide  
 XX  
 SQ Sequence 7 AA;  
 XX  
 Query Match 100.0%; Score 16; DB 6; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FID 3  
 DB 4 FID 6  
 XX  
 RESULT 13  
 ABU96535  
 ID ABU96535 standard; peptide; 7 AA.  
 AC ABU96535;  
 XX  
 DT 28-JUL-2003 (first entry)  
 XX  
 DE Human cytochrome P450 polypeptide 2C8 wild type peptide #7.  
 XX  
 KW Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;  
 KW cancer; cardiovascular disease; cytostatic; cardiovascular; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2000299099-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 31-MAY-2002; 2002WO-EP006000.  
 PR 01-JUN-2001; 2001EP-00112899.  
 XX  
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
 XX  
 PI Penger A, Sprenger R, Brinkmann U;  
 XX  
 DR WPI; 2003-167344/16.  
 XX



XX New polymorphic variants of the gene encoding Cytochrome P450 polypeptide  
PT 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.  
PT arachidonic acid metabolism, cancer or cardiovascular diseases.  
XX  
PS Disclosure, Page 58; 178pp; English.  
XX  
XX The invention describes a new polynucleotide comprises a polynucleotide:  
CC (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined  
CC in the specification; (b) encoding any of seven polypeptides having 7  
CC amino acids, or a polypeptide with 3 amino acids; (c) capable of  
CC hybridizing to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)  
CC encoding a molecular CYP2C8 variant polypeptide or its fragment. The  
CC polynucleotide, gene, vector, polypeptide or antibody is useful for  
CC diagnosing or treating a disease, for preparing a diagnostic composition  
CC for diagnosing a disease, or for preparing a pharmaceutical composition  
CC for treating a disease. This disease includes arachidonic acid  
CC metabolism, cancer or cardiovascular diseases. This is the amino acid  
CC sequence of a human cytochrome P450 polypeptide 2C8 (CYP2C8) wild type  
XX peptide  
XX  
SQ Sequence 7 AA;  
  
Query Match 100.0%; Score 16; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FID 3  
Db 3 FID 5  
  
RESULT 14  
AAB06597  
ID AAB06597 standard; peptide; 8 AA.  
XX  
AC AAB06597;  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 230.  
XX  
XX Claudin-3 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
XX WO200026360-A1.  
PN  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA001029.  
XX  
PR 03-NOV-1998; 98US-00185908.  
PR 30-MAR-1999; 99US-00282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
XX WPI; 2000-365610/31.  
XX  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin.  
XX  
XX Claim 55; Page 99; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides

CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation  
XX  
SQ Sequence 8 AA;  
  
Query Match 100.0%; Score 16; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FID 3  
Db 6 FID 8  
  
RESULT 15  
AAB06777  
ID AAB06777 standard; peptide; 8 AA.  
XX  
AC AAB06777;  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 348.  
XX  
XX Claudin-6 modulating agent; claudin-9 modulating agent;  
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;  
KW inflammatory disease; cancer; graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
XX WO200026360-A1.  
PN  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA001029.  
XX  
PR 03-NOV-1998; 98US-00185908.  
PR 30-MAR-1999; 99US-00282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
XX WPI; 2000-365610/31.  
XX  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin.  
XX  
XX Claim 73; Page 103; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins  
CC are cadherins, which are membrane glycoproteins involved in cell  
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,  
CC and these peptides can be used to modulate these levels, and thus treat  
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound  
CC healing and implant adhesion. In addition, they can also be used to  
CC facilitate drug delivery to the desired target site. The present sequence  
CC has a cyclic conformation  
XX  
SQ Sequence 8 AA;  
  
Query Match 100.0%; Score 16; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FID 3  
Db 6 FID 8

Thu Sep 30 13:18:33 2004

us-09-674-716b-13.open.rag

Page 8

Search completed: September 30, 2004, 06:06:24  
Job time : 16.6441 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:01:30 ; Search time 50.339 Seconds  
(without alignments)  
19.178 Million cell updates/sec

Title: US-09-674-716B-13  
Perfect score: 16  
Sequence: 1 FID 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*\*

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pap.\*
- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US05\_NEW\_PUB.pap.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pap.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pap.\*
- 6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pap.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pap.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pap.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US09A\_PUBCOMB.pap.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pap.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pap.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pap.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pap.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pap.\*
- 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pap.\*
- 16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pap.\*
- 17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pap.\*
- 18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	5	8	US-08-484-409-36
2	16	100.0	5	12	US-09-920-306-25
3	16	100.0	6	11	US-09-943-944E-130
4	16	100.0	7	9	US-09-185-908-174
5	16	100.0	7	9	US-09-185-908-227
6	16	100.0	7	14	US-10-190-082-567
7	16	100.0	8	9	US-09-946-678-8
8	16	100.0	8	9	US-09-791-378-511
9	16	100.0	8	9	US-09-185-908-177
10	16	100.0	8	9	US-09-185-908-230
11	16	100.0	8	10	US-09-880-748-2842
12	16	100.0	8	12	US-10-293-418-2842
13	16	100.0	8	12	US-10-601-100-92
14	16	100.0	8	12	US-10-601-100-108
15	16	100.0	8	12	US-09-791-377-511

16	16	100.0	8	14	US-10-190-082-501	Sequence 501, App
17	16	100.0	8	16	US-10-712-425-1352	Sequence 1352, App
18	16	100.0	9	9	US-09-185-908-180	Sequence 180, App
19	16	100.0	9	9	US-09-185-908-233	Sequence 233, App
20	16	100.0	9	10	US-09-932-165-862	Sequence 862, App
21	16	100.0	9	10	US-09-932-165-1235	Sequence 1235, App
22	16	100.0	9	12	US-10-363-791-121	Sequence 121, App
23	16	100.0	10	9	US-09-757-417-45	Sequence 45, App1
24	16	100.0	10	10	US-09-572-404B-644	Sequence 644, App
25	16	100.0	10	10	US-09-572-404B-1464	Sequence 1464, App
26	16	100.0	10	10	US-09-572-404B-2015	Sequence 2015, App
27	16	100.0	10	10	US-09-572-404B-2017	Sequence 2017, App
28	16	100.0	10	10	US-09-572-404B-3882	Sequence 3882, App
29	16	100.0	10	10	US-09-572-404B-3883	Sequence 3883, App
30	16	100.0	10	10	US-09-932-165-153	Sequence 153, App
31	16	100.0	10	10	US-09-932-165-356	Sequence 356, App
32	16	100.0	10	10	US-09-932-165-563	Sequence 563, App
33	16	100.0	10	10	US-09-932-165-583	Sequence 583, App
34	16	100.0	10	10	US-09-932-165-1361	Sequence 1361, App
35	16	100.0	10	10	US-09-573-822C-8	Sequence 8, App11
36	16	100.0	10	10	US-09-573-822C-693	Sequence 693, App
37	16	100.0	10	14	US-10-042-945-45	Sequence 45, App1
38	16	100.0	10	16	US-10-327-598-462	Sequence 462, App
39	16	100.0	11	9	US-09-817-310-5	Sequence 5, App11
40	16	100.0	11	12	US-10-372-876-560	Sequence 560, App
41	16	100.0	11	14	US-10-097-065-560	Sequence 560, App
42	16	100.0	12	9	US-09-214-371-27	Sequence 27, App1
43	16	100.0	12	9	US-09-214-371-63	Sequence 63, App1
44	16	100.0	12	12	US-10-609-217-136	Sequence 136, App
45	16	100.0	12	12	US-10-632-388-136	Sequence 136, App

ALIGNMENTS

RESULT 1

US-08-484-409-36  
; Sequence 36, Application US/08484409  
; Publication No. US20020076412A1  
; GENERAL INFORMATION:  
; APPLICANT: Steinman, Lawrence  
; APPLICANT: Zamvil, Scott  
; TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7032  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,409  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 690068.409C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear

US-08-484-409-36

Query Match 100.0%; Score 16; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 3 FID 5

## RESULT 2

US-09-920-306-25  
; Sequence 25, Application US/09920306  
; Publication No. US20040029808A1  
; GENERAL INFORMATION:  
; APPLICANT: Unilever PLC  
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for  
; FILE REFERENCE: Peptide Mimotopes  
; CURRENT APPLICATION NUMBER: US/09/920-306  
; CURRENT FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: EP00306613.1  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-920-306-25

Query Match 100.0%; Score 16; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 3 FID 5

## RESULT 3

US-09-943-944E-130  
; Sequence 130, Application US/09943944E  
; Publication No. US20040014036A1  
; GENERAL INFORMATION:  
; APPLICANT: Ptashne, et al.,  
; TITLE OF INVENTION: Transcriptional Activation System, Activators, and Uses  
; FILE REFERENCE: Therefor  
; FILE REFERENCE: 0342941-0065  
; CURRENT APPLICATION NUMBER: US/09/943,944E  
; CURRENT FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 238  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 130  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Random peptide  
US-09-943-944E-130

Query Match 100.0%; Score 16; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||

Db 1 FID 3

## RESULT 4

US-09-185-908-174  
; Sequence 174, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185,908A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 174  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R  
; OTHER INFORMATION: sequences  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-185-908-174

Query Match 100.0%; Score 16; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 5 FID 7

## RESULT 5

US-09-185-908-227  
; Sequence 227, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185,908A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 227  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-185-908-227

Query Match 100.0%; Score 16; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 5 FID 7

## RESULT 6

US-10-190-082-567  
 ; Sequence 567, Application US/10190082  
 ; Publication No. US20030148264A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lasky, Lawrence A.  
 ; APPLICANT: Sidhu, Sachdev S.  
 ; APPLICANT: Held, Heike A.  
 ; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS  
 ; FILE REFERENCE: P190581  
 ; CURRENT APPLICATION NUMBER: US/10/190,082  
 ; CURRENT FILING DATE: 2002-07-03  
 ; PRIOR APPLICATION NUMBER: US 60/303,634  
 ; PRIOR FILING DATE: 2001-07-06  
 ; NUMBER OF SEQ ID NOS: 683  
 ; SEQ ID NO 567  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 US-10-190-082-567

Query Match 100.0%; Score 16; DB 14; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 DB 4 FID 6

RESULT 7

US-09-946-678-8  
 ; Sequence 8, Application US/09946678  
 ; Patent No. US20020106782A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ITO, Kotaro  
 ; APPLICANT: UMITSUJI, Genryou  
 ; APPLICANT: KOYAMA, Yasuji  
 ; TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same  
 ; FILE REFERENCE: 0283-0158P  
 ; CURRENT APPLICATION NUMBER: US/09/946,678  
 ; CURRENT FILING DATE: 2001-09-06  
 ; PRIOR APPLICATION NUMBER: JP 2000-270371  
 ; PRIOR FILING DATE: 2000-09-06  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 8  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Cryptococcus rodansensis  
 US-09-946-678-8

Query Match 100.0%; Score 16; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 DB 2 FID 4

RESULT 8

US-09-791-378-511  
 ; Sequence 511, Application US/09791378  
 ; Patent No. US20020142303A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Parekh, Rajesh  
 ; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF  
 ; TITLE OF INVENTION: SCHIZOPHRENIA  
 ; FILE REFERENCE: 9195-061-999  
 ; CURRENT APPLICATION NUMBER: US/09/791,378  
 ; CURRENT FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: 09/750,395  
 ; PRIOR FILING DATE: 2000-12-28  
 ; NUMBER OF SEQ ID NOS: 677  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 511  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-791-378-511

Query Match 100.0%; Score 16; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 DB 2 FID 4

RESULT 9

US-09-185-908-177  
 ; Sequence 177, Application US/09185908A  
 ; Publication No. US20020193294A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blaschuk, Orest W.  
 ; APPLICANT: Gour, Barbara J.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
 ; TITLE OF INVENTION: FUNCTIONS  
 ; FILE REFERENCE: 100086.409  
 ; CURRENT APPLICATION NUMBER: US/09/185,908A  
 ; CURRENT FILING DATE: 1998-11-03  
 ; NUMBER OF SEQ ID NOS: 269  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 177  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Product of  
 ; OTHER INFORMATION: syntheses based on human, mouse and monkey CPE-R  
 ; OTHER INFORMATION: sequences  
 ; FEATURE:  
 ; OTHER INFORMATION: Cyclic Peptide  
 US-09-185-908-177

Query Match 100.0%; Score 16; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 DB 6 FID 8

RESULT 10

US-09-185-908-230  
 ; Sequence 230, Application US/09185908A  
 ; Publication No. US20020193294A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blaschuk, Orest W.  
 ; APPLICANT: Gour, Barbara J.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
 ; TITLE OF INVENTION: FUNCTIONS  
 ; FILE REFERENCE: 100086.409  
 ; CURRENT APPLICATION NUMBER: US/09/185,908A  
 ; CURRENT FILING DATE: 1998-11-03  
 ; NUMBER OF SEQ ID NOS: 269  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 230  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Product of  
 ; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences  
 ; FEATURE:  
 ; OTHER INFORMATION: Cyclic Peptide  
 US-09-183-908-230

Query Match 100.0%; Score 16; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 Db 6 FID 8

RESULT 11  
 US-09-880-748-2842  
 ; Sequence 2842, Application US/09880748  
 ; Publication No. US2003005937A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
 ; FILE REFERENCE: PF523  
 ; CURRENT APPLICATION NUMBER: US/09/880,748  
 ; CURRENT FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/212,210  
 ; PRIOR FILING DATE: 2000-06-15  
 ; PRIOR APPLICATION NUMBER: 60/240,816  
 ; PRIOR FILING DATE: 2000-10-17  
 ; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; NUMBER OF SEQ ID NOS: 3239  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2842  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-880-748-2842

Query Match 100.0%; Score 16; DB 10; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 Db 5 FID 7

RESULT 12  
 US-10-293-418-2842  
 ; Sequence 2842, Application US/10293418  
 ; Publication No. US2003023996A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
 ; FILE REFERENCE: PF523P2  
 ; CURRENT APPLICATION NUMBER: US/10/293,418  
 ; CURRENT FILING DATE: 2002-11-27  
 ; PRIOR APPLICATION NUMBER: 60/331,469  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: 60/340,817  
 ; PRIOR FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 09/880,748  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/240,816  
 ; PRIOR FILING DATE: 2000-10-17  
 ; PRIOR APPLICATION NUMBER: 60/212,210  
 ; PRIOR FILING DATE: 2000-06-16  
 ; NUMBER OF SEQ ID NOS: 3247  
 ; SEQ ID NO 2842  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-293-418-2842

Query Match 100.0%; Score 16; DB 12; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 Db 5 FID 7

RESULT 13  
 US-10-601-100-92  
 ; Sequence 92, Application US/10601100  
 ; Publication No. US20040072261A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INNOGENETICS N.V.  
 ; TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of  
 ; FILE REFERENCE: 11362.0038.NFUS01  
 ; CURRENT APPLICATION NUMBER: US/10/601,100  
 ; CURRENT FILING DATE: 2003-06-20  
 ; PRIOR APPLICATION NUMBER: EP 02447121.1  
 ; PRIOR FILING DATE: 2002-06-21  
 ; PRIOR APPLICATION NUMBER: US 60/396,437  
 ; PRIOR FILING DATE: 2002-07-17  
 ; NUMBER OF SEQ ID NOS: 113  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 92  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-10-601-100-92

Query Match 100.0%; Score 16; DB 12; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 Db 2 FID 4

RESULT 14  
 US-10-601-100-108  
 ; Sequence 108, Application US/10601100  
 ; Publication No. US20040072261A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INNOGENETICS N.V.  
 ; TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of  
 ; FILE REFERENCE: 11362.0038.NFUS01  
 ; CURRENT APPLICATION NUMBER: US/10/601,100  
 ; CURRENT FILING DATE: 2003-06-20  
 ; PRIOR APPLICATION NUMBER: EP 02447121.1  
 ; PRIOR FILING DATE: 2002-06-21  
 ; PRIOR APPLICATION NUMBER: US 60/396,437  
 ; PRIOR FILING DATE: 2002-07-17  
 ; NUMBER OF SEQ ID NOS: 113  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 108  
 ; LENGTH: 8  
 ; TYPE: PRT

; ORGANISM: homo sapiens  
US-10-601-100-108

Query Match 100.0%; Score 16; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. NO. 1.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 5 FID 7

## RESULT 15

US-09-791-377-511  
; Sequence 511, Application US/09791377  
; Publication No. US20040110938A1  
; GENERAL INFORMATION:  
; APPLICANT: Parekh, Rajesh  
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF  
; FILE REFERENCE: 9195-060-999  
; CURRENT APPLICATION NUMBER: US/09/791,377  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/750,395  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 677  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 511  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-377-511

Query Match 100.0%; Score 16; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. NO. 1.2e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 2 FID 4

Search completed: September 30, 2004, 06:54:53  
Job time : 50.339 secs

Blank Sheet





Db 61 TyrluGlnlyProGlyGlnSerProGlnLeuLeuLeuTyrluGlySerAsnArgAla 80  
 QY 181 TCAGGGTCCCTGACAGTTCAGTGGAGTGGATTCAGGCACAGATTTTACATGAAATC 240  
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 Db 101 SerArgValGluAlaGluAspValGlyValTyrrCysMetGlnAlaLeuGlnThrPro 120  
 QY 301 TTCAGTTCGCCCAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 348  
 Db 121 TrpThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 136

## RESULT 2

S40342  
 Ig kappa chain - human  
 C:Species: Homo sapiens (man)  
 C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S40342  
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A>Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A:Reference number: S40342; MUID:94080891; PMID:8258341  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-135 <KLE>  
 A:Cross-references: EMBL:X72452; NID:9441372; PID:9441373  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:29-108/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 3,04e-44 Length: 135  
 Score: 518.00 Matches: 101  
 Percent Similarity: 92.24% Conservative: 6  
 Best Local Similarity: 87.07% Mismatches: 9  
 Query Match: 83.68% Indels: 0  
 DB: 2 Gaps: 0

US-09-674-716B-17 (1-348) x S40342 (1-135)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTGAGGAGCGGCTCC 60  
 Db 14 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 33  
 QY 61 ATCTCTCTGCTCGAGTAAAGTCTCCTGTATTAAGGATGGGAAGACATCTGAATTGG 120  
 Db 34 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrrAsnTyrrLeuAspTrp 53  
 QY 121 TACCTGAGAACGAGGAGTCTCCAGTCTCCAGTCTCCCTGCCGTGAGGAGCGGCTCC 180  
 Db 54 TyrluGlnlyProGlyGlnSerProGlnLeuLeuLeuTyrluGlySerAsnArgAla 73  
 QY 181 TCAGGGTCCCTGACAGTTCAGTGGAGTGGATTCAGGCACAGATTTTACATGAAATC 240  
 Db 74 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 93  
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 Db 94 SerArgValGluAlaGluAspValGlyValTyrrCysMetGlnAlaLeuGlnThrPro 113  
 QY 301 TTCAGTTCGCCCAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 348  
 Db 114 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 129

## RESULT 3

S40356  
 Ig kappa chain - human  
 C:Species: Homo sapiens (man)  
 C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40356  
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A>Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A:Reference number: S40312; MUID:94080891; PMID:8258341  
 C:Accession: S40356  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-125 <KLE>  
 A:Cross-references: EMBL:X72466; NID:9441400; PID:CAAS1134.1; PID:9441401  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:25-104/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 3,83e-44 Length: 125  
 Score: 517.00 Matches: 100  
 Percent Similarity: 92.24% Conservative: 7  
 Best Local Similarity: 86.21% Mismatches: 9  
 Query Match: 83.52% Indels: 0  
 DB: 2 Gaps: 0

US-09-674-716B-17 (1-348) x S40356 (1-125)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTGAGGAGCGGCTCC 60  
 Db 10 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 29  
 QY 61 ATCTCTCTGCTCGAGTAAAGTCTCCTGTATTAAGGATGGGAAGACATCTGAATTGG 120  
 Db 30 IleSerCysArgSerSerGlnSerLeuLeuHisAsnGlyTyrrAsnTyrrLeuAspTrp 49  
 QY 121 TACCTGAGAACGAGGAGTCTCCAGTCTCCAGTCTCCTGTATTAAGTGTCCACCCGGGCA 180  
 Db 50 TyrluGlnlyProGlyGlnSerProGlnLeuLeuLeuTyrluGlySerAsnArgAla 69  
 QY 181 TCAGGGTCCCTGACAGTTCAGTGGAGTGGATTCAGGCACAGATTTTACATGAAATC 240  
 Db 70 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 89  
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 Db 90 SerArgValGluAlaGluAspValGlyValTyrrCysMetGlnValLeuGlnIlePro 109  
 QY 301 TTCAGTTCGCCCAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 348  
 Db 110 LeuThrPheGlyGlyGlyThrLysValGluLeuLysArgThrValAla 125

## RESULT 4

K2HUTW  
 Ig kappa chain V-II region (Tew) - human (tentative sequence)  
 C:Species: Homo sapiens (man)  
 C>Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 31-Mar-2000  
 C:Accession: A90370; A92764; R01888  
 R:Putnam, F.W.; Whitley Jr., E.J.; Paul, C.; Davidson, J.N.  
 Biochemistry 12, 3763-3780, 1973  
 A>Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloid  
 A:Reference number: A90370; MUID:74148480; PMID:4596149  
 A:Contents: Bence Jones protein Tew  
 A:Accession: A90370  
 A:Molecule type: protein  
 A:Residues: 1-113 <PUT>  
 A>Note: this protein was isolated from the urine of a patient with plasma cell dyscrasia  
 R:Berry, W.D.; Pegg, D.B.; Kimura, S.; Isobe, T.; Osseman, E.F.; Glenner, G.G.  
 J. Clin. Invest. 52, 1276-1281, 1973  
 A>Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient with  
 A:Reference number: A92764; MUID:73166638; PMID:4700495  
 A:Contents: amyloid protein Tew  
 A:Accession: A92764  
 A:Molecule type: protein  
 A:Residues: 1-27 <TER>  
 A>Note: the major amyloid protein appears to be identical with the Bence Jones protein is

C;Genetics:  
A;Gene: GDB:IGKV2  
A;Cross-references: GDB:136265  
A;Map position: 2p12-2p12  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: amyloid; heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>  
F;23-93/Disulfide bonds: #status predicted

Alignment Scores:  
Pred. No.: 4,94e-43 Length: 113  
Score: 506.00 Matches: 95  
Percent Similarity: 92.04% Conservative: 9  
Best Local Similarity: 84.07% Mismatches: 3  
Query Match: 81.74% Indels: 0  
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x K2HUTW (1-113)

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QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCCCTGAGAGCGGCTCC 60
D 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
QY 61 ATCTCTGCTGCTCGAGTAAGAGTCTCTCTGATAAGAGTGGAGACATATCTGAT 120
D 21 IleSerCysArgSerGlnSerLeuLeuHisSerAspGlyPheAspTyrLeuAsnTrp 40
QY 121 TACTTCGAGAACGAGCGAGTCTCCAGCTCTCCCTGAGAGCGGCTCC 180
D 41 TyLeuGlnLysProGlyGlnSerPro***LeuLeuIleTyrAlaLeuSerAsnArgAla 60
QY 181 TCAGGGTCTCCTCAGAGTTCAGTGGCAGTGGATGAGTGGAGTGGAGTGGAGT 240
D 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATCTGTTTATCTGTTTATCTGTT 300
D 81 SerArgValGluAlaGluAspValGlyValTyrCysMet***AlaLeuGlnAlaPro 100
QY 301 TTCAGTTCGCGCCCAAGGACCAAGTGGAGTCAAA 336
D 101 TrpThrPheGlyGlnGlyThrLysValGluLys 112
```

RESULT 5

S58207  
Ig light chain V region anti-F(ab')<sub>2</sub> - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1996 #sequence\_revision 19-Apr-1996 #text\_change 21-Jan-2000  
C;Accession: S58207  
R;Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, submitted to the EMBL Data Library, July 1995  
A;Description: Characterization of heavy and light chain immunoglobulin variable region  
A;Reference number: S58206  
A;Accession: S58207  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-112 <WEL>  
A;Cross-references: EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PID:g929643  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 7.87e-43 Length: 112  
Score: 504.00 Matches: 97  
Percent Similarity: 92.86% Conservative: 7  
Best Local Similarity: 86.61% Mismatches: 8  
Query Match: 81.42% Indels: 0  
DB: 2 Gaps: 0

US-09-674-716B-17 (1-348) x S58207 (1-112)

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QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCCCTGAGAGCGGCTCC 60
D 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
QY 61 ATCTCTGCTGCTCGAGTAAGAGTCTCTCTGATAAGAGTGGAGACATATCTGAT 120
D 21 IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40
QY 121 TACTTCGAGAACGAGCGGCTCTCCAGCTCTCCCTGAGAGCGGCTCC 180
D 41 TyLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 60
QY 181 TCAGGGTCTCCTCAGAGTTCAGTGGCAGTGGATGAGTGGAGTGGAGTGGAGT 240
D 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATCTGTTTATCTGTTTATCTGTT 300
D 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 100
QY 301 TTCAGTTCGCGCCCAAGGACCAAGTGGAGTCAAA 336
D 101 TrpThrPheGlyGlnGlyThrLysValGluLys 112
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RESULT 6

S40321  
Ig kappa chain - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40321  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:9408091; PMID:8258341  
A;Accession: S40321  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-130 <KLB>  
A;Cross-references: EMBL:X72431  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;31-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1.12e-42 Length: 130  
Score: 502.50 Matches: 97  
Percent Similarity: 92.17% Conservative: 9  
Best Local Similarity: 84.35% Mismatches: 8  
Query Match: 81.18% Indels: 1  
DB: 2 Gaps: 1

US-09-674-716B-17 (1-348) x S40321 (1-130)

```
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCCCTGAGAGCGGCTCC 60
D 16 AspIleValMetThrGlnThrProLeuSerLeuProValThrProGlyGluProAlaSer 35
QY 61 ATCTCTGCTGCTCGAGTAAGAGTCTCTG---TATAAGGATGGAGACATATCTGA 117
D 36 IleSerCysArgSerGlnSerLeuLeuHisSerAspGlyAsnThrTyrLeuAsp 55
QY 118 TGGTACCTGTCAGAACGAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTC 177
D 56 TrpTyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrThrLeuSerTyrArg 75
QY 178 GCATCAGGGGTCCTGACAGAGTTCAGTGGCAGTGGATGAGTGGACAGATTTAC 237
D 76 AlaSerGlyValProAspArgPheSerGlySerGlyThrAlaPheThrLeuLys 95
QY 238 ATCAGCAGAGTGGAGCTGAGGATGTTGGGGTTTATCTGTTTATCTGTTTAT 297
D 96 IleSerArgValGluAlaGluAspValGlyLeuTyrCysMetGlnArgIleGluPhe 115
```



DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x K2HUCM (1-117)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60

Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24

QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTGTAAGATGGAAGACATCTTGAATTGG 120

Db 25 IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 44

QY 121 TACTGACAGAGCAGGAGGAGTCTCCAGCTCTCCAGCTCTGATCTATTGATGTCACCCGGCA 180

Db 45 TyrLeuGlnLysProGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 64

QY 181 TCAGGGTCTCCACAGGTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240

Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84

QY 241 AGCAGAGTGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300

Db 85 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyLeuGlnThrPro 104

QY 301 TTCACGTCGCGCAAGGACCAAGGTGGAGATCAAAAGT 339

Db 105 GlnThrPheGlyGlnGlyThrLysValGluLeuArg 117

RESULT 10

K2HUCM

Ig kappa chain V-II region (Cum) - human

C:Species: Homo sapiens (man)

C:Date: 24-Apr-1984 #sequence\_revision 02-Jul-1998 #text\_change 02-Jul-1998

C:Accession: B91639; A93409; A01885; S02576

R:Hiltschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967

A:Title: Die voltaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).

A:Reference number: A91639; MUID:68242259; PMID:5586923

A:Accession: B91639

A:Molecule type: protein

A:Residues: 1-49, 'Q', 'S', '53-95, 'QM', '98-115 <HIL>

A:Note: the sequence of the C region, which has the Inv (3) marker, is also given

R:Hiltschmann, N.

Naturwissenschaften 56, 195-205, 1969

A:Title: Die molekularen Grundlagen der Antikoeperbildung.

A:Reference number: A93409; MUID:70063440; PMID:4186189

A:Accession: A93409

A:Molecule type: protein

A:Residues: 1-115 <Hiz>

R:Steiner, V.; Chang, J.Y.

FEBS Lett. 222, 6-10, 1987

A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the

A:Reference number: S02572; MUID:88005152; PMID:3115831

A:Contents: annotation

C:Comment: This is a Bence Jones protein.

C:Genetics:

A:Gene: GDB:IGKV2

A:Cross-references: GDB:136265

A:Map position: 2p12-2p12

C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds; in some cases, such as Iga and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:17-97/Domain: immunoglobulin homology <IMM>

F:24-95/Disulfide bonds: #status predicted

Alignment Scores:

Pred. No.:	9,07e-42	Length:	115
Score:	493.50	Matches:	96
Percent Similarity:	91.23%	Conservative:	8
Best Local Similarity:	84.21%	Mismatches:	9
Query Match:	79.73%	Indels:	1
DB:	1	Gaps:	1

US-09-674-716B-17 (1-348) x K2HUCM (1-115)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60

Db 2 AspIleValMetThrGlnThrProLeuSerLeuProValThrProGlyGluProAlaSer 21

QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTGTAAG---GATGGAAGACATCTTGAAT 117

Db 22 IleSerCysArgSerGlnSerLeuLeuAspSerGlyAspGlyAsnThrTyrLeuAsn 41

QY 118 TGGTACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGG 177

Db 42 TrpTyrLeuGlnLysAlaGlyGlnSerProGlnLeuLeuLeuTyrThrLeuSerTyrArg 61

QY 178 GCATCAGGGTCCCTGCAGAGCTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAA 237

Db 62 AlaSerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLys 81

QY 238 ATCAGCAGAGTGGAGGTGAGATGTTGGGGTTTATTACTGTCAACAGCTGCTAGAGTAT 297

Db 82 IleSerArgValGlnAlaGluAspValGlyValTyrCysMetGlnArgLeuGluLeu 101

QY 298 CCATTACGTTCCGCGCAAGGACCAAGGTGGAGATCAAAAGT 339

Db 102 ProTyrThrPheGlyGlnGlyThrLysLeuGluLeuArgArg 115

RESULT 11

S58206

Ig light chain V region anti-F(ab')2 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 21-Jan-2000

C:Accession: S58206

R:Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, F.

submitted to the EMBL Data Library, July 1995

A:Description: Characterization of heavy and light chain immunoglobulin variable region

A:Reference number: S58206

A:Accession: S58206

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 <WEL>

A:Cross-references: EMBL:X89054; NID:G929640; PID:CAA61441.1; PID:G929641

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	1,29e-41	Length:	112
Score:	492.00	Matches:	95
Percent Similarity:	90.18%	Conservative:	6
Best Local Similarity:	84.82%	Mismatches:	11
Query Match:	79.48%	Indels:	0
DB:	2	Gaps:	0

US-09-674-716B-17 (1-348) x S58206 (1-112)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60

Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20

QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTGTAAGGATGGAGACATCTTGAATTGG 120

Db 21 IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrPheAspTrp 40

QY 121 TACTGTCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGCA 180

Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 60

QY 181 TCAGGGTCTCCGACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGCTAGATATCCA 300



Db 21 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluSerAlaSer 40  
Qy 61 ATCTCTGTCGTCGAGTAAAGTCTCCGTGTATAGAGTGGGAAGACATCTGTAATTGG 120  
Db 41 PheSerCysIysThrSerGlnSerLeuLeuHisSerAsnGlyHisAsnTyrLeuAspTrp 60  
Qy 121 TACTCTCAGAACCCAGGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180  
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLetyrLeuGlySerThrArgAla 80  
Qy 181 TCAGGGGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100  
Qy 241 AGCAGATGCGAGGCTGAGGATGTGGGTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnProLeuGlnThrPro 120  
Qy 301 TTCACGTTCCGCCCAAGGACCAAGGTGGAGATC 333  
Db 121 TyrThrPheGlyGlnGlyThrLysLeuGluIle 131

RESULT 15  
KWS16  
Ig kappa chain V region (M167) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 16-Aug-1996  
C:Accession: A01908  
R:Rudikoff, S.; Potter, M.  
Biochemistry 17, 2703-2707, 1978  
A:Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma protein  
A:Reference number: A01908; MUID:79000273; PMID:99160  
A:Accession: A01908  
A:Molecule type: protein  
A:Residues: 1-112 <RUD>  
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-95/Domain: immunoglobulin homology <IMM>  
F:23-93/Disulfide bonds: #status predicted

Alignment Scores:  
Pred. No.: 1.04e-40 Length: 112  
Score: 483.00 Matches: 94  
Percent Similarity: 90.18% Conservative: 7  
Best Local Similarity: 83.93% Mismatches: 11  
Query Match: 78.03% Indels: 0  
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x KWS16 (1-112)

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCAGCCCTCGAGAGCGGCTCC 60  
Db 1 AspileValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
Qy 61 ATCTCTGTCGTCGAGTAAAGTCTCCGTGTATAGAGTGGGAAGACATCTGTAATTGG 120  
Db 21 IleSerCysArgSerSerLysSerLeuLetyrLysAspGlyLysThrTyrLeuAsnTrp 40  
Qy 121 TACTCTCAGAACCCAGGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180  
Db 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLetyrLeuGlySerThrArgAla 60  
Qy 181 TCAGGGGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 61 SerGlyValSerAspArgPheSerGlySerGlySerArgThrAspPheThrLeuGluIle 80  
Qy 241 AGCAGATGCGAGGCTGAGGATGTGGGTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
Db 81 SerArgValLysAlaGluAspValGlyValTyrCysGlnGlnLeuValGluLuryPro 100

Qy 301 TTCACGTTCCGCCCAAGGACCAAGGTGGAGATCAAA 336  
Db 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuLys 112

Search completed: September 30, 2004, 08:57:03  
Job time : 15.7964 secs

Blank Sheet



OM protein - protein search, using sw model

Run on: September 30, 2004, 06:00:45 ; Search time 5.08475 Seconds  
(without alignments)  
30.459 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/2/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/6C COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/6D COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	16	100.0	7	1	US-08-197-792-25
2	16	100.0	7	1	US-08-459-850-25
3	16	100.0	7	1	US-08-459-214-25
4	16	100.0	8	3	US-09-042-071-52
5	16	100.0	8	4	US-09-946-678-8
6	16	100.0	9	4	US-09-359-304B-2
7	16	100.0	9	4	US-09-359-304B-5
8	16	100.0	9	4	US-09-359-304B-7
9	16	100.0	9	4	US-09-000-217-2
10	16	100.0	9	4	US-09-341-982-67
11	16	100.0	10	1	US-08-277-007-1
12	16	100.0	10	1	US-08-485-181-1
13	16	100.0	10	2	US-08-964-338-1
14	16	100.0	10	3	US-08-975-917-1
15	16	100.0	11	4	US-09-817-310-5
16	16	100.0	11	5	PCT-US92-01433A-6
17	16	100.0	12	1	US-08-434-255-15
18	16	100.0	12	1	US-08-459-967-15
19	16	100.0	12	1	US-08-460-327-15
20	16	100.0	12	1	US-08-459-871-15
21	16	100.0	12	4	US-09-517-439-27
22	16	100.0	12	4	US-09-428-082B-136
23	16	100.0	12	5	PCT-US91-02942-70
24	16	100.0	13	4	US-09-690-454-84
25	16	100.0	13	4	US-10-053-485-55
26	16	100.0	13	4	US-09-834-759-501
27	16	100.0	14	1	US-07-620-426B-15

28 16 100.0 14 1 US-07-620-426B-16 Sequence 16, Appl  
29 16 100.0 14 1 US-07-662-007B-15 Sequence 15, Appl  
30 16 100.0 14 1 US-07-662-007B-15 Sequence 16, Appl  
31 16 100.0 14 1 US-07-824-247-15 Sequence 15, Appl  
32 16 100.0 14 1 US-07-824-247-16 Sequence 16, Appl  
33 16 100.0 14 2 US-08-695-412B-7 Sequence 7, Appl  
34 16 100.0 14 2 US-08-574-959A-18 Sequence 18, Appl  
35 16 100.0 14 3 US-08-470-204A-15 Sequence 15, Appl  
36 16 100.0 14 3 US-08-470-204A-16 Sequence 16, Appl  
37 16 100.0 14 3 US-08-622 INFORMATION FOR  
38 16 100.0 14 3 US-09-357-014-18 Sequence 18, Appl  
39 16 100.0 14 4 US-09-165-922A-7 Sequence 7, Appl  
40 16 100.0 15 1 US-08-325-553-10 Sequence 10, Appl  
41 16 100.0 15 1 US-08-527-113-1 Sequence 1, Appl  
42 16 100.0 15 2 US-08-432-871C-88 Sequence 88, Appl  
43 16 100.0 15 2 US-08-934-222-52 Sequence 52, Appl  
44 16 100.0 15 2 US-08-394-152A-10 Sequence 10, Appl  
45 16 100.0 15 2 US-08-933-402-52 Sequence 52, Appl

ALIGNMENTS

RESULT 1  
US-08-197-792-25  
; Sequence 25, Application US/08197792  
; Patent No. 5525488  
; GENERAL INFORMATION:  
; APPLICANT: Anthony J. Mason  
; APPLICANT: Peter H. Seeburg  
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin and  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,792  
; FILING DATE: 16-FEB-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/958414  
; FILING DATE: 08-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744207  
; FILING DATE: 12-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/215466  
; FILING DATE: 05-JUL-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 06/906729  
; FILING DATE: 31-DEC-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 06/827710  
; FILING DATE: 07-FEB-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 06/783910  
; FILING DATE: 03-OCT-1985  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 297P2D4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881

TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 25;  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-197-792-25

Query Match 100.0%; Score 16; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
Db 4 FID 6

RESULT 2  
US-08-459-850-25  
; Sequence 25, Application US/08459850  
; Patent No. 5665568  
; GENERAL INFORMATION:  
; APPLICANT: Anthony J. Mason  
; APPLICANT: Peter H. Seeburg  
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or  
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptides  
; TITLE OF INVENTION: Using such Nucleic Acid  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,850  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/197792  
FILING DATE: 17-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/958414  
FILING DATE: 08-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744207  
FILING DATE: 12-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/215466  
FILING DATE: 05-JUL-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/906729  
FILING DATE: 31-DEC-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/827710  
FILING DATE: 07-FEB-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/783910  
FILING DATE: 03-OCT-1985  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 2972D5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 25;  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-459-850-25

Query Match 100.0%; Score 16; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
Db 4 FID 6

RESULT 3  
US-08-459-214-25  
; Sequence 25, Application US/08459214  
; Patent No. 5716810  
; GENERAL INFORMATION:  
; APPLICANT: Anthony J. Mason  
; APPLICANT: Peter H. Seeburg  
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or  
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptides  
; TITLE OF INVENTION: Using such Nucleic Acid  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,214  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/197792  
FILING DATE: 17-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/958414  
FILING DATE: 08-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744207  
FILING DATE: 12-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/215466  
FILING DATE: 05-JUL-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/906729  
FILING DATE: 31-DEC-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/827710  
FILING DATE: 07-FEB-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/783910  
FILING DATE: 03-OCT-1985  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 2972D6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 25.

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-214-25

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 7;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3-
Db 4 FID 6

RESULT 4
US-09-042-071-52
; Sequence 52, Application US/09042071
; Patent No. 6294372
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Kay, William W.
; TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM
; TITLE OF INVENTION: SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING
; TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,071
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.407
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-042-071-52

Query Match
Best Local Similarity 100.0%; Score 16; DB 3; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 2 FID 4

RESULT 5
US-09-946-678-8
; Sequence 8, Application US/09946678
; Patent No. 6541236
; GENERAL INFORMATION:
; APPLICANT: ITO, Kotaro
; APPLICANT: UMITSUKI, Genryou

; APPLICANT: KOYAMA, Yasuji
; TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same
; FILE REFERENCE: 0283-0158P
; CURRENT APPLICATION NUMBER: US/09/946,678
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: JP 2000-270371
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Cryptococcus nodaensis
US-09-946-678-8

Query Match
Best Local Similarity 100.0%; Score 16; DB 4; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 2 FID 4

RESULT 6
US-09-359-304B-2
; Sequence 2, Application US/09359304B
; Patent No. 6468745
; GENERAL INFORMATION:
; APPLICANT: FITZMAURICE, Wayne P.
; APPLICANT: LINDBO, John A.
; APPLICANT: PADGETT, Hal S.
; APPLICANT: POGUE, Gregory P.
; TITLE OF INVENTION: METHOD FOR EXPRESSING A LIBRARY OF
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE VARIANTS AND SELECTING DESIRED TRAITS
; FILE REFERENCE: 008010137US02
; CURRENT APPLICATION NUMBER: US/09/359,304B
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Tobacco mosaic virus
US-09-359-304B-2

Query Match
Best Local Similarity 100.0%; Score 16; DB 4; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 3 FID 5

RESULT 7
US-09-359-304B-5
; Sequence 5, Application US/09359304B
; Patent No. 6468745
; GENERAL INFORMATION:
; APPLICANT: FITZMAURICE, Wayne P.
; APPLICANT: LINDBO, John A.
; APPLICANT: PADGETT, Hal S.
; APPLICANT: POGUE, Gregory P.
; TITLE OF INVENTION: METHOD FOR EXPRESSING A LIBRARY OF
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE VARIANTS AND SELECTING DESIRED TRAITS
; FILE REFERENCE: 008010137US02
; CURRENT APPLICATION NUMBER: US/09/359,304B
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 9

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; TYPE: PRT  
; ORGANISM: Tobacco mosaic virus  
US-09-359-304B-5

Query Match 100.0%; Score 16; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
Db 3 FID 5

RESULT 8  
US-09-359-304B-7

; Sequence 7, Application US/09359304B  
; Patent No. 6468745

; GENERAL INFORMATION:

; APPLICANT: FITZMAURICE, Wayne P.

; APPLICANT: LINDBO, John A.

; APPLICANT: PADGETT, Hal S.

; APPLICANT: POQUE, Gregory P.

; TITLE OF INVENTION: METHOD FOR EXPRESSING A LIBRARY OF

; FILE REFERENCE: 008010137US02

; CURRENT APPLICATION NUMBER: US/09/359,304B

; CURRENT FILING DATE: 1999-07-21

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Tobacco mosaic virus

US-09-359-304B-7

Query Match 100.0%; Score 16; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
Db 3 FID 5

RESULT 9

US-09-000-217-2

; Sequence 2, Application US/09000217A

; Patent No. 6521598

; GENERAL INFORMATION:

; APPLICANT: Goulmy, Ils A.J.M.

; APPLICANT: Hunt, Donald F.

; APPLICANT: Engelhard, Victor H.

; TITLE OF INVENTION: The H-Y Antigen

; FILE REFERENCE: Sequence ID No. 6521598. 1-9 for 294-43

; Patent No. 6521598

; CURRENT APPLICATION NUMBER: US/09/000,217A

; CURRENT FILING DATE: 1998-06-26

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-000-217-2

Query Match 100.0%; Score 16; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
Db 1 FID 3

RESULT 10  
US-09-341-982-67  
; Sequence 67, Application US/09341982  
; Patent No. 6858671  
; GENERAL INFORMATION:  
; APPLICANT: SLINGLUFF, Craig L.  
; APPLICANT: HUNT, Donald F.  
; APPLICANT: ENGELHARD, Victor H.  
; APPLICANT: KITTLESEN, David  
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED  
; FILE REFERENCE: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR  
; FILE REFERENCE: SLINGLUFF=3B  
; CURRENT APPLICATION NUMBER: US/09/341,982  
; CURRENT FILING DATE: 1999-09-20  
; EARLIER APPLICATION NUMBER: PCT/US98/01592  
; EARLIER FILING DATE: 1998-01-29  
; EARLIER APPLICATION NUMBER: 60/037,781  
; EARLIER FILING DATE: 1997-01-31  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 67  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
; OTHER INFORMATION: human protein  
US-09-341-982-67

Query Match 100.0%; Score 16; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
Db 1 FID 3

RESULT 11

US-08-277-007-1

; Sequence 1, Application US/08277007

; Patent No. 5538883

; GENERAL INFORMATION:

; APPLICANT: NISHIMOTO, Tomoyuki

; APPLICANT: CHAEN, Hiroto

; APPLICANT: SUGIMOTO, Toshiyuki

; APPLICANT: MIYAKE, Toshio

; TITLE OF INVENTION: MALTOSE-TREHALOSE CONVERTING ENZYME, AND

; PREPARATION AND USES THEREOF

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/277,007

; FILING DATE: 19-JUL-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 199971/1993

; FILING DATE: 20-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 144092/1994

; FILING DATE: 03-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: NEIMARK, Sheridan  
REGISTRATION NUMBER: 20,520  
REFERENCE/DOCKET NUMBER: NISHIMOTO-2  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-277-007-1

Query Match 100.0%; Score 16; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
DB 8 FID 10

#### RESULT 12

US-08-485-181-1  
Sequence 1, Application US/08485181  
Patent No. 5736380  
GENERAL INFORMATION:  
APPLICANT: NISHIMOTO, Tomoyuki  
APPLICANT: CHAEN, Hiroto  
APPLICANT: SUGIMOTO, Toshiyuki  
APPLICANT: MIYAKE, Toshio  
TITLE OF INVENTION: MALTOSSE-TREHALOSE CONVERTING ENZYME, AND  
TITLE OF INVENTION: PREPARATION AND USES THEREOF  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,181  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,007  
FILING DATE: 19-JUL-1994  
APPLICATION NUMBER: JP 199971/1993  
FILING DATE: 20-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 144092/1994  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: NEIMARK, Sheridan  
REGISTRATION NUMBER: 20,520  
REFERENCE/DOCKET NUMBER: NISHIMOTO=2  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-485-181-1

Query Match 100.0%; Score 16; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
DB 8 FID 10

#### RESULT 13

US-08-964-338-1  
Sequence 1, Application US/08964338  
Patent No. 5965411  
GENERAL INFORMATION:  
APPLICANT: NISHIMOTO, Tomoyuki  
APPLICANT: CHAEN, Hiroto  
APPLICANT: SUGIMOTO, Toshiyuki  
APPLICANT: MIYAKE, Toshio  
TITLE OF INVENTION: MALTOSSE-TREHALOSE CONVERTING ENZYME, AND  
TITLE OF INVENTION: PREPARATION AND USES THEREOF  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,338  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/277,007  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 144092/1994  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: NEIMARK, Sheridan  
REGISTRATION NUMBER: 20,520  
REFERENCE/DOCKET NUMBER: NISHIMOTO=2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-964-338-1

Query Match 100.0%; Score 16; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
DB 8 FID 10

RESULT 14  
US-08-975-917-1  
; Sequence 1, Application US/08975917  
; Patent No. 6090792  
; GENERAL INFORMATION:  
; APPLICANT: NISHIMOTO, Tomoyuki  
; APPLICANT: CHAEN, Hiroto  
; APPLICANT: SUGIMOTO, Toshiyuki  
; APPLICANT: MIYAKE, Toshio  
; TITLE OF INVENTION: MALTOSYL-TREHALOSE CONVERTING ENZYME, AND  
; TITLE OF INVENTION: PREPARATION AND USES THEREOF  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/975,917  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,007  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: JP 199971/1993  
; FILING DATE: 20-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 144092/1994  
; FILING DATE: 03-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NEIMARK, Sheridan  
; REGISTRATION NUMBER: 20,520  
; REFERENCE/DOCKET NUMBER: NISHIMOTO=2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-975-917-1

Query Match 100.0%; Score 16; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 8 FID 10

RESULT 15  
US-09-817-310-5  
; Sequence 5, Application US/09817310  
; Patent No. 6534311  
; GENERAL INFORMATION:  
; APPLICANT: Stewart, Mary  
; APPLICANT: Kozma, Sarah  
; APPLICANT: Thomas, George  
; TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase

FILE REFERENCE: 4-20971/A  
; CURRENT APPLICATION NUMBER: US/09/817,310  
; CURRENT FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: 09/230,247  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:mammalian  
; OTHER INFORMATION: autoinhibitory domain  
US-09-817-310-5

Query Match 100.0%; Score 16; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred.No. 3.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 6 FID 8

Search completed: September 30, 2004, 06:38:21  
Job time : 6.08475 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:20:22 ; Search time 7.5503 Seconds  
(without alignments)  
4799.922 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 619

Sequence: 1 gatattgtgactcagtc.....agatcaaacgtacggtggct 348

Scoring table: BLOSUM62  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DRV=xlp  
-Q=/cgn2.1/USPTO.spool\_p/US09674716/runat\_30092004\_070257\_25855/app\_query.fasta\_1.3164  
-DB=SwissProt 42 -QFMT=fastan -SUFFIX=rs -MINMATCH=0.1 -IOPCFI=0 -LOOPEXT=0  
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-OUTFMT=ptc -NORW=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09674716@cgn 1.1.82@runat\_30092004\_070257\_25855 -NCPUE=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	506	81.7	113	1 KV2D_HUMAN	P01617 homo sapien
2	494	79.8	117	1 KV2E_HUMAN	P06309 homo sapien
3	493.5	79.7	115	1 KV2A_HUMAN	P01614 homo sapien
4	490	79.2	113	1 KV2C_MOUSE	P01628 mus musculus
5	483	78.0	112	1 KV2A_MOUSE	P01626 mus musculus
6	481	77.7	113	1 KV2B_HUMAN	P01615 homo sapien
7	473	76.4	133	1 KV2F_HUMAN	P06310 homo sapien
8	463.5	74.9	112	1 KV2C_HUMAN	P01616 homo sapien
9	455	73.5	120	1 KV2B_MOUSE	P01627 mus musculus
10	444	71.7	113	1 KV2G_MOUSE	P01631 mus musculus
11	443	71.6	113	1 KV2F_MOUSE	P01630 mus musculus
12	439	70.9	113	1 KV2E_MOUSE	P03976 mus musculus
13	432	69.8	112	1 KV2D_MOUSE	P01629 mus musculus
14	416.5	67.3	108	1 KV1_CANFA	P01618 canis famil
15	415.5	67.1	134	1 KV4C_HUMAN	P06314 homo sapien
16	403.5	65.2	114	1 KV4A_HUMAN	P01625 homo sapien
17	388	62.7	133	1 KV4B_HUMAN	P06313 homo sapien
18	379	61.2	109	1 KV3D_HUMAN	P01622 homo sapien

19	378	61.1	129	1 KV3L_HUMAN	P18135 homo sapien
20	377	60.9	129	1 KV3M_HUMAN	P18136 homo sapien
21	372	60.1	109	1 KV3B_HUMAN	P01620 homo sapien
22	370.5	59.9	111	1 KV3M_MOUSE	P01665 mus musculus
23	370	59.8	109	1 KV3E_HUMAN	P01623 homo sapien
24	368.5	59.5	109	1 KV4D_HUMAN	P83593 homo sapien
25	366	59.1	109	1 KV3F_HUMAN	P01624 homo sapien
26	365.5	59.0	111	1 KV3O_MOUSE	P01667 mus musculus
27	365	59.0	108	1 KV3A_HUMAN	P01619 homo sapien
28	362	58.5	109	1 KV3G_HUMAN	P04206 homo sapien
29	361.5	58.4	111	1 KV3N_MOUSE	P01666 mus musculus
30	361	58.3	129	1 KV3H_HUMAN	P04207 homo sapien
31	360.5	58.2	111	1 KV3L_MOUSE	P01664 mus musculus
32	358.5	57.9	111	1 KV3Q_MOUSE	P01669 mus musculus
33	358.5	57.9	111	1 KV3U_HUMAN	P01673 mus musculus
34	356.5	57.6	128	1 KV3K_HUMAN	P06311 homo sapien
35	356	57.5	110	1 KV3P_MOUSE	P01668 mus musculus
36	353.5	57.1	111	1 KV3S_MOUSE	P01671 mus musculus
37	351.5	56.8	111	1 KV3R_MOUSE	P01670 mus musculus
38	346.5	56.0	108	1 KV1M_HUMAN	P01605 homo sapien
39	346.5	56.0	121	1 KV4O_HUMAN	P06312 homo sapien
40	344.5	55.7	111	1 KV3T_MOUSE	P01672 mus musculus
41	343.5	55.5	111	1 KV3H_MOUSE	P01660 mus musculus
42	339.5	54.8	111	1 KV3C_MOUSE	P01656 mus musculus
43	339.5	54.8	111	1 KV3J_MOUSE	P01662 mus musculus
44	337.5	54.5	131	1 KV3I_MOUSE	P01661 mus musculus
45	336.5	54.4	111	1 KV3A_MOUSE	P01654 mus musculus

#### ALIGNMENTS

RESULT 1	KV2D_HUMAN	STANDARD;	PRT;	113 AA.
ID	KV2D_HUMAN			
AC	P01617;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-II region TEW.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (BENCE-JONES PROTEIN TEW).			
RX	MEDLINE=74148480; PubMed=4596149;			
RA	Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;			
RT	Amino acid sequence of a kappa Bence Jones protein from a case of			
RT	Primary amyloidosis.";			
RL	Biochemistry 12:3763-3780(1973).			
RN	[2]			
RP	SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).			
RX	MEDLINE=73166638; PubMed=4700495;			
RA	Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,			
RA	Glenner G.G.;			
RT	Structural identity of Bence Jones and amyloid fibril proteins in a			
RT	patient with plasma cell dyscrasia and amyloidosis.";			
RL	J. Clin. Invest. 52:1276-1281(1973).			
CC	-!- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL			
CC	WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.			
CC	-!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A			
CC	PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.			
CC	-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)			
CC	MARKER.			
DR	PIR; A90370; K2HTW7.			
DR	HSSP; P01607; 1RE1.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; IG; 1.			
DR	SMART; SM00406; IGV; 1.			

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DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 FRAMEWORK-2.
FT DOMAIN 40 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 61 FRAMEWORK-2.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 94 102 FRAMEWORK-3.
FT DOMAIN 103 112 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 113 93 FRAMEWORK-4.
FT NON_TER 23 93 BY SIMILARITY.
SQ SEQUENCE 113 AA; 12316 MW; 0C3C39F81F1843CA CRC64;

Alignment Scores:
Pred. No.: 1.2e-48 Length: 113
Score: 506.00 Matches: 95
Percent Similarity: 92.04% Conservativeness: 9
Best Local Similarity: 84.07% Mismatches: 9
Query Match: 81.74% Indels: 0
DB: 1 Gaps: 0

US-09-674-716b-17 (1-348) x KV2D_HUMAN (1-113)
QY 1 GATATTGATGACTCAGTCTCCACTCTCCCTGCCCTCAGCCCTGAGAGCGGCGCTCC 60
Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
QY 61 ATCTCTGCTGCTCGAGTAAGAGTCTCTGTATAGGATGGAGACATATCTTGAATTGG 120
Db 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAspGlyPheAspTyrLeuAsnTyr 40
QY 121 TACTCTGAGAGAGCGAGGAGTCTCCAGCTCTCCCTGCCCTCAGCCCTGAGAGCGGCGCTCC 180
Db 41 TyrLeuGlnLysProGlyGlnSerPro**LeuLeuIleTyrAlaLeuSerAsnArgAla 60
QY 181 TCAGGGTCCCTGACAGTTCAGTGGCAGTGGATCGAGACAGATTTTACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGGTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMet**AlaLeuGlnAlaPro 100
QY 301 TTCAGTTCGGCCAGGAGGACAGGTGGAGATCAACAGT 339
Db 101 IleThrPheGlyGlnGlyThrArgLeuGluLeuLysArg 113

RESULT 2
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RL Nature 309:73-76(1984).
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or send an email to license@isb-sib.ch).
CC EMBL; Z00009; -; NOT ANNOTATED_CDS.
CC PIR; A01889; K2HUGM.
DR HSSP; P80362; LWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK-1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 58 FRAMEWORK-2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 66 97 FRAMEWORK-3.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 27 97 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Alignment Scores:
Pred. No.: 2.68e-47 Length: 117
Score: 494.00 Matches: 97
Percent Similarity: 91.15% Conservativeness: 6
Best Local Similarity: 85.84% Mismatches: 10
Query Match: 79.81% Indels: 0
DB: 1 Gaps: 0

US-09-674-716b-17 (1-348) x KV2E_HUMAN (1-117)
QY 1 GATATTGATGACTCAGTCTCCACTCTCCCTGCCCTCAGCCCTGAGAGCGGCGCTCC 60
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24
QY 61 ATCTCTGCTGCTCGAGTAAGAGTCTCTGTATAGGATGGAGACATATCTTGAATTGG 120
Db 25 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAsnTyr 44
QY 121 TACTCTGAGAGAGCGGAGTCTCCAGCTCTCCCTGCCCTCAGCCCTGAGAGCGGCGCTCC 180
Db 45 TyrLeuGlnLysProGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 64
QY 181 TCAGGGTCCCTGACAGTTCAGTGGCAGTGGATCGAGACAGATTTTACACTGAAATC 240
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84
QY 241 AGCAGAGTGGAGGTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 85 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyLeuGlnThrPro 104
QY 301 TTCAGTTCGGCCAGGAGGACAGGTGGAGATCAACAGT 339
Db 105 GlnThrPheGlyGlnGlyThrLysValGluLeuLysArg 117

RESULT 3
KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=68242259; PubMed=5586923;  
RA Hilschmann N.;  
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
RN [2]  
RP REVISIONS TO 50; 52; 96 AND 97.  
RX MEDLINE=70063440; PubMed=4188189;  
RA Hilschmann N.;  
RT "Molecular basis of antibody formation.";  
RL Naturwissenschaften 56:195-205(1969).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PIR; B31639; K2HUCM.  
DR HSP; P01607; IREI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR Pfam; PF00047; IG\_v.  
DR SMART; SMO0406; IG; 1.  
DR PROSITE; PS0835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DISULFID 24 95  
FT NON TER 115 115  
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Alignment Scores:  
Pred. No.: 3.04e-47 Length: 115  
Score: 493.50 Matches: 96  
Percent Similarity: 91.23% Conservative: 8  
Best Local Similarity: 84.21% Mismatches: 9  
Query Match: 79.73% Indels: 1  
DB: 1 Gaps: 1

US-09-674-716b-17 (1-348) x KV2C\_HUMAN (1-115)

QY 1 GATATTGTGATGACTAGTCTCCACTCTCCCTGCTCCCTGAGAGCGGCTCC 60  
Db 2 AspileValMetThrGlnThrProLeuSerLeuProValThrProGlyGluProAlaSer 21  
QY 61 ATCTCTCTGCTCGAGTAAAGTCTCTGTATAAG---GATGGAGACATCTTGAAT 117  
Db 22 IleserCysArgSerSerLeuLeuAspSerGlyAspGlyAsnThrLeuAsn 41  
QY 118 TGGTACTTCGAGAGCCAGGCGAGTCTCCAGCTCTCTGATCTATTGATGTCACCCCG 177  
Db 42 TrpTyrLeuGlnLysAlaGlyGlnSerProGlnLeuLeuIleTyrThrLeuSerTyrArg 61  
QY 178 GCATCAGGGTCCCTGACAGGTTTCAGTGGCAGTGATCGGCACAGATTTTACACTGAA 237  
Db 62 AlaserGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLys 81  
QY 238 ATCAGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTCTCAACAGCTGGTAGAGTAT 297  
Db 82 IleserArgValGlnAlaGluAspValGlyValTyrTyrCysMetGlnArgLeuGluLeu 101  
QY 298 CCATTACGTTCCCGCAGGACCAAGTGGAGATCAACGCT 339  
Db 102 ProTyrThrPheGlyGlyGlyThrLysLeuGluLeuArg 115

RESULT 4  
KV2C\_MOUSE  
ID KV2C\_MOUSE STANDARD; PRT; 113 AA.  
AC P01628;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG kappa chain V-II region MOPC 511.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81052016; PubMed=6776396;  
RA Appella E.;  
RT "Amino acid sequence of the light chain variable region of MS11, a phosphorylcholine-binding murine myeloma protein.";  
RL Mol. Immunol. 17:711-718(1980).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE.  
DR PIR; A01910; KVM551.  
DR HSP; P80362; 1WTL.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SMO0406; IGv; 1.  
DR PROSITE; PS0835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 55 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON TER 113 113  
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Alignment Scores:  
Pred. No.: 7.47e-47 Length: 113  
Score: 490.00 Matches: 95  
Percent Similarity: 90.27% Conservative: 7  
Best Local Similarity: 84.07% Mismatches: 11  
Query Match: 79.16% Indels: 0  
DB: 1 Gaps: 0

US-09-674-716b-17 (1-348) x KV2C\_MOUSE (1-113)

QY 1 GATATTGTGATGACTAGTCTCCACTCTCCCTGCTCCCTGAGAGCGGCTCC 60  
Db 1 AspileValIleThrGlnAspGluLeuSerLysProValThrSerGlyGluSerValSer 20  
QY 61 ATCTCTCTGCTCGAGTAAAGTCTCTGTATAAGGATGGAGACATCTTGAATGG 120  
Db 21 IleserCysArgSerSerLysSerLeuLeuTyrLysAspGlyLysThrTyrLeuAsnTrp 40  
QY 121 TACTTCGAGAGCCAGGCGAGTCTCCAGCTCTCTGATCTATTGATGTCACCCCGGCA 180  
Db 41 PheLeuGlnGlyProGlnGlnSerProArgLeuLeuIleTyrLeuMetSerThrArgAla 60  
QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLeu 80  
QY 241 ACCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCA 300  
Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnGlnLeuValGluTyrPro 100  
QY 301 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAACGCT 339  
Db 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuArg 113

RESULT 5  
KV2A\_MOUSE  
ID KV2A\_MOUSE STANDARD; PRT; 112 AA.  
AC P01626;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region MOPC 167.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=79000273; PubMed=99160;  
RA Rudikoff S., Potter M.;  
RT "Kappa Chain variable region from M167, a phosphorylcholine binding  
RL myeloma protein."  
RL Biochemistry 17:2703-2707(1978).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY  
CC CHAIN HAS ALSO BEEN DETERMINED.  
CC PIR; A01908; KMS16.  
DR HSSP; P80362; 1MTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00466; Igv\_1.  
DR PROSITE; PS50835; IG LIKE; 1.  
DR Immunoglobulin V region.  
KW DOMAIN 1 23  
FT DOMAIN 1 23  
FT FRAMEWORK-1.  
FT COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 24 39  
FT FRAMEWORK-2.  
FT DOMAIN 40 54  
FT FRAMEWORK-3.  
FT DOMAIN 55 61  
FT COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 62 93  
FT FRAMEWORK-3.  
FT DOMAIN 94 102  
FT COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 103 112  
FT FRAMEWORK-4.  
FT DISULFID 23 93  
FT NON TER 112 112  
FT BY SIMILARITY.  
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;  
Alignment Scores:  
Pred. No.: 4.54e-46 Length: 112  
Score: 483.00 Matches: 94  
Percent Similarity: 90.18% Conservatives: 7  
Best Local Similarity: 83.93% Mismatches: 11  
Query Match: 78.03% Indels: 0  
DB: 1 Gaps: 0  
US-09-674-716B-17 (1-348) x KV2A\_MOUSE (1-112)  
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACTCCCTGGAGAGCGGCTCC 60  
DB 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
QY 61 ATCTCTGTCTGCTGAGTAAGAGTCTCTGTATAAGGATGGGAGACATACCTTGAATTGG 120  
DB 21 IleSerCysArgSerSerLysSerLeuLeuTyLysAspGlyLysThrYrLeuAsnTrp 40  
QY 121 TACCTGCAGAGCAGGCGAGTCTCCACAGCTCTCATCTATTGATGTCACCGCGGCA 180  
DB 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleSerLeuMetSerThrArgAla 60  
QY 181 TCAGGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGACAGATTTTACATGAAATC 240  
DB 61 SerGlyValSerAspArgPheSerGlySerGlySerArgThrAspPheThrLeuGluIle 80  
QY 241 AGCAGAGTGGAGCTCAGAGTGTGGGTTTACTGTCACAGCTGGTAGAGTATCCA 300  
DB 81 SerArgValIysAlaGluAspValGlyValTyTyTyCysGlnGlnLeuValGluTyPro 100  
QY 301 TTCACGTTCCGCGCAGGACCAAGGTGGAGATCAA 336  
DB 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuLys 112  
RESULT 6  
KV2B\_HUMAN  
ID KV2B\_HUMAN STANDARD; PRT; 113 AA.  
AC F01615;  
DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region FR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=76253627; PubMed=821524;  
RA Riessen W.F., Jaton J.-C.;  
RT "Variable region sequence of the light chain from a Waldenstroms Igm  
RL with specificity for phosphorylcholine."  
RL Biochemistry 15:3829-3833(1976).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.  
CC PIR; A01886; K2HUPR.  
DR HSSP; P01607; IREI.  
DR GO; GO:0005576; Extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; Igv\_1.  
DR PROSITE; PS50835; IG LIKE; 1.  
DR Immunoglobulin V region.  
KW DOMAIN 1 23  
FT DOMAIN 1 23  
FT FRAMEWORK-1.  
FT COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 24 39  
FT FRAMEWORK-2.  
FT DOMAIN 40 54  
FT FRAMEWORK-3.  
FT DOMAIN 55 61  
FT COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 62 93  
FT FRAMEWORK-3.  
FT DOMAIN 94 102  
FT COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON TER 113 113  
FT BY SIMILARITY.  
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39B46DB96BE CRC64;  
Alignment Scores:  
Pred. No.: 7.63e-46 Length: 113  
Score: 481.00 Matches: 88  
Percent Similarity: 89.38% Conservatives: 13  
Best Local Similarity: 77.88% Mismatches: 12  
Query Match: 77.71% Indels: 0  
DB: 1 Gaps: 0  
US-09-674-716B-17 (1-348) x KV2B\_HUMAN (1-113)  
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACTCCCTGGAGAGCGGCTCC 60  
DB 1 AspValValMetThrGlnSerProLeuPheLeuProValThrLeuGlyGluProAlaSer 20  
QY 61 ATCTCTGTCTGCTGAGTAAGAGTCTCTGTATAAGGATGGGAGACATACCTTGAATTGG 120  
DB 21 IleGlnCysArgSerSerGlnSerLeuValTyArg\*\*\*Gly\*\*\*ThrTyLeu\*\*\*Trp 40  
QY 121 TACCTGCAGAGCAGGCGAGTCTCCACAGCTCTCATCTATTGATGTCACCGCGGCA 180  
DB 41 TyrLeuGlnLysProGlyGlnSerProGluLeuLeuIleTyLeuSerSerTyArgAsp 60  
QY 181 TCAGGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGACAGATTTTACATGAAATC 240  
DB 61 SerGlyValProAspArgPheSerAspSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGCTCAGAGTGTGGGTTTACTGTCACAGCTGGTAGAGTATCCA 300  
DB 81 ThrArgValGlnAlaGluAspValGlyValTyTyTyCysMetGlnAlaThr\*\*\*SerPro 100  
QY 301 TTCACGTTCCGCGCAGGACCAAGGTGGAGATCAAACGT 339  
DB 101 TyThrPheGlyGlnGlyThrLysLeu\*\*\*IleLysArg 113  
RESULT 7

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KV2F_HUMAN          STANDARD;          PRT;          133 AA.
ID   P06310;
AC   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG kappa chain V-II region RPMI 6410 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041852; PubMed=2997711;
RA   Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT   "Human immunoglobulin kappa light chain genes of subgroups II and
RT   III.";
RL   Nucleic Acids Res. 13:6499-6513 (1985).
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@sib-sib.ch).
CC   -----
DR   ENBL; Z00020; CAA77315.1; -.
DR   PIR; A01890; K2HURP.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003596; IG_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG LIKE; 1.
DR   Immunoglobulin V region; Signal.
FT   SIGNAL          1
FT   CHAIN           20
FT   DOMAIN          21 133
FT   DOMAIN          21 43
FT   DOMAIN          44 59
FT   DOMAIN          60 74
FT   DOMAIN          75 81
FT   DOMAIN          82 113
FT   DOMAIN          114 122
FT   DOMAIN          123 132
FT   DISULFID        43 113
FT   NON_TER         133
SQ   SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Alignment Scores:
Pred. No.:          6,2e-45          Length:          133
Score:              473.00          Matches:          90
Percent Similarity: 88.50%          Conservative:    10
Best Local Similarity: 79.65%          Mismatches:     13
Query Match:        76.41%          Indels:          0
DB:                  1              Gaps:            0

US-09-674-716B-17 (1-348) x KV2F_HUMAN (1-133)

QY   1 GATATTGTGACTGACTGCTCCACTCTCCCTGCCCGTCCACCCCTGGAGAGCGGCTCC 60
DB   21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40

QY   61 ATCTCTGTCGCTCGAGTAAAGTCTCTCTGTAAGGATGGGAACATACATTGAATTGG 120
DB   41 ILeserCysArgSerSerGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60

QY   121 TACCTGCAGAACCCAGGCGAGCTCCACAGCTCTGATCTATTGATGTCACCCGGGCA 180
DB   61 PheGlnGlnArgProGlyGlnSerProArgGlyLeuIleTyrLysValSerAsnArgAsp 80

KV2F_HUMAN          STANDARD;          PRT;          112 AA.
ID   KV2C_HUMAN
AC   P01616;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG kappa chain V-II region MIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RA   Dreyer W.J., Gray W.R., Hood L.E.;
RT   "The genetic, molecular, and cellular basis of antibody formation:
RT   some facts and a unifying hypothesis.";
RL   Cold Spring Harb. Symp. Quant Biol. 32:353-367 (1967).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01887; K2HUML.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003596; IG_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG LIKE; 1.
DR   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN          1 23
FT   DOMAIN          24 38
FT   DOMAIN          39 53
FT   DOMAIN          54 60
FT   DOMAIN          61 92
FT   DOMAIN          93 101
FT   DOMAIN          102 111
FT   DISULFID        23 92
FT   NON_TER         112
SQ   SEQUENCE 112 AA; 12055 MW; E5B2E2EFA7ABE481 CRC64;

Alignment Scores:
Pred. No.:          6,98e-44          Length:          112
Score:              463.50          Matches:          86
Percent Similarity: 89.38%          Conservative:    15
Best Local Similarity: 76.11%          Mismatches:     11
Query Match:        74.88%          Indels:          1
DB:                  1              Gaps:            1

US-09-674-716B-17 (1-348) x KV2C_HUMAN (1-112)

QY   1 GATATTGTGACTGACTGCTCCACTCTCCCTGCCCGTCCACCCCTGGAGAGCGGCTCC 60
DB   1 AspIleValLeuThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20

QY   61 ATCTCTGTCGCTCGAGTAAAGTCTCTCTGTAAGGATGGGAACATACATTGAATTGG 120
DB   21 ILeserCysArgSerSerGlnSerLeuLeu***Ser***Gly***---TyrLeuAspTrp 39

QY   121 TACCTGCAGAACCCAGGCGAGCTCCACAGCTCTGATCTATTGATGTCACCCGGGCA 180
DB   40 TyrLeu***LysProGly***SerPro***LeuLeuIleTyrLeuGlySerAsnArgAla 59

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QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGCATCAGGCACAGATTTTACACTGAAATC 240
Db 60 SerGlyValProAsnArgPheSerGlySerGlyThr***PheThrLeuLysValle 79
QY 241 AGCAGAGTGGAGGTGAGAGTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 80 SerArgVal***Ala*****ValGlyValTyrCysMetGlnAlaLeuGlnThrPro 99
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAACT 339
Db 100 LeuThrPheGlyGlyThrAsnValGluLeuLysArg 112

RESULT 9
KV2B_MOUSE
ID KV2B_MOUSE STANDARD; PRT: 120 AA.
AC P01627;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region VKappa167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.; PubMed=6791832;
RA MEDLINE=8200223; PubMed=6791832;
RA Seising E., Storb U.;
RT "Somatic mutation of immunoglobulin light-chain variable-region
genes."
RL Cell 25:47-58(1981).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00562; AAA39032.1; -.
DR EMBL; K02415; AAA39051.1; -.
DR PIR; A01909; KWS67.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 120 IG KAPPA CHAIN V-II REGION VKAPPA167.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 60 74 FRAMEWORK-2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-3.
FT DOMAIN 114 120 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 113 BY SIMILARITY.
SQ SEQUENCE 120 AA; 13280 MW; 63B3571F0E4DE3E8 CRC64;

Alignment Scores:
Pred. No.: 6,34e-43 Length: 120
Score: 455.00 Matches: 88
Percent Similarity: 93.00% Conservative: 5
Best Local Similarity: 88.00% Mismatches: 7
Query Match: 73.51% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x KV2B_MOUSE (1-120)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
Db 1 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20

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Db 21 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 40
QY 61 ATCTCTGTCGTCGAGTAAGAGTCTCTGATATAAGGATGGAGACATCTACTGTAATGG 120
Db 41 IleSerCysArgSerSerLysSerLeuLeuTyrLysAspGlyLysThrThrLeuAsnTrp 60
QY 121 TACCTCCAGAACCCAGGCGAGTCTCCACAGCTCCCTGATCTATTGATCTCCACCCGGCA 180
Db 61 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleTyrLeuMetSerThrArgAla 80
QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGCATCAGGCACAGATTTTACACTGAAATC 240
Db 81 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLeu 100
QY 241 AGCAGAGTGGAGGTGAGAGTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 101 SerArgValLysAlaGluAspValGlyValTyrCysGlnGlnLeuValGluTyrPro 120

RESULT 10
KV2G_MOUSE
ID KV2G_MOUSE STANDARD; PRT: 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RT anti-digoxin hybridoma antibody."
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
CC PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KWS26.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Alignment Scores:
Pred. No.: 1.07e-41 Length: 113
Score: 444.00 Matches: 84
Percent Similarity: 86.73% Conservative: 14
Best Local Similarity: 74.34% Mismatches: 15
Query Match: 71.73% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x KV2G_MOUSE (1-113)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
Db 1 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20

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QY 61 ATCTCTGCTCGCTAGAGTCTCCCTGATTAAGGATGGGAAGACATCTTGAATTGG 120
Db 21 IleserCysArgSerSerGlnSerLeuValHisSerAsnGlyAsnThrTyrLeuAsnTrp 40
QY 121 TACCTCGAAGCAGGAGGAGTCTCCAGCTCCCTGATCTATTGATGTCACCCGGGCA 180
Db 41 TyrLeuGlnLysAlaGlyGlnSerProLysLeuLeuLysValSerAsnArgPhe 60
QY 181 TCAGGGGTCCTCGACAGGTTTCAGTGGCAGTCAGGACAGACAGATTTTACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 81 SerArgValGluAlaGluAspLeuGlyIleTyrPheCysSerGlnThrHisValPro 100
QY 301 TTCACCTTCGGCCCAAGGACCAAGTGGAGATCAAAAGT 339
Db 101 ProThrPheGlyGlyThrLysLeuGluLeuLysArg 113

RESULT 11
KV2F_MOUSE
ID_KV2F_MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 7334.1.
CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KMS78.
DR HSSP; P80362; IWTL.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 103 112 BY SIMILARITY.
FT DISULFID 23 93
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91/CRC64;

Alignment Scores:
Pred. No.: 1,39e-41 Length: 113
Score: 443.00 Matches: 87
Percent Similarity: 84.07% Conservative: 8
Best Local Similarity: 76.99% Mismatches: 18
Query Match: 71.57% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x KV2F_MOUSE (1-113)
```

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QY 1 GATATTGTGATGATCTCAGTCTCCACTCTCCCTGCCCTCCACCTCTGGAGAGCGCGCTCC 60
Db 1 AspIleValMetThrGlnThrAlaProSerAlaLeuValThrProGlyGluSerValSer 20
QY 61 ATCTCTGCTCGCTAGAGTCTCCCTGATTAAGGATGGGAAGACATCTTGAATTGG 120
Db 21 IleserCysArgSerSerLysSerLeuLeuHisSerAsnGlyAsnThrTyrLeuTrp 40
QY 121 TACCTCGAAGCAGGAGGAGTCTCCAGCTCCCTGATCTATTGATGTCACCCGGGCA 180
Db 41 PheLeuGlnArgProGlyGlnCysProGlnLeuLeuLysValSerAsnLeuAla 60
QY 181 TCAGGGGTCCTCGACAGGTTTCAGTGGCAGTCAGGACAGACAGATTTTACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAlaPheThrLeuArgIle 80
QY 241 AGCAGAGTGGAGCTGAGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnGlnArgGluTyrPro 100
QY 301 TTCACCTTCGGCCCAAGGACCAAGTGGAGATCAAAAGT 339
Db 101 TyrThrPheGlyGlyThrLysLeuGluLeuLysArg 113

RESULT 12
KV2E_MOUSE
ID_KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17829.1.
CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=85128968; PubMed=6441768;
RA Abersold R., Herbst H., Grutter T., Chang J.-Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 2S25.1 specific for the
RT group A-streptococcal polysaccharide."
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR; A01912; KMS17.
DR HSSP; P01607; IRE1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E939797046F8DB33/CRC64;

Alignment Scores:
Pred. No.: 3.9e-41 Length: 113
Score: 439.00 Matches: 87
Percent Similarity: 84.07% Conservative: 8
Best Local Similarity: 76.99% Mismatches: 18
Query Match: 70.92% Indels: 0
DB: 1 Gaps: 0
```





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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:27:18 ; Search time 44.0663 Seconds  
(without alignments)  
4983.418 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 619

Sequence: 1 gatattgtgactcagtc.....agatcaaacgtacgtggct 348

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US09674716/runat\_30092004\_070258\_25867/app\_query.fasta\_1.3164  
-DB=SPTREMBL\_25 -QWMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=pcpt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pc -NORM=ext -HEAPSZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09674716@cgn\_1\_1\_499@runat\_30092004\_070258\_25867 -NCPU=3  
-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SPTREMBL\_25:

1:	sp_archaea.*
2:	sp_bacteria.*
3:	sp_fungi.*
4:	sp_human.*
5:	sp_invertebrate.*
6:	sp_mammal.*
7:	sp_mhc.*
8:	sp_organelle.*
9:	sp_phage.*
10:	sp_plant.*
11:	sp_rodent.*
12:	sp_virus.*
13:	sp_vertibrate.*
14:	sp_unclassified.*
15:	sp_virus.*
16:	sp_bacteriaph.*
17:	sp_archaea.*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	%	Score	Match	Length	DB	ID	Description
1	516	83.4	239	4	Q8NEK0	Q8NEK0	homo sapien	

#### ALIGNMENTS

##### RESULT 1

ID	Q8NEK0	PRELIMINARY;	PRT;	239	AA.
AC	Q8NEK0;				
DT	01-OCT-2002 (TrEMBLrel. 22, Created)				
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_taxID=9606;				
RN	[1]_taxID=9606;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Prostate;				
RA	Straussberg R.;				
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC030814; AAH30814.1; -				
DR	PIR; S23638; S23638.				
DR	PIR; S34091; S34091.				
DR	PIR; S40357; S40357.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003597; Ig cl.				
DR	InterPro; IPR003006; Ig MHC.				
DR	InterPro; IPR003596; Ig_v.				

Q8TCD0	homo sapien
Q8VC55	mus musculus
Q9U180	homo sapien
Q99M37	mus musculus
Q8VC16	mus musculus
Q8K0F8	mus musculus
Q8K122	mus musculus
Q9J182	mus musculus
Q9U178	homo sapien
Q9U186	homo sapien
Q9U186	homo sapien
Q920E9	mus musculus
Q72473	homo sapien
Q811U6	mus musculus
Q9U177	homo sapien
Q9U185	homo sapien
Q8K1F2	mus musculus
Q9ERZ9	mus musculus
Q8K1F1	mus musculus
Q72336	mus musculus
Q9U410	mus musculus
Q723Y4	homo sapien
Q723Y5	homo sapien
Q8K1F3	mus musculus
Q8K1F1	mus musculus
Q96SA9	homo sapien
Q9U181	homo sapien
Q9U170	homo sapien
Q91A5	mus musculus
Q9QYF0	mus musculus
Q8VCP0	mus musculus
Q920E6	mus musculus
Q8VJ0	mus musculus
Q8VDD0	mus musculus
Q7E98	mus musculus
Q8R062	mus musculus
Q7Tmk3	mus musculus
Q811C3	mus musculus
Q9J180	mus musculus
Q91WS9	mus musculus
Q96PF6	homo sapien
Q7Tmk0	mus musculus
Q91W12	mus musculus







DR DB; 1KN2; 13-MAR-02.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002198; ADH\_short.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_cl.  
DR InterPro; IPR003596; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRO64;  
  
Alignment Scores:  
Pred. No.: 5,25e-42 Length: 239  
Score: 433.00 Matches: 83  
Percent Similarity: 84.48% Conservative: 15  
Best Local Similarity: 71.55% Mismatches: 18  
Query Match: 69.95% Indels: 0  
DB: 11 Gaps: 0  
  
US-09-674-716B-17 (1-348) x Q8K0F8 (1-239)  
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACCCCTGGAGAGCGCGCTCC 60  
DB 21 AspValValMetThrGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSer 40  
QY 61 ATCTCTGTCGCTCGAGTAAGACTCTCCCTGTATAGGATGGGAACACATCTTGATTGG 120  
DB 41 IleSerCysLysSerGlnSerLeuPheThrAsnGlyLysMetTyrLeuSerTrp 60  
QY 121 TACTCTGAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCCGGCA 180  
DB 61 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleSerLeuValSerLysLeuAsp 80  
QY 181 TCAGGGTCCCTGACAGTTTCAGTGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
DB 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100  
QY 241 AGCAGAGTGAGGCTCAGAGTGTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
DB 101 SerArgValGluAlaGluAspLeuGlyValTyrCysLeuGlnSerThrHisPhePro 120  
QY 301 TTCAGGTTCCGCAAGGACCAAGGTCAGATCAAAACGTACGGTGGCT 348  
DB 121 TyrPheGlyGlyThrLysLeuGluIleLysArgAlaAspAla 136  
  
RESULT 8  
Q8K122 PRELIMINARY; PRT; 148 AA.  
ID Q8K122 AC Q8K122  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP TISSUE=Salivary gland;  
RC Strauberg R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC028925; AAB28925.1; -  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
FT NON TER 1









Pred. No.: 4,1e-32 Length: 108  
Score: 348.50 Matches: 69  
Percent Similarity: 72.57% Conservative: 13  
Best Local Similarity: 61.06% Mismatches: 26  
Query Match: 56.30% Indels: 5  
DB: 4 Gaps: 1

US-09-674-716B-17 (1-348) x Q9UL79 (1-108)

QY	1	GATATTGTGACTCAGTCTCCCTGCCCCGTCACCCCTGGAGAGCCGGCCTCC	60
Db	1	AspIleValMetThrGlnSerProSerLeuLeuSerAlaSerThrGlyAspArgValThr	20
QY	61	ATCTCTCTGCTCGAGTAAGAGTCTCCTGTATAAGGATGGAGACATCTTGAATTGG	120
Db	21	IleSerCysArgMetSerGlnGlyLe-----SerSerTyLeuAlaTrp	35
QY	121	TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATCTCCACCCGGGCA	180
Db	36	TyrGlnGlnLysProGlyLysAlaProGluLeuLeuTyrAlaAlaSerThrLeuGln	55
QY	181	TCAGGGGTCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC	240
Db	56	SerGlyValProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIle	75
QY	241	AGCAGAGTGGAGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA	300
Db	76	SerCysLeuGlnSerGluAspPheAlaThrTyrTyrcysGlnGlnTyrTyrcSerPhePro	95
QY	301	TTCAGTTTCGGCCAGGACCAAGGTGGAGATCAACGT	339
Db	96	ProThrPheGlyGlnGlyThrLysValGluIleLysArg	108

Search completed: September 30, 2004, 08:53:40  
Job time : 45.0663 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:19:42 ; Search time 41.458 Seconds  
(without alignments)  
4743.430 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 619

Sequence: 1 gatattgtgactcagtc.....agatcaaacgtacgtggtc 348

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q/cgn2\_1/USPTO\_spool\_P/US09674716/runat\_30092004\_070257\_25848/app\_query.fasta\_1.3164  
-DB=A\_Geneseq\_29Jan04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=oct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09674716@cgn\_1\_1\_475@runat\_30092004\_070257\_25848 -NCPUS=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	601	97.1	116	3 AAY32262	Aay32262 Humanised
2	522	84.3	239	7 ADE28461	Ad28461 Human ant
3	519.5	83.9	170	5 ABP64972	Abp64972 Human pro
4	519	83.8	239	3 AAY82615	Aay82615 Human PTH
5	518	83.7	239	7 ADE28405	Ad28405 Human ant
6	518	83.7	114	5 ABB57576	Abb57576 HLA-DR-sp
7	518	83.7	239	7 ADE28465	Ad28465 Human ant
8	516	83.4	145	3 AAY32261	Aay32261 Mouse ant
9	513	82.9	239	7 ADE28397	Ad28397 Human ant
10	512	82.7	239	7 ADE28421	Ad28421 Human ant

11	511	82.6	239	3 AAY82611	Aay82611 Human PTH
12	511	82.6	239	7 ADE28469	Ad28469 Human ant
13	510	82.4	238	4 AAB72235	Aab72235 Humanised
14	510	82.4	238	4 AAB72231	Aab72231 Humanised
15	510	82.4	238	4 AAB72227	Aab72227 Humanised
16	510	82.4	238	4 AAB72233	Aab72233 Humanised
17	510	82.4	239	3 AAY82617	Aay82617 Human PTH
18	510	82.4	239	7 ADE28521	Ad28521 Human ant
19	510	82.4	239	7 ADE28477	Ad28477 Human ant
20	507	81.9	114	2 AAW27544	Aaw27544 Human Ab
21	507	81.9	281	2 AAW27560	Aaw27560 Consensus
22	506	81.7	239	3 AAY82614	Aay82614 Human PTH
23	506	81.7	239	3 AAY82610	Aay82610 Human PTH
24	505	81.6	239	3 AAY82616	Aay82616 Human PTH
25	504	81.4	112	7 ADE28437	Ad28437 Human ant
26	504	81.4	113	7 ADD28282	Add28282 Human het
27	503	81.3	112	2 AAW53586	Aaw53586 Light cha
28	502.5	81.2	113	2 AAR88508	Aar88508 Vlkappa f
29	502	81.1	113	6 ABU18680	Abj18680 Antibody
30	502	81.1	139	4 AAB99117	Aab99117 Human pro
31	501	80.9	112	7 ADE28487	Ad28487 Human ant
32	501	80.9	112	7 ADE28409	Ad28409 Human ant
33	501	80.9	127	5 AAU79809	Aau79809 Light cha
34	501	80.9	239	3 AAY82618	Aay82618 Human PTH
35	501	80.9	239	6 ABR48456	Abr48456 Human Cal
36	500	80.8	112	2 AAW54015	Aaw54015 Human ant
37	500	80.8	112	7 ADE28441	Ad28441 Human ant
38	500	80.8	125	5 ABG76926	Abg76926 Humanised
39	500	80.8	247	5 ABG70338	Abg70338 Human MDD
40	499.5	80.7	114	3 AAY95186	Aay95186 Anti-plat
41	499.5	80.7	131	3 AAY95226	Aay95226 Anti-plat
42	499	80.6	113	6 ADA89172	Ada89172 Human ant
43	499	80.6	219	6 ABR39484	Abr39484 Humanised
44	499	80.6	219	6 ABU08310	Abu08310 Humanised
45	499	80.6	219	6 ABR39792	Abr39792 Humanised

ALIGNMENTS

RESULT 1

AAAY32262

ID AAAY32262 standard; protein; 116 AA.

AC AAAY32262;

DT 15-FEB-2000 (first entry)

DE Humanised anti-CD23 MAb C11 light chain variable region.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;

XX monoclonal antibody; chimeric antibody; humanised antibody;

XX complementarity determining region; CDR; autoimmune disease;

XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;

XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

XX urticaria; nephrotic syndrome; glomerulonephritis;

XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;

XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX therapy.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Region 1..23 "framework region 1"

XX Region 24..39 "framework region 1"

XX Region 40..54 "note= "CDR 1"

XX Region 55..61 "note= "framework region 2"

XX Region 62..93 "note= "CDR 2"

FT Region /note= "framework region 3"

FT 94.102

FT /note= "CDR 3"

FT 103.113

FT /note= "framework region 4"

XX W09958679-A1.

XX 18-NOV-1999.

XX

XX 07-MAY-1999; 99WO-GB001434.

XX

XX 09-MAY-1998; 98GB-00009839.

XX

XX (GLAX ) GLAXO GROUP LTD.

XX

XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX

XX WPI; 2000-053101/04.

XX

XX N-PSDB; AA234747.

XX

XX Cell receptor specific antibodies useful for treating e.g. arthritis,

XX diabetes, multiple sclerosis and psoriasis.

XX

XX Claim 9; Fig 3; 81pp; English.

XX

XX This sequence represents the light chain variable region (VL) of

CC humanised anti-CD23 (PCERII) monoclonal antibody C11, composed of a human

CC framework (HSICKVII) and the light chain complementarity determining

CC regions (see AAY32254-56) of murine antibody C11. The DNA was constructed

CC by splice overlap PCR. The invention provides altered antibodies, such as

CC chimeric or humanised antibodies, which comprise sufficient of the amino

CC acid sequences of the C11 light and heavy chain complementarity

CC determining regions to render them capable of binding to the CD23 type II

CC molecule expressed on haematopoietic cells. The antibodies are used to

CC block soluble CD23 formation in human therapy, for the treatment of

CC arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple

CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic

CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative

CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,

CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-

CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic

CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell

CC malignancies (claimed). They are also useful for studying interactions

CC between CD23 and various ligands and determining the binding agents

XX

XX Sequence 116 AA;

XX

Alignment Scores:

Pred. No.: 6.6e-56 Length: 116

Score: 601.00 Matches: 116

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 97.09% Indels: 0

DB: 3 Gaps: 0

US-09-674-716B-17 (1-348) x AAY32262 (1-116)

QY 1 GATATTGATGACTCAGTCTCCACTCTCCCTGCGGTCCACCCCTGGAGAGCGGCTCC 60

DB 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20

QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTGTATAGGATGGGAACATACCTGAATTGG 120

DB 21 IleSerCysArgSerSerLysSerLeuLeuTyrlLysAspGlyLysThrTyrlLeuAsnTrp 40

QY 121 TACCTCGAAGCCAGGCGAGTCTCCACAGTCTCTGATCTTATTTGATGTCCACCGGGCA 180

DB 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLysLeuMetSerThrArgala 60

QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300

DB 81 SerArgValGluAlaGluaspValGlyValTyrlLysCysGlnGlnLeuValGluTyrlPro 100

QY 301 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAAAACGTACGGTGGCT 348

DB 101 PheThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 116

RESULT 2

ADE28461

ID ADE28461 standard; protein; 239 AA.

XX

XX ADE28461;

XX

XX 29-JAN-2004 (first entry)

XX

XX Human anti-CD40 antibody 23-28-1 variable region light chain protein.

XX

XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;

XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;

XX bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;

XX human; variable region light chain; 23-28-1.

XX

XX Homo sapiens.

XX

XX WO2003040170-A2.

XX

XX 15-MAY-2003.

XX

XX 08-NOV-2002; 2002WO-US036107.

XX

XX 09-NOV-2001; 2001US-0348980P.

XX

XX (PFIZ ) PFIZER PROD INC.

XX

XX (ABGE-) ABGENIX INC.

XX

XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX

XX WPI; 2003-441521/41.

XX

XX N-PSDB; ADE28460.

XX

XX New chimeric or human monoclonal antibody or its antigen-binding portion

PT that specifically binds to and activates human CD40, useful for enhancing

PT an immune response in a human, or treating cancer, HIV, neutropenia or

PT viral infections.

XX

XX Claim 1; SEQ ID NO 68; 177pp; English.

XX

XX The invention relates to a novel chimeric or human monoclonal antibody or

CC its antigen-binding portion that specifically binds to and activates

CC human CD40. The anti-CD40 antibody of the invention demonstrates

CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV

CC activities and may be useful for treating a hyperproliferative disorder

CC such as cancer, viral and bacterial infection or genetic, primary or

CC combined immunodeficiency conditions including neutropenia or HIV

CC infection. The anti-CD40 antibodies may also be useful for detecting CD40

CC in a biological sample in vitro or in vivo, as well as during gene

CC therapy procedures. The current sequence is that of the human anti-CD40

CC antibody variable region light chain protein of the invention.

XX

XX Sequence 239 AA;

XX

Alignment Scores:

Pred. No.: 2.33e-47 Length: 239

Score: 522.00 Matches: 100

Percent Similarity: 93.10% Conservative: 8

Best Local Similarity: 86.21% Mismatches: 8

Query Match: 84.33% Indels: 0

DB: 7 Gaps: 0

US-09-674-716B-17 (1-348) x ADE28461 (1-239)



OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Misc-difference 155 /note= "possible Ala"  
 FT  
 XX JF2000080100-A.  
 XX  
 XX 21-MAR-2000.  
 XX  
 XX 12-OCT-1998; 98JP-00304793.  
 XX  
 XX 17-JUN-1998; 98JP-00188196.  
 PR  
 XX 26-JUN-1998; 98JP-00196729.  
 XX  
 XX (NLSB ) JAPAN TOBACCO INC.  
 PA  
 XX WPI; 2000-286723/25.  
 XX  
 DR N-PSDB; AAA13925.  
 XX  
 XX A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain.  
 XX  
 XX Claim 31; Page 45-46; 89pp; Japanese.  
 XX  
 XX The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment of  
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a human  
 CC PTHrP monoclonal antibody clone protein sequence from the present  
 CC invention  
 XX  
 XX Sequence 239 AA;  
 Alignment Scores:  
 Pred. No.: 4,9e-47 Length: 239  
 Score: 519.00 Matches: 99  
 Percent Similarity: 92.24% Conservative: 8  
 Best Local Similarity: 85.34% Mismatches: 9  
 Query Match: 83.84% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-674-716B-17 (1-348) x AAY82615 (1-239)  
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCCGCGCTCC 60  
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40  
 QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCCGTATAGGTGGGAGACATCTTGAATTGG 120  
 Db 41 IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyAsnThrLeuAspTyr 60  
 QY 121 TACCTCAGAACCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCCACCGCGGCA 180  
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgAla 80  
 QY 181 TCAGGGGTCCTCCACAGGTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC 240  
 Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 100  
 QY 241 AGCAGAGTGGAGCTGAGGATGTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300  
 Db 101 SerArgValGluAlaGluAspValGlyIleTyrTyrCysMetGlnAlaLeuGlnThrPro 120  
 QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAACACGTACGGTGGCT 348

Db 121 PheThrPheGlyProGlyThrLysValAspIleLysArgThrValAla 136  
 RESULT 5  
 ADE28405  
 ID ADE28405 standard; protein; 239 AA.  
 XX  
 XX ADE28405;  
 XX  
 XX 29-JAN-2004 (first entry)  
 DT  
 XX Human anti-CD40 antibody 7-1-2 variable region light chain protein.  
 DE  
 XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
 KW human; variable region light chain; 7-1-2.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2003040170-A2.  
 PN  
 XX 15-MAY-2003.  
 PD  
 XX 08-NOV-2002; 2002WO-US036107.  
 PF  
 XX 09-NOV-2001; 2001US-0348980P.  
 PR  
 XX (PRTZ ) PRTZER PROD INC.  
 PA (ABGE-) ABGENIX INC.  
 XX  
 XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
 PI WPI; 2003-441521/41.  
 XX N-PSDB; ADE28404.  
 DR  
 XX New chimeric or human monoclonal antibody or its antigen-binding portion  
 PT that specifically binds to and activates human CD40, useful for enhancing  
 PT an immune response in a human, or treating cancer, HIV, neutropenia or  
 PT viral infections.  
 XX  
 XX Claim 1; SEQ ID NO 12; 177pp; English.  
 PS  
 XX The invention relates to a novel chimeric or human monoclonal antibody or  
 CC its antigen-binding portion that specifically binds to and activates  
 CC human CD40. The anti-CD40 antibody of the invention demonstrates  
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
 CC activities and may be useful for treating a hyperproliferative disorder  
 CC such as cancer, viral and bacterial infection or genetic, primary or  
 CC combined immunodeficiency conditions including neutropenia or HIV  
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
 CC in a biological sample in vitro or in vivo, as well as during gene  
 CC therapy procedures. The current sequence is that of the human anti-CD40  
 CC antibody variable region light chain protein of the invention.  
 XX  
 XX Sequence 239 AA;  
 Alignment Scores:  
 Pred. No.: 4,9e-47 Length: 239  
 Score: 519.00 Matches: 101  
 Percent Similarity: 92.24% Conservative: 6  
 Best Local Similarity: 87.07% Mismatches: 9  
 Query Match: 83.84% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-674-716B-17 (1-348) x ADE28405 (1-239)  
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCCGCGCTCC 60  
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40  
 QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCCGTATAGGTGGGAGACATCTTGAATTGG 120

Db 41 IleSerCysArgSerSerGlnSerLeuLeuTyrSerAsnGlyTyrAsnPheLeuAspTyr 60  
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCCGGCA 180  
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 80  
QY 181 TCAGGGGTCCTGCAGCTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 100  
QY 241 AGCAGAGTGGAGCTGAGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGATCCCA 300  
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 120  
QY 301 TTCAGTTTCGGCCAGGACCAAGTGGAGATCAAACTACGGTGGCT 348  
Db 121 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 136

RESULT 6  
ABBS5756  
ID ABB57576 standard; peptide; 114 AA.  
XX AC ABB57576;  
XX DT 18-MAR-2002 (first entry)  
XX DE HLA-DR-specific protein MS-GPIC16 VL sequence.  
XX KW Immunomodulatory human MHC class II antigen-binding protein; HLA;  
KW human leukocyte antigen; immune system; immunosuppression; antibody;  
KW major histocompatibility complex; antirheumatic; antiarthritic;  
KW neuroprotective; antinflammatory; antidiabetic; antipsoriatic;  
KW immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;  
KW thymimetic; hepatotropic; immune response suppressor; narcolepsy;  
KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;  
KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;  
KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;  
KW transplant rejection; graft versus host disease; pemphigus vulgaris;  
KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;  
KW irritable bowel disease; Sjogren's syndrome.

XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WC200187338-A1.  
XX PD 22-NOV-2001.  
XX PF 14-MAY-2001; 2001WO-US015626.  
XX PR 12-MAY-2000; 2000EP-00110063.  
XX PR 06-OCT-2000; 2000US-0238762P.  
XX PA (GPCB-) GPC BIOTECH AG.  
XX PA (MORP-) MORPHOSYS AG.  
XX PI Nagy Z, Tessa M, Thomassen-Wolf E;  
XX WPI; 2002-075289/10.  
XX PT Composition for suppressing immune response, treating diseases of immune  
XX system, has polypeptide comprising antibody-based antigen-binding domain  
XX of human composition, which binds antigen expressed on a cell surface.  
XX PS Example; Fig 15; 139pp; English.  
XX CC The present invention describes a composition (I), comprising a  
XX polypeptide comprising an antibody-based antigen-binding domain of human  
XX composition with binding specificity for an antigen expressed on the  
XX surface of a cell, where treating cells expressing the antigen with the  
XX polypeptides leads to suppression of an immune response, and the IC50 for  
XX the suppression of immune response is 1 microM or less. (I) has  
XX antirheumatic, antiarthritic, neuroprotective, antinflammatory,

CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,  
CC antithyroid, nephrotropic, thymimetic and hepatotropic activities, and  
CC can be used as a suppressor of immune response. (I) is useful for  
CC suppressing activation or proliferation of a cell of the immune system,  
CC suppressing IL-2 secretion by a cell, the interaction of a cell of the  
CC immune system with another cell, immunosuppressing a patient and for  
CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on  
CC the surface of the cell, where neither cytotoxic entities nor  
CC immunological mechanisms are needed to cause or lead to the killing. (I)  
CC (optionally linked to cytotoxic or immunogenic agent) is useful for  
CC preparing a pharmaceutical preparation for the treatment of rheumatoid  
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,  
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus  
CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus  
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,  
CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary  
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.  
CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in  
CC the exemplification of the present invention

XX SQ Sequence 114 AA;

Alignment Scores:  
Pred. No.: 5,61e-47 Length: 114  
Score: 518.00 Matches: 101  
Percent Similarity: 92.11% Conservative: 4  
Best Local Similarity: 88.60% Mismatches: 9  
Query Match: 83.68% Indels: 0  
DB: Gaps: 0

US-09-674-716B-17 (1-348) x ABB57576 (1-114)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCTCCGCTACCCCTCGAGAGCGGCTCC 60  
Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20  
QY 61 ATCTCTCTGCTCGCTAGTAAAGTCTCTCTATATAGGATGGGAGACATCTTGAATTGG 120  
Db 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTyr 40  
QY 121 TACTGTCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCCGGCA 180  
Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 60  
QY 181 TCAGGGGTCCTGCAGCTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 80  
QY 241 AGCAGAGTGGAGCTGAGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGATCCCA 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysGlnGlnTyrAsnSerTyrPro 100  
QY 301 TTCAGTTTCGGCCAGGACCAAGTGGAGATCAAACTACGGTGGCT 342  
Db 101 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThr 114

RESULT 7  
ADE28465  
ID ADE28465 standard; protein; 239 AA.  
XX AC ADE28465;  
XX DT 29-JAN-2004 (first entry)  
XX DE Human anti-CD40 antibody 23-28-1 full length light chain protein.  
XX KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; light chain; 23-28-1.  
XX OS Homo sapiens.

PN WO2003040170-A2.  
 XX  
 PD  
 XX 15-MAY-2003.  
 XX  
 PF 08-NOV-2002; 2002WO-US036107.  
 XX  
 XX 09-NOV-2001; 2001US-0348980P.  
 XX  
 XX (PIZ ) PRIZER PROD INC.  
 PA (ABGE-) ABGENIX INC.  
 XX  
 XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
 XX WPI; 2003-441521/41.  
 XX N-PSDB; ADE28464.  
 XX  
 PT New chimeric or human monoclonal antibody or its antigen-binding portion  
 PT that specifically binds to and activates human CD40, useful for enhancing  
 PT an immune response in a human, or treating cancer, HIV, neutropenia or  
 PT viral infections.  
 XX  
 XX Claim 7; SEQ ID NO 72; 177bp; English.  
 XX  
 CC The invention relates to a novel chimeric or human monoclonal antibody or  
 CC its antigen-binding portion that specifically binds to and activates  
 CC human CD40. The anti-CD40 antibody of the invention demonstrates  
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
 CC activities and may be useful for treating a hyperproliferative disorder  
 CC such as cancer, viral and bacterial infection or genetic, primary or  
 CC combined immunodeficiency conditions including neutropenia or HIV  
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
 CC in a biological sample in vitro or in vivo, as well as during gene  
 CC therapy procedures. The current sequence is that of the human anti-CD40  
 CC antibody full length light chain protein of the invention.  
 XX  
 SQ Sequence 239 AA;  
 Alignment Scores:  
 Pred. No.: 6,28e-47 Length: 239  
 Score: 518.00 Matches: 101  
 Percent Similarity: 91.38% Conservative: 5  
 Best Local Similarity: 87.07% Mismatches: 10  
 Query Match: 83.68% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-674-716B-17 (1-348) x ADE28465 (1-239)  
 QY 1 GATATTGTGATGACTCAGTCTCTCACTCTCCCTGCCCGTCACCCCTGGAGAGCGCGCTCC 60  
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40  
 QY 61 ATCTCTGTCTGCTCAGTGAAGAGTCTCTGTTAGGATGGAGACATCTTGAATGG 120  
 Db 41 IleSerCysArgSerSerGlnSerLeuLeuTyrSerAsnGlyTyrAsnTyrLeuAspTrp 60  
 QY 121 TACCTGCAGAACGCGGCGAGTCTCACAGCTCTGATCTATTGATGTCCACCGCGGCA 180  
 Db 61 TyrLeuGlnLysProGlyGlnSerProHisLeuLeuLeuTyrLeuGlySerAsnArgAla 80  
 QY 181 TGAGGGTCCCTCAGAGTTCAGTGGCAGTGGATCAGGCACAGATTTACCTGAAATC 240  
 Db 81 SerGlyValProAspArgPheSerGlySerGlyTyrAspPheThrLeuLysIle 100  
 QY 241 AGCAGATGGAGCTGAGCATGTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 Db 101 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnAlaLeuGlnThrPro 120  
 QY 301 TTCAGTTCGGCCAGGGACCGAGTGGAGATCAACGTCACGTGGCT 348  
 Db 121 ArgThrPheGlyGlnGlyThrLysValGluIleLysArgThrValAla 136  
 RESULT 8  
 AAY32261

ID AAY32261 standard; protein; 145 AA.  
 XX  
 AC AAY32261;  
 XX  
 DT 15-FEB-2000 (first entry)  
 XX  
 DE Mouse anti-CD23 MAb C11 light chain variable region.  
 XX  
 XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 55..70  
 FT /note= "CDR L1"  
 FT Region 83..92  
 FT /note= "CDR L2"  
 FT Region 125..134  
 FT /note= "CDR L3"  
 XX  
 PN WO9958679-A1.  
 XX 18-NOV-1999.  
 PD  
 XX 07-MAY-1999; 99WO-GB001434.  
 PF  
 XX 09-MAY-1998; 98GB-00009839.  
 PR  
 XX (GLAX ) GLAXO GROUP LTD.  
 PA  
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 FI  
 XX WPI: 2000-053101/04.  
 XX N-PSDB; AAZ34746.  
 DR  
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.  
 XX  
 PS Claim 8; Fig 2; 81pp; English.  
 CC This sequence represents the light chain variable region (VL) of murine  
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides  
 CC altered antibodies, such as chimeric or humanised antibodies (see  
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions (see AAY32254-59) to render them capable of binding to the CD23  
 CC type II molecule expressed on haematopoietic cells. The antibodies are  
 CC used to block soluble CD23 formation in human therapy for the treatment  
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents  
 XX  
 SQ Sequence 145 AA;  
 Alignment Scores:  
 Pred. No.: 9,55e-47 Length: 145  
 Score: 516.00 Matches: 99  
 Percent Similarity: 92.98% Conservative: 7



CC	cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC	activities and may be useful for treating a hyperproliferative disorder
CC	such as cancer, viral and bacterial infection or genetic, primary or
CC	combined immunodeficiency conditions including neutropenia or HIV
CC	infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC	in a biological sample in vitro or in vivo, as well as during gene
CC	therapy procedures. The current sequence is that of the human anti-CD40
CC	antibody variable region light chain protein of the invention.
XX	
SQ	Sequence 239 AA;
Alignment Scores:	
Pred. No.:	2,17e-46
Score:	513.00
Percent Similarity:	92.24%
Best Local Similarity:	85.34%
Query Match:	82.88%
DB:	7
US-09-674-716B-17 (1-348) x ADE28397 (1-239)	
QY	1 GATATTGTGATGACTCAGTCTCCACCTCTCCCTGCCCTGACCCCTGAGAGCCGGCTCC 60
DB	21 AspIleValLeuThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
QY	61 ATCTCTGTCGCTCGAGTAAGATCTCTCTATTAAGATGCGAAGACATCTTGAATTGG 120
DB	41 IleSerCysArgSerGlnSerLeuLeuTySerAsnGlyTyrAsnPheLeuAspTrp 60
QY	121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGCCA 180
DB	61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLysLeuGlySerAsnArgAla 80
QY	181 TCAGGGTCCCTGCACAGTTTCAGTGGCAGTGGATGAGGCACAGATTTTACCTGAAAATC 240
DB	81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
QY	241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGTAGTATCCA 300
DB	101 SerArgLeuGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 120
QY	301 TTCACTGTCGGCCCAAGGACCAAGGTGGAGATCAAAAGCTACGGTGGCT 348
DB	121 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 136
RESULT 10	
ADE28421	
ID	ADE28421 standard; protein; 239 AA.
XX	
AC	ADE28421;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Human anti-CD40 antibody 15-1-1 variable region light chain protein.
XX	
KW	anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW	immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW	bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW	human; variable region light chain; 15-1-1.
OS	Homo sapiens.
XX	
PN	WO2003040170-A2.
XX	
PD	15-MAY-2003.
XX	
PF	08-NOV-2002; 2002WO-US036107.
XX	
PR	09-NOV-2001; 2001US-0348980P.
XX	
PA	(PFIZ ) PFIZER PROD INC.
PA	(ABGE-) ABGENIX INC.
XX	
PI	Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX	
DR	WPI; 2003-441521/41.
DR	N-PSDB; ADE28396.
XX	
PT	New chimeric or human monoclonal antibody or its antigen-binding portion
PT	that specifically binds to and activates human CD40, useful for enhancing
PT	an immune response in a human, or treating cancer, HIV, neutropenia or
PT	viral infections.
XX	
PS	Claim 1; SEQ ID NO 4; 177pp; English.
XX	
CC	The invention relates to a novel chimeric or human monoclonal antibody or
CC	its antigen-binding portion that specifically binds to and activates
CC	human CD40. The anti-CD40 antibody of the invention demonstrates

Best Local Similarity:	86.84%	Mismatches:	8
Query Match:	83.36%	Indels:	0
DB:	3	Gaps:	0
US-09-674-716B-17 (1-348) x AAY32261 (1-145)			
QY	1	GATATTGTGATGACTCAGTCTCCCTGCGCGTCA	60
DB	32	AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer	51
QY	61	ATCTCTGTCGCTCGAGTAAGATCTCTGTATAGGATGGAAGACATCTTGAATTGG	120
DB	52	IleSerCysArgSerSerLysSerLeuLeuTyLysAspGlyLysThrTyrLeuAsnTrp	71
QY	121	TACTGCGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTTCATGTCCACCCGGCCA	180
DB	72	PheLeuGlnArgProGlyGlnSerProGlnLeuLeuMetTyrLeuMetSerThrArgAla	91
QY	181	TCAGGGTCCCTGCACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC	240
DB	92	SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile	111
QY	241	AGCAGAGTGGAGCTGAGGATCTTGGGTTTATTACTGTCAACAGCTGTAGATATCCA	300
DB	112	SerArgValLysAlaGluAspValGlyValTyrCysGlnGlnLeuValGluTyrPro	131
QY	301	TTCACGTTCCGGCCCAAGGACCAAGGTGGAGATCAAAAGCTACG	342
DB	132	PheThrPheGlySerGlyThrLysLeuGluileLysArgThr	145
RESULT 9			
ADE28397			
ID	ADE28397 standard; protein; 239 AA.		
AC	ADE28397;		
XX	29-JAN-2004 (first entry)		
XX	Human anti-CD40 antibody 3-1-1 variable region light chain protein.		
DE	anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;		
KW	immunostimulant; anti-HIV; hyperproliferative; cancer; viral;		
KW	bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;		
KW	human; variable region light chain; 3-1-1.		
OS	Homo sapiens.		
XX	WO2003040170-A2.		
XX	15-MAY-2003.		
PD	08-NOV-2002; 2002WO-US036107.		
PF	09-NOV-2001; 2001US-0348980P.		
XX	(PFIZ ) PFIZER PROD INC.		
XX	(ABGE-) ABGENIX INC.		
PA	Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;		
XX	WPI; 2003-441521/41.		
XX	N-PSDB; ADE28396.		
DR	New chimeric or human monoclonal antibody or its antigen-binding portion		
PT	that specifically binds to and activates human CD40, useful for enhancing		
PT	an immune response in a human, or treating cancer, HIV, neutropenia or		
PT	viral infections.		
XX	Claim 1; SEQ ID NO 4; 177pp; English.		
PS	The invention relates to a novel chimeric or human monoclonal antibody or		
XX	its antigen-binding portion that specifically binds to and activates		
CC	human CD40. The anti-CD40 antibody of the invention demonstrates		

PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
 XX WPI: 2003-441521/41.  
 DR N-PSDB; ADE28420.  
 XX  
 PT New chimeric or human monoclonal antibody or its antigen-binding portion  
 PT that specifically binds to and activates human CD40, useful for enhancing  
 PT an immune response in a human, or treating cancer, HIV, neutropenia or  
 PT viral infections.  
 XX  
 XX Claim 1; SEQ ID NO 28; 177pp; English.  
 PS  
 CC The invention relates to a novel chimeric or human monoclonal antibody or  
 CC its antigen-binding portion that specifically binds to and activates  
 CC human CD40. The anti-CD40 antibody of the invention demonstrates  
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
 CC activities and may be useful for treating a hyperproliferative disorder  
 CC such as cancer, viral and bacterial infection or genetic, primary or  
 CC combined immunodeficiency conditions including neutropenia or HIV  
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
 CC in a biological sample in vitro or in vivo, as well as during gene  
 CC therapy procedures. The current sequence is that of the human anti-CD40  
 CC antibody variable region light chain protein of the invention.  
 XX  
 XX Sequence 239 AA;

Alignment Scores:  
 Pred. No.: 2,78e-46 Length: 239  
 Score: 512.00 Matches: 98  
 Percent Similarity: 92.24% Conservative: 9  
 Best Local Similarity: 84.48% Mismatches: 9  
 Query Match: 82.71% Indels: 0  
 DB: 7 Gaps: 0

US-09-674-716B-17 (1-348) x ADE28421 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCTCC 60  
 Db |||||ValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProlaser 40  
 QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTGTATTAAGATGGGAAGACATCTGAATTGG 120  
 Db |||||ValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProlaser 40  
 QY 41 IleSerCysArgSerGlnSerLeuLeuHisThrAsnGlyTyrAsnTyrPheAspTrp 60  
 QY 121 TACCTCAGAGCCAGGCGAGTCTCCACAGCTCCCTGATCTATTGATGTCACCCGGGCA 180  
 Db |||||ValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProlaser 40  
 QY 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu 80  
 QY 181 TCAGGGGTCCCTGACAGGTTCAAGTTCCTGTATTAAGATGGGAAGACATCTGAATTGG 240  
 Db |||||ValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProlaser 40  
 QY 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 241 AGCAGAGTGGAGCTCAGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 Db |||||ValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProlaser 40  
 QY 101 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnAlaLeuGlnThrPro 120  
 QY 301 TTCACGTTCCGGCCCAAGGACCAAGTGGAGATCAAAACGTACCGTGGCT 348  
 Db |||||ValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProlaser 40  
 QY 121 TyrSerPheGlyGlnGlyThrLysLeuGluLeuLysArgThrValAla 136

RESULT 11  
 ID AAY82611  
 AC AAY82611; standard; protein; 239 AA.  
 XX  
 XX AAY82611; (first entry)  
 DT 02-AUG-2000  
 XX Human PTHrP monoclonal antibody clone 16B12-6 protein SEQ ID NO:6.  
 DE Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;

KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
 KW antiarthritic; cytostatic; antiinflammatory.  
 OS Homo sapiens.  
 XX JP2000080100-A.  
 XX 21-MAR-2000.  
 XX 12-OCT-1998; 98JP-00304793.  
 XX 17-JUN-1998; 98JP-00188196.  
 XX 26-JUN-1998; 98JP-00196729.  
 XX (NISR) JAPAN TOBACCO INC.  
 DR WPI: 2000-286723/25.  
 XX N-PSDB; AAI13921.  
 PT A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain.  
 XX  
 PS Claim 31; Page 34-35; 88pp; Japanese.

The present invention describes a human monoclonal antibody to  
 parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 its fragments, following the stimulation of PTHrP has the following  
 properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 the release of calcium from bone; or (c) inhibits elevation of blood  
 calcium content. The monoclonal antibody can be used in the treatment of  
 hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 antiinflammatory activities. The present sequence represents a human  
 PTHrP monoclonal antibody clone protein sequence from the present  
 invention

Sequence 239 AA;

Alignment Scores:  
 Pred. No.: 3,56e-46 Length: 239  
 Score: 511.00 Matches: 96  
 Percent Similarity: 93.10% Conservative: 12  
 Best Local Similarity: 82.76% Mismatches: 8  
 Query Match: 82.55% Indels: 0  
 DB: 3 Gaps: 0

US-09-674-716B-17 (1-348) x AAY82611 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCTCC 60  
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProlaser 40  
 QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTGTATTAAGATGGGAAGACATCTGAATTGG 120  
 Db 41 IleSerCysArgSerGlnSerLeuLeuHisThrAsnGlyTyrAsnTyrPheAspTrp 60  
 QY 121 TACCTCAGAGCCAGGCGAGTCTCCACAGCTCCCTGATCTATTGATGTCACCCGGGCA 180  
 Db 61 PheLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu 80  
 QY 181 TCAGGGGTCCCTGACAGGTTCAAGTTCCTGTATTAAGATGGGAAGACATCTGAATTGG 240  
 Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 241 AGCAGAGTGGAGCTCAGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 Db 101 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnAlaLeuGlnThrPro 120  
 QY 301 TTCACGTTCCGGCCCAAGGACCAAGTGGAGATCAAAACGTACCGTGGCT 348

```

Db      121 PheThrPheGlyProGlyThrLysValAspLeuLysArgThrValAla 136
RESULT 12
ADE28469
ID      ADE28469 standard; protein; 239 AA.
XX
AC      ADE28469;
XX
DT      29-JAN-2004 (first entry)
XX
DE      Human anti-CD40 antibody 23-29-1 variable region light chain protein.
XX
DE      anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
XX      immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
XX      bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
XX      human; variable region light chain; 23-29-1.
XX
OS      Homo sapiens.
XX
XX      WO2003040170-A2.
XX
XX      15-MAY-2003.
XX
XX      08-NOV-2002; 2002WO-US036107.
XX
XX      09-NOV-2001; 2001US-0348980P.
XX
XX      (PFIZ ) PFIZER PROD INC.
XX
XX      (ABGE-) ABGENIX INC.
XX
XX      Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
XX      WPI: 2003-441521/41.
XX      N-PSDB; ADE28468.
XX
XX      New chimeric or human monoclonal antibody or its antigen-binding portion
XX      that specifically binds to and activates human CD40, useful for enhancing
XX      an immune response in a human, or treating cancer, HIV, neutropenia or
XX      viral infections.
XX
XX      Claim 1; SEQ ID NO 76; 177pp; English.
XX
XX      The invention relates to a novel chimeric or human monoclonal antibody or
XX      its antigen-binding portion that specifically binds to and activates
XX      human CD40. The anti-CD40 antibody of the invention demonstrates
XX      cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
XX      activities and may be useful for treating a hyperproliferative disorder
XX      such as cancer, viral and bacterial infection or genetic, primary or
XX      combined immunodeficiency conditions including neutropenia or HIV
XX      infection. The anti-CD40 antibodies may also be useful for detecting CD40
XX      in a biological sample in vitro or in vivo, as well as during gene
XX      therapy procedures. The current sequence is that of the human anti-CD40
XX      antibody variable region light chain protein of the invention.
XX
XX      Sequence 239 AA;

Alignment Scores:
Pred. No.:      3,56e-46      Length:      239
Score:          511.00      Matches:    101
Percent Similarity: 91.38%      Conservative: 5
Best Local Similarity: 87.07%      Mismatches: 10
Query Match:    82.55%      Indels:    0
DB:             7      Gaps:      0

US-09-674-716B-17 (1-348) x ADE28469 (1-239)

QY      1 GATATTGTGATGACTCAGTCTCCCTGCGCGTCACCCCTGGAGAGCGGCGCTCC 60
Db      21 AspIleVal.MethrGlnSerProLeuSerLeuProValThrProGlyGluProlaser 40
QY      61 ATCTCTGTCGTCGAGTGAAGTCTCTCTGATATAAGGATGGGAAGACATCTGTAATTCG 120
Db      41 IleSerCysArgSerGlnSerLeuLeuProGlyAsnGlyTyrAsnTyrLeuAspTrp 60

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QY      121 TACTCAGAACGCCAGGCGAGTCTCCACAGTCTCCTGATCTATTGTGATGTCACCCCGGCA 180
Db      61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 80
QY      181 TCAGGGGTCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Db      81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY      241 AGCAGAGTGAGGCTCAGGATGTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db      101 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnAlaLeuGlnThrPro 120
QY      301 TTCAGTTGGCCCAAGGACCGAGGTGGAGATCAACAGTACGGTGGCT 348
Db      121 ArgThrPheGlyGlnGlyThrLysValGluIleLysArgThrValAla 136

RESULT 13
AAB72235
ID      AAB72235 standard; protein; 238 AA.
XX
AC      AAB72235;
XX
DT      10-MAY-2001 (first entry)
XX
DE      Humanised 323/A3 (IgG2cys) antibody kappa light chain amino acid.
XX
XX      Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
XX      chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
XX      light chain.
XX
XX      Mus sp.
XX      Homo sapiens.
XX
XX      WO200107082-A1.
XX
XX      01-FEB-2001.
XX
XX      23-JUL-1999; 99WO-EP005271.
XX
XX      23-JUL-1999; 99WO-EP005271.
XX
XX      (GLAX ) GLAXO GROUP LTD.
XX
XX      Knick VC, Stimmel JB, Thurmond LM;
XX
XX      WPI; 2001-182729/18.
XX
XX      Combination for treating cancer (e.g. breast, gastric or prostate
XX      cancers), or in the manufacture of a medicament for anti-cancer therapy,
XX      comprises an anti-Ep-cyclic adenosine monophosphate antibody with a
XX      chemotherapeutic agent.
XX
XX      Example 8; Fig 13; 103pp; English.
XX
XX      This invention relates to a combination of an anti-Ep-CAM (cyclic
XX      adenosine monophosphate) antibody with a chemotherapeutic agent, that is
XX      capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
XX      phase or the second growth phase (M) of cell enlargement (G2)/DNA
XX      replication. The antibody exhibits cytostatic activity and is useful in
XX      the manufacture of a medicament for use in anti-cancer therapy.
XX      characterised in that a chemotherapeutic agent, which is capable of
XX      arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-
XX      administered to a patient with an anti-Ep-CAM antibody. The combination
XX      is useful for treating cancer, particularly colorectal cancer, breast
XX      cancer, gastric cancer, prostate cancer or non-small-cell lung cancer.
XX      The present sequence represents the kappa light chain of anti-Ep-CAM
XX      antibody known as humanised 323/A3 (IgG2cys) which can be used in the
XX      combination of the invention
XX
XX      Sequence 238 AA;
Alignment Scores:

```



XX (GLAXO) GLAXO GROUP LTD.  
XX PA  
XX PI Knick VC, Stimmel JB, Thurmond LM;  
XX DR  
XX DR WPI; 2001-182729/18.  
XX DR N-PSDB; AAF63373.  
XX PT  
XX PT Combination for treating cancer (e.g. breast, gastric or prostate  
XX PT cancers), or in the manufacture of a medicament for anti-cancer therapy,  
XX PT comprises an anti-Ep-cyclic adenosine monophosphate antibody with a  
XX PT chemotherapeutic agent.  
XX PS  
XX PS Disclosure; Fig 15; 103pp; English.  
XX CC  
XX CC This invention relates to a combination of an anti-Ep-CAM (cyclic  
XX CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is  
XX CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)  
XX CC phase or the second growth phase (M) of cell enlargement (G2)/DNA  
XX CC replication. The antibody exhibits cytostatic activity and is useful in  
XX CC the manufacture of a medicament for use in anti-cancer therapy,  
XX CC characterised in that a chemotherapeutic agent, which is capable of  
XX CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-  
XX CC administered to a patient with an anti-Ep-CAM antibody. The combination  
XX CC is useful for treating cancer, particularly colorectal cancer, breast  
XX CC cancer, gastric cancer, prostate cancer or non-small-cell lung cancer.  
XX CC The present sequence represents the light chain of anti-Ep-CAM antibody  
XX CC known as humanised 323/A3 (IgG1) which can be used in the combination of  
XX CC the invention  
XX SQ Sequence 238 AA;

Alignment Scores:  
Pred. No.: 4,566-46 Length: 238  
Score: 510.00 Matches: 101  
Percent Similarity: 90.52% Conservative: 4  
Best Local Similarity: 87.07% Mismatches: 11  
Query Match: 82.39% Indels: 0  
DB: 4 Gaps: 0

US-09-674-716B-17 (1-348) x AAB72227 (1-238)

QY 1 GATATTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGGCTCC 60  
Db 20 AsplleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 39  
QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAGACATCTTGAATTGG 120  
Db 40 IleSerCysArgSerSerIysAsnLeuLeuHisSerAsnGlyIleThrTyrLeuTyrTrp 59  
QY 121 TACCTGCAGACGAGCGAGCTCCACAGCTCCTGATCTATTGATGCTCCACCGGSCA 180  
Db 60 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrGlnMetSerAsnLeuAla 79  
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGCAGTGATCAGGCACAGATTTACACTGAAATC 240  
Db 80 SerGlyValProAspArgPheSerSerSerGlySerGlyThrAspPheThrLeuLysIle 99  
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300  
Db 100 SerArgValGluAlaGluAspValGlyValTyrTyrCysAlaGlnAsnLeuGluIlePro 119  
QY 301 TTCACGTTCCGCCAGGACCAAGGTGGAGATCAACAGTACGGTGGCT 348  
Db 120 ArgThrPheGlyGlnGlyThrLysValGluIleLysArgThrValAla 135

Search completed: September 30, 2004, 08:40:57  
Job time : 45.458 secs

Blank sheet

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:54:09 ; Search time 45.645 Seconds  
(without alignments)

4906.833 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 619

Sequence: 1 gatattgtgactcagtc.....agatcaaacgtacgttggt 348

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Xgapop 10.0 , Xgapext 0.5

Xgapop 6.0 , Xgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 2702124

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0  
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Database : Published Applications AA:\*

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8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
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16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
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1	522	84.3	239	12	US-10-292-088-40	Sequence 40, Appl
2	519	83.8	239	12	US-10-292-088-16	Sequence 16, Appl
3	518	83.7	114	15	US-10-275-046-83	Sequence 83, Appl
4	518	83.7	239	12	US-10-292-088-56	Sequence 56, Appl
5	516	83.4	238	16	US-10-663-244-149	Sequence 149, App
6	513	82.9	238	16	US-10-663-244-145	Sequence 145, App
7	513	82.9	239	12	US-10-292-088-8	Sequence 8, Appl
8	512	82.7	239	12	US-10-292-088-32	Sequence 32, Appl
9	511	82.6	239	12	US-10-292-088-64	Sequence 64, Appl
10	510	82.4	239	12	US-10-292-088-80	Sequence 80, Appl
11	510	82.4	239	12	US-10-292-088-102	Sequence 102, App
12	510	82.4	239	12	US-10-404-724-12	Sequence 12, Appl
13	505	81.6	113	15	US-10-453-698-177	Sequence 177, App
14	505	81.6	113	15	US-10-308-817-177	Sequence 177, App
15	505	81.6	238	16	US-10-663-244-148	Sequence 148, App
16	504	81.4	112	12	US-10-292-088-36	Sequence 36, Appl
17	504	81.4	112	12	US-10-292-088-103	Sequence 103, App
18	504	81.4	112	12	US-10-292-088-111	Sequence 111, App
19	504	81.4	113	15	US-10-364-743-60	Sequence 60, Appl
20	504	81.4	238	16	US-10-663-244-144	Sequence 144, App
21	503	81.3	112	12	US-10-292-088-104	Sequence 104, App
22	502	81.1	113	14	US-10-125-687-9	Sequence 9, Appl
23	501	80.9	112	12	US-10-292-088-12	Sequence 12, Appl
24	501	80.9	112	12	US-10-292-088-94	Sequence 94, Appl
25	501	80.9	127	16	US-10-380-082-4	Sequence 4, Appl
26	501	80.9	239	10	US-09-992-600A-8	Sequence 8, Appl
27	501	80.9	239	10	US-09-924-340-8	Sequence 8, Appl
28	501	80.9	239	10	US-09-992-095B-8	Sequence 8, Appl
29	501	80.9	239	10	US-09-993-570-8	Sequence 8, Appl
30	501	80.9	239	14	US-10-000-489-8	Sequence 8, Appl
31	501	80.9	239	14	US-10-000-986-8	Sequence 8, Appl
32	501	80.9	239	14	US-10-154-678-8	Sequence 8, Appl
33	500	80.8	112	12	US-10-292-088-52	Sequence 52, Appl
34	500	80.8	112	12	US-10-292-088-112	Sequence 112, App
35	500	80.8	125	14	US-10-010-942B-6	Sequence 6, Appl
36	500	80.8	125	16	US-10-388-389-6	Sequence 6, Appl
37	500	80.8	125	16	US-10-703-713-6	Sequence 6, Appl
38	500	80.8	125	16	US-10-704-070-6	Sequence 6, Appl
39	500	80.8	247	12	US-10-466-164-69	Sequence 69, Appl
40	499.5	80.7	237	16	US-10-663-244-146	Sequence 146, App
41	499.5	80.7	237	16	US-10-663-244-153	Sequence 153, App
42	499	80.6	113	12	US-10-371-942-16	Sequence 16, Appl
43	499	80.6	219	12	US-10-226-435A-11	Sequence 11, Appl
44	499	80.6	238	16	US-10-663-244-147	Sequence 147, App
45	498	80.5	112	16	US-10-663-244-75	Sequence 75, Appl

#### ALIGNMENTS

RESULT 1  
US-10-292-088-40  
; Sequence 40, Application US/10292088  
; Publication NO. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-Pf/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-088-40

Alignment Scores:  
 Pred. No.: 3,83e-45 Length: 239  
 Score: 522.00 Matches: 100  
 Percent Similarity: 93.10% Conservative: 8  
 Best Local Similarity: 86.21% Mismatches: 8  
 Query Match: 84.33% Indels: 0  
 DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-292-088-40 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGCGCTCC 60  
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40  
 QY 61 ATCTCTGTGCTCGAGTAAAGTCTCCTGTATAAGAGTGGGAACACATCTTGAATTGG 120  
 Db 41 IleSerCysArgSerGlnSerValLeuTyrSerAsnGlyTyrAsnTyrLeuAspTrp 60  
 QY 121 TACCTGCAGAACCGAGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCGCGCA 180  
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgAla 80  
 QY 181 TCAGGGTCCCTCAGAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnValLeuGlnThrPro 120  
 QY 301 TTCACGTTGGCCAGGACCAAGGTGGAGATCAACGTACGTTGGCT 348  
 Db 121 PheThrPheGlyProGlyThrLysValAspIleLysArgThrValAla 136

## RESULT 2

US-10-292-088-16  
 ; Sequence 16, Application US/10292088  
 ; Publication No. US2003021100A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BEDIAN, VAHE  
 ; APPLICANT: GLADUE, RONALD P.  
 ; APPLICANT: CORVALAN, JOSE  
 ; APPLICANT: JIA, XIAO-CHI  
 ; APPLICANT: FENG, XIAO  
 ; TITLE OF INVENTION: ANTIBODIES TO CD40  
 ; FILE REFERENCE: ABX-PF/3 US  
 ; CURRENT APPLICATION NUMBER: US/10/292,088  
 ; CURRENT FILING DATE: 2003-03-14  
 ; PRIOR APPLICATION NUMBER: 60/348,980  
 ; PRIOR FILING DATE: 2001-11-09  
 ; NUMBER OF SEQ ID NOS: 147  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 16  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; ORGANISM: Homo sapiens  
 ; LENGTH: 239  
 ; US-10-292-088-16

Alignment Scores:  
 Pred. No.: 7.81e-45 Length: 239  
 Score: 519.00 Matches: 101  
 Percent Similarity: 92.24% Conservative: 6  
 Best Local Similarity: 87.07% Mismatches: 9  
 Query Match: 83.84% Indels: 0  
 DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-292-088-16 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGCGCTCC 60  
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40  
 QY 61 ATCTCTGTGCTCGAGTAAAGTCTCCTGTATAAGAGTGGGAACACATCTTGAATTGG 120

Db 41 IleSerCysArgSerGlnSerLeuTyrSerAsnGlyTyrAsnPheLeuAspTrp 60  
 QY 121 TACCTGCAGAACCGAGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCGCGCA 180  
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgAla 80  
 QY 181 TCAGGGTCCCTCAGAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 120  
 QY 301 TTCACGTTGGCCAGGACCAAGGTGGAGATCAACGTACGTTGGCT 348  
 Db 121 ArgThrPheGlyGlnGlyThrLysValGluLysArgThrValAla 136

## RESULT 3

US-10-275-046-83  
 ; Sequence 83, Application US/10275046  
 ; Publication No. US20040019187A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nagy et al.  
 ; TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPTIDES  
 ; FILE REFERENCE: GPCG-P01-260  
 ; CURRENT APPLICATION NUMBER: US/10/275,046  
 ; CURRENT FILING DATE: 2002-10-31  
 ; PRIOR APPLICATION NUMBER: 00110063.5  
 ; PRIOR FILING DATE: 2000-05-12  
 ; NUMBER OF SEQ ID NOS: 97  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 83  
 ; LENGTH: 114  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: MS-GPIC16 VL  
 ; US-10-275-046-83

## Alignment Scores:

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 Score: 518.00 Matches: 101  
 Percent Similarity: 92.11% Conservative: 4  
 Best Local Similarity: 88.60% Mismatches: 9  
 Query Match: 83.68% Indels: 0  
 DB: 15 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-275-046-83 (1-114)

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 Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20  
 QY 61 ATCTCTGTGCTCGAGTAAAGTCTCCTGTATAAGAGTGGGAACACATCTTGAATTGG 120  
 Db 21 IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40  
 QY 121 TACCTGCAGAACCGAGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCGCGCA 180  
 Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgAla 60  
 QY 181 TCAGGGTCCCTCAGAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
 Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 80  
 QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 Db 81 SerArgValGluAlaGluAspValGlyValTyrCysGlnGlnTyrAsnSerTyrPro 100  
 QY 301 TTCACGTTGGCCAGGACCAAGGTGGAGATCAACGTACGTTAGC 342



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Db 101 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThr 114
RESULT 4
US-10-292-088-56
; Sequence 56, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PP/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-56
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Pred. No.: 9,91e-45 Length: 239
Score: 518.00 Matches: 101
Percent Similarity: 91.38% Conservative: 5
Best Local Similarity: 87.07% Mismatches: 10
Query Match: 83.68% Indels: 0
DB: 12 Gaps: 0
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QY 61 ATCTCTCTGCTCGAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
Db 41 IleSerCysArgSerSerGlnSerLeuLeuTyrSerAsnGlyTyrAsnTyrLeuAspTyr 60
QY 121 TACCTGCAAGACCGGCGAGTCTCCAGCTCTCTGATCTATTGATGTCACCCGGCA 180
Db 61 TyrLeuGlnLysProGlyGlnSerProHisLeuLeuIleTyrLeuGlySerAsnArgAla 80
QY 181 TCAGGGGTCCCTGCACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY 241 AGCAGAGTGAGGCTGAGAGTGTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 120
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAACTACGTGGCT 348
Db 121 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 136
RESULT 5
US-10-663-244-149
; Sequence 149, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-149
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; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide.
US-10-663-244-149
Alignment Scores:
Pred. No.: 1.59e-44 Length: 238
Score: 516.00 Matches: 100
Percent Similarity: 92.24% Conservative: 7
Best Local Similarity: 86.21% Mismatches: 9
Query Match: 83.36% Indels: 0
DB: 16 Gaps: 0
US-09-674-716B-17 (1-348) x US-10-663-244-149 (1-238)
QY 1 GATATTGTGACTCAGTCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGGCTCC 60
Db 20 AsplleGlnMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 39
QY 61 ATCTCTCTGCTCGAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
Db 40 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTyr 59
QY 121 TACCTGCAAGACCGGCGAGTCTCCAGCTCTCTGATCTATTGATGTCACCCGGCA 180
Db 60 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgAla 79
QY 181 TCAGGGGTCCCTGCACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Db 80 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 99
QY 241 AGCAGAGTGAGGCTGAGAGTGTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 100 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 119
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAACTACGTGGCT 348
Db 120 TrpThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 135
RESULT 6
US-10-663-244-145
; Sequence 145, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-145
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US-10-292-088-102

Alignment Scores:

Pred. No.: 6,64e-44 Length: 239  
 Score: 510.00 Matches: 100  
 Percent Similarity: 91.38% Conservative: 6  
 Best Local Similarity: 86.21% Mismatches: 10  
 Query Match: 82.39% Indels: 0  
 DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-292-088-102 (1-239)

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 DB 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40  
 QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCCTGTATAGAGTGGGAAGACATACCTGAATTGG 120  
 DB 41 IleSerCysArgSerSerGlnSerLeuLeuProGlyAsnGlyTyAsnTyLeuAspTrp 60  
 QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGGCA 180  
 DB 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyLeuGlySerAsnArgala 80  
 QY 181 TCAGGGGTCCCTGCACAGTTCAGTGGCAGTGGATCAGGCACACAGATTTACACTGAAATC 240  
 DB 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 241 ACAGAGTGGAGCTCAGAGTGTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 DB 101 SerArgValGluAlaGluAspValGlyIleTyTyTyCysMetGlnAlaLeuGlnThrPro 120  
 QY 301 TTCACGTTCCGCAAGGACCAAGTGGAGATCAACAGCTACCGTGGCT 348  
 DB 121 ArgThrPheGlyGlnGlyThrLysValGluLysArgThrValAla 136

RESULT 12

US-10-404-724-12  
 ; Sequence 12, Application US/10404724  
 ; Publication No. US20030203447A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horwitz, Arnold H.  
 ; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant  
 ; FILE REFERENCE: 13698US01  
 ; CURRENT APPLICATION NUMBER: US/10/404,724  
 ; PRIOR FILING DATE: 2003-03-31  
 ; PRIOR FILING DATE: 2002-03-29  
 ; NUMBER OF SEQ ID NOS: 79  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 12  
 ; LENGTH: 239  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-404-724-12

Alignment Scores:

Pred. No.: 6,64e-44 Length: 239  
 Score: 510.00 Matches: 100  
 Percent Similarity: 90.52% Conservative: 5  
 Best Local Similarity: 86.21% Mismatches: 11  
 Query Match: 82.39% Indels: 0  
 DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-404-724-12 (1-239)

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 DB 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProGlySer 40  
 QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCCTGTATAGAGTGGGAAGACATACCTGAATTGG 120

Db 41 IleSerCysArgSerSerLysSerLeuLeuHisSerAsnGlyIleThrTyLeuTyTrp 60  
 QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGGCA 180  
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyLeuGlySerAsnArgala 80  
 QY 181 TCAGGGGTCCCTGCACAGTTCAGTGGCAGTGGATCAGGCACACAGATTTACACTGAAATC 240  
 Db 81 SerGlyValProAspArgPheSerSerSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 241 AGCAGAGTGGAGCTCAGAGTGTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 Db 101 SerArgValGluAlaGluAspValGlyIleTyTyTyCysMetGlnAlaLeuGlnThrPro 120  
 QY 301 TTCACGTTCCGCAAGGACCAAGTGGAGATCAACAGCTACCGTGGCT 348  
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RESULT 13

US-10-453-698-177  
 ; Sequence 177, Application US/10453698  
 ; Publication No. US20040038308A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rother, Russell  
 ; TITLE OF INVENTION: HYBRID ANTIBODIES  
 ; FILE REFERENCE: 92 CIP (1087-37 CIP)  
 ; CURRENT APPLICATION NUMBER: US/10/453,698  
 ; CURRENT FILING DATE: 2003-06-03  
 ; NUMBER OF SEQ ID NOS: 196  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 177  
 ; LENGTH: 113  
 ; TYPE: PRT  
 ; ORGANISM: human  
 US-10-453-698-177

Alignment Scores:

Pred. No.: 1,99e-43 Length: 113  
 Score: 505.00 Matches: 98  
 Percent Similarity: 92.04% Conservative: 6  
 Best Local Similarity: 86.73% Mismatches: 9  
 Query Match: 81.58% Indels: 0  
 DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-453-698-177 (1-113)

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 Db 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyAsnTyLeuAspTrp 40  
 QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGGCA 180  
 Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyLeuGlySerAsnArgala 60  
 QY 181 TCAGGGGTCCCTGCACAGTTCAGTGGCAGTGGATCAGGCACACAGATTTACACTGAAATC 240  
 Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 80  
 QY 241 AGCAGAGTGGAGCTCAGAGTGTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 Db 81 SerArgValGluAlaGluAspValGlyIleTyTyTyCysMetGlnAlaLeuGlnThrPro 100  
 QY 301 TTCACGTTCCGCAAGGACCAAGTGGAGATCAACAGCT 339  
 Db 101 GlnThrPheGlyGlnGlyThrLysValGluLysArg 113

RESULT 14

US-10-308-817-177  
 ; Sequence 177, Application US/10308817

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; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 177
; LENGTH: 113
; TYPE: PRT
; ORGANISM: human
US-10-308-817-177

Alignment Scores:
Pred. No.: 1,99e-43 Length: 113
Score: 505.00 Matches: 98
Percent Similarity: 92.04% Conservative: 6
Best Local Similarity: 86.73% Mismatches: 9
Query Match: 81.58% Indels: 0
DB: 15 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-308-817-177 (1-113)
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DB 1 AsplleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCCTGTATAGGATGGAGACATCTGAATTGG 120
DB 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCGGSCA 180
DB 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 60
QY 181 TCAGGGGTCCTTCACAGTTCAGTGGCAGTGATCAGGCAGGACAGATTTTACACTGAAATC 240
DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 80
QY 241 ACCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
DB 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 100
QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAAACGT 339
DB 101 GlnThrPheGlyGlnGlyThrLysValGluLysArg 113

RESULT 15
US-10-663-244-148
; Sequence 148, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-148

Alignment Scores:
Pred. No.: 2,18e-43 Length: 238
Score: 505.00 Matches: 99
Percent Similarity: 90.52% Conservative: 6
Best Local Similarity: 85.34% Mismatches: 11
Query Match: 81.58% Indels: 0
DB: 16 Gaps: 0

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QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCCTGTATAGGATGGAGACATCTGAATTGG 120
DB 40 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 59
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCGGSCA 180
DB 60 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 79
QY 181 TCAGGGGTCCTTCACAGTTCAGTGGCAGTGATCAGGCAGGACAGATTTTACACTGAAATC 240
DB 80 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 99
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
DB 100 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 119
QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAAACGTACGTTGGCT 348
DB 120 ArgThrPheGlyGlyThrLysValGluLysArgThrValAla 135

Search completed: September 30, 2004, 09:48:32
Job time : 47.645 secs
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ALIGNMENTS

RESULT 1  
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; Sequence 15, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Illeg, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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(without alignments)  
4221.672 Million cell updates/sec

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Minimum DB seq length: 0  
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Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	507	81.9	114	4	US-09-025-769B-29 Sequence 29, Appl
3	507	81.9	114	4	US-09-025-769B-45 Sequence 45, Appl
4	507	81.9	281	4	US-09-025-769B-178 Sequence 178, Appl
5	505	81.6	112	1	US-08-053-171-16 Sequence 16, Appl
6	502.5	81.2	113	1	US-08-264-093-10 Sequence 10, Appl
7	500	80.8	112	1	US-08-478-039-88 Sequence 88, Appl
8	500	80.8	112	1	US-08-476-349A-88 Sequence 88, Appl
9	498	80.5	116	1	US-08-482-882-66 Sequence 66, Appl
10	498	80.5	116	2	US-08-483-389-66 Sequence 66, Appl
11	498	80.5	116	2	US-08-487-113D-66 Sequence 66, Appl
12	498	80.5	116	2	US-08-473-503-66 Sequence 66, Appl

TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9090  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 113 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-025-769B-15

Alignment Scores:  
 Pred. No.: 4,87e-55 Length: 113  
 Score: 508.00 Matches: 97  
 Percent Similarity: 92.92% Conservative: 8  
 Best Local Similarity: 85.84% Mismatches: 8  
 Query Match: 82.07% Indels: 0  
 DB: 4 Gaps: 0

US-09-674-716B-17 (1-348) x US-09-025-769B-15 (1-113)

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QY 61 ATCTCTCTGCTCGCTGAGTAAGAGTCTCTCTGTATAGGATGGGAAGACATACTTGAATTGG 120
Db 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40
QY 121 TACCTCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTCATGTCACCCGGGCA 180
Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLiefTyrLeuGlySerAsnArgala 50
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QY 301 TTCACGTTCCGCAAGGACCAAGGTGGAGATCAAAACGT 339
Db 101 TyrThrPheGlyGlnGlyThrLysLeuGluLiefLysArg 113

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#### RESULT 2

US-09-025-769B-29  
 Sequence 29, Application US/09025769B  
 Patent No. 6300064

GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 APPLICANT: Pack, Peter  
 APPLICANT: Ilag, Vic  
 APPLICANT: Ge, Liming  
 APPLICANT: Moroney, Simon  
 APPLICANT: Plueckthun, Andreas  
 TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/025,769B  
 FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: MOREHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9090  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 114 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-025-769B-29

Alignment Scores:  
 Pred. No.: 6,51e-55 Length: 114  
 Score: 507.00 Matches: 100  
 Percent Similarity: 91.23% Conservative: 4  
 Best Local Similarity: 87.72% Mismatches: 10  
 Query Match: 81.91% Indels: 0  
 DB: 4 Gaps: 0

US-09-674-716B-17 (1-348) x US-09-025-769B-29 (1-114)

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QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGGCTCC 60
Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
QY 61 ATCTCTCTGCTCGCTGAGTAAGAGTCTCTCTGTATAGGATGGGAAGACATACTTGAATTGG 120
Db 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40
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Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLiefTyrLeuGlySerAsnArgala 50
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
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QY 301 TTCACGTTCCGCAAGGACCAAGGTGGAGATCAAAACGTACG 342
Db 101 ProThrPheGlyGlnGlyThrLysValGluLiefLysArgThr 114

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#### RESULT 3

US-09-025-769B-45  
 Sequence 45, Application US/09025769B  
 Patent No. 6300064

GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 APPLICANT: Pack, Peter  
 APPLICANT: Ilag, Vic  
 APPLICANT: Ge, Liming  
 APPLICANT: Moroney, Simon  
 APPLICANT: Plueckthun, Andreas  
 TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-45

Alignment Scores:  
Pred. No.: 6,518-55 Length: 114  
Score: 507.00 Matches: 100  
Percent Similarity: 91.23% Conservative: 4  
Best Local Similarity: 87.72% Mismatches: 10  
Query Match: 81.91% Indels: 0  
DB: 4 Gaps: 0

US-09-674-716B-17 (1-348) x US-09-025-769B-45 (1-114)

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DB 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20  
QY 61 ATCTCTGCTCGCTCAGTAAGAGTCTCCTGTATAGGATGGAGACATCTGTAATTGG 120  
DB 21 IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40  
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTGATCTATTTGATCTCCACCCGGGCA 180  
DB 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 60  
QY 181 TCAGGGTCCCTGACAGGTTCACTGCGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 240  
DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 300  
DB 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysGlnGlnHisTyrThrThrPro 100  
QY 301 TTCACGTTCCGCGCAAGGACCAAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 342  
DB 101 ProThrPheGlyGlnGlyThrLysValGluIleLysArgThr 114

#### RESULT 4

US-09-025-769B-178  
Sequence 178, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 178:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-178

Alignment Scores:  
Pred. No.: 9,318-55 Length: 281  
Score: 507.00 Matches: 100  
Percent Similarity: 91.23% Conservative: 4  
Best Local Similarity: 87.72% Mismatches: 10  
Query Match: 81.91% Indels: 0  
DB: 4 Gaps: 0

US-09-674-716B-17 (1-348) x US-09-025-769B-178 (1-281)

QY 1 GATATTGTGATGACTCAGTCTCCATCTCCCTGCGCTCACCCCTGGAGAGCCGCGCTCC 60  
DB 166 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 185  
QY 61 ATCTCTGCTCGCTCAGTAAGAGTCTCCTGTATAGGATGGAGACATCTGTAATTGG 120  
DB 186 IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 205  
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTGATCTATTTGATCTCCACCCGGGCA 180  
DB 206 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 225  
QY 181 TCAGGGTCCCTGACAGGTTCACTGCGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 240  
DB 226 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 245  
QY 241 AGCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 300  
DB 246 SerArgValGluAlaGluAspValGlyValTyrTyrCysGlnGlnHisTyrThrThrPro 265  
QY 301 TTCACGTTCCGCGCAAGGACCAAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 342  
DB 266 ProThrPheGlyGlnGlyThrLysValGluIleLysArgThr 279

#### RESULT 5

US-08-053-171-16  
Sequence 16, Application US/08053171  
Patent No. 5562903  
GENERAL INFORMATION:  
APPLICANT: Co, Leibner

;; TITLE OF INVENTION: Antibody Derivatives  
;; NUMBER OF SEQUENCES: 32  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend Khourie and Crew  
;; STREET: 379 Lytton Avenue  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: US  
;; ZIP: 94301  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/053,171  
;; FILING DATE: 22-APR-1993  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Smith, William M.  
;; REGISTRATION NUMBER: 30,223  
;; REFERENCE/DOCKET NUMBER: 11823-54-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 326-2400  
;; TELEFAX: (415) 326-2422  
;; INFORMATION FOR SEQ ID NO: 16:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 112 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..112  
;; OTHER INFORMATION: /note= "Sequence of Tew antibody  
;; Patent No. 5562903  
;; OTHER INFORMATION: fragment"  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..112  
;; OTHER INFORMATION: /note= "E.A. Kabat, et al.,  
;; OTHER INFORMATION: Sequences of Protein of Immunological Interest,  
;; OTHER INFORMATION: 4th Ed. (1987), US Dept. of Health and Human Services  
US-08-053-171-16

Alignment Scores:  
Pred. No.: 1,15e-54 Length: 112  
Score: 505.00 Matches: 96  
Percent Similarity: 91.9e% Conservative: 7  
Best Local Similarity: 85.71% Mismatches: 9  
Query Match: 81.58% Indels: 0  
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x US-08-053-171-16 (1-112)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGACCGCGCTCC 60  
Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20  
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTGTATAAGGATGGAGACATACCTGCAATTGG 120  
Db 21 IleSerCysArgSerSerGlnSerLeuLeuIleSerAspGlyPheAspTyrLeuAsnTyr 40  
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCACCCCGGCA 180  
Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrAlaLeuSerAsnArgAla 60  
QY 181 TCAGGGGTCCTTGACAGTTTCAGTGGCAGTGGATCAGGCAGAGATTTTACACTGAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGAGTTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300

Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnAlaPro 100  
QY 301 TTCACGTTCCGCCAAGGGACCAAGGTGGAGATCAAA 336  
Db 101 IleThrPheGlyGlnGlyThrArgLeuGluLeuLys 112  
RESULT 6  
US-08-264-093-10  
; Sequence 10, Application US/08264093  
; Patent No. 5639863  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. Dan  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO  
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ridout & Maybee  
; STREET: 2300 Richmond-Adelaide Centre  
; STREET: 101 Richmond Street West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 2J7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS 6.00  
; SOFTWARE: ASCII Editor  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/264,093  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA: No. 5639863 applicable  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lake, James R.  
; REGISTRATION NUMBER: 31081  
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 868-1482  
; TELEFAX: (416) 362-0823  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not applicable  
; TOPOLOGY: linear  
US-08-264-093-10  
Alignment Scores:  
Pred. No.: 2,37e-54 Length: 113  
Score: 502.50 Matches: 98  
Percent Similarity: 92.04% Conservative: 6  
Best Local Similarity: 86.73% Mismatches: 8  
Query Match: 81.18% Indels: 1  
DB: 1 Gaps: 1  
US-09-674-716B-17 (1-348) x US-08-264-093-10 (1-113)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGACCGCGCTCC 60  
Db 1 AspIleValMetThrGlnThrProLeuSerLeuProValThrProGlyGluProAlaSer 20  
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTCTG---TATAAGGATGGGAAGACATCTTGAAT 117  
Db 21 IleSerCysArgSerSerGlnSerLeuLeuAspSerAspGlyAsnThrTyrLeuAsp 40  
QY 118 TGGTACTCCAGAACCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCACCCCGG 177  
Db 41 TrpTyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrThrLeuSerTyrArg 60  
QY 178 GCATCAGGGGTCCTGTCACAGGTTTCAGTGGCAGTGGATCAGGCAGACATTTTACACTGAAA 237

Db 61 AlaSerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLys 80  
QY 238 ATCAGCAGAGTGGAGGTGGAGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTAT 297  
Db 81 IleSerArgValGluAlaGluAspValGlyValTyrCysMetGlnArgIleGluPhe 100  
QY 298 CCATTCAGTTCGCGCAAGGACCAAGTGGAGATCAAA 336  
Db 101 ProPheThrPheGlyGlyThrLysValGluIleLys 113  
RESULT 7  
US-08-478-039-88  
; Sequence 88, Application US/08478039  
; Patent No. 5681722  
; GENERAL INFORMATION:  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Raab, Ronald W.  
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,039  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/379,072  
; FILING DATE: 25-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/912,292  
; FILING DATE: 10-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/856,281  
; FILING DATE: 23-MAR-1992  
; APPLICATION NUMBER: US 07/735,064  
; FILING DATE: 25-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin Esq., Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-160  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: VK2 consensus  
US-08-478-039-88  
Alignment Scores:  
P-red. No.: 4.85e-54 Length: 112  
Score: 500.00 Matches: 95  
Percent Similarity: 91.96% Conservative: 8

Best Local Similarity: 84.82% Mismatches: 9  
Query Match: 80.78% Indels: 0  
DB: 1 Gaps: 0  
US-09-674-716B-17 (1-348) x US-08-478-039-88 (1-112)  
QY 1 GATATTGTGATCAGTCAGTCTCCACTCTCCCTGCGCCGTACCCCTGGAGAGCGGCTCC 60  
Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20  
QY 61 ATCTCTCTGCTCGCTCGAGTAAGAGTCTCTCTGTATAAGAGTGGGAGACACATCTGAATTGG 120  
Db 21 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAsnThrTyrLeuAsnTyr 40  
QY 121 TACCTCAGAACGACGAGGAGCTCTCCAGAGCTCTCCAGCTCTGATCTATTGATGTCCACCGGGCA 180  
Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 60  
QY 181 TCAGGGCTCCCTGACAGAGTTCAGTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGCTGAGAGTGTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCA 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnSerPro 100  
QY 301 TTCACGTTCCGCGCAAGGACCAAGTGGAGATCAAA 336  
Db 101 TyrThrPheGlyGlnGlyThrLysAsnGluIleLys 112  
RESULT 8  
US-08-478-349A-88  
; Sequence 88, Application US/08476349A  
; Patent No. 5750105  
; GENERAL INFORMATION:  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Raab, Ronald W.  
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,349A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/379,072  
; FILING DATE: 25-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/912,292  
; FILING DATE: 10-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/856,281  
; FILING DATE: 23-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/735,064  
; FILING DATE: 25-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin Esq., Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-161  
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VK2 consensus
US-08-476-349A-88
Alignment Scores:
Pred. No.: 4,85e-54 Length: 112
Score: 500.00 Matches: 95
Percent Similarity: 91.96% Conservative: 8
Best Local Similarity: 84.82% Mismatches: 9
Query Match: 80.78% Indels: 0
DB: 1 Gaps: 0
US-09-674-716B-17 (1-348) x US-08-476-349A-88 (1-112)
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
Db 1 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
QY 61 ATCTCTCTCGCTCGAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTGATTGG 120
Db 21 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAsnThrTyrLeuAsnTrp 40
QY 121 TACCTGCAGAACCGAGGCGAGTCTCCACAGCTCTGATCTATTGATCTCCACCGGGCA 180
Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 60
QY 181 TCAGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 80
QY 241 AGCAGAGTGGAGGCTCAGGATCTGGGTATTACTCTCAACAGCTGGTAGATATCCA 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnSerPro 100
QY 301 TTCAGTTCGGCCAAAGGACCAAGTGGAGATCAA 336
Db 101 TyrThrPheGlyGlnGlyThrLysAsnGluLleLys 112
RESULT 9
US-08-482-882-66
; Sequence 66, Application US/08482882
; Patent No. 5773218
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,882
; FILING DATE: 07-JUN-1995

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5773218and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-882-66
Alignment Scores:
Pred. No.: 8,75e-54 Length: 116
Score: 498.00 Matches: 95
Percent Similarity: 91.07% Conservative: 7
Best Local Similarity: 84.82% Mismatches: 10
Query Match: 80.45% Indels: 0
DB: 1 Gaps: 0
US-09-674-716B-17 (1-348) x US-08-482-882-66 (1-116)
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
Db 5 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24
QY 61 ATCTCTCTCGCTCGAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTGATTGG 120
Db 25 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44
QY 121 TACCTGCAGAACCGAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCCACCGGGCA 180
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 64
QY 181 TCAGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 84
QY 241 AGCAGAGTGGAGGCTCAGGATCTGGGTATTACTCTCAACAGCTGGTAGATATCCA 300
Db 85 SerArgValGluAlaGluAspValGlyValTyrCysSerGlnSerThrHisValPro 104
QY 301 TTCAGTTCGGCCAAAGGACCAAGTGGAGATCAA 336
Db 105 TyrThrPheGlyGlnGlyThrLysValGluLleLys 116
RESULT 10
US-08-483-389-66
; Sequence 66, Application US/08483389
; Patent No. 5811517
; GENERAL INFORMATION:

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QY 181 TCAGGGGTCCTGACAGAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLys 84  
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGTAGATATCCA 300  
Db 85 SerArgValGluAlaGluAspValGlyValTyrCysSerGlnSerThrHisValPro 104  
QY 301 TTCACGTTGGCCAGGACGACCAAGTGGAGATCAA 336  
Db 105 TyrThrPheGlyGlnGlyThrLysValGluLeuLys 116  
RESULT 11  
; Sequence 66, Application US/08487113D  
; Patent No. 5837822  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Vazeux, Rosemay  
; TITLE OF INVENTION: ICAM-Related Materials and Methods  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,113D  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,754  
; FILING DATE: 05-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/102,852  
; FILING DATE: 05-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/009,266  
; FILING DATE: 22-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/894,061  
; FILING DATE: 05-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/889,724  
; FILING DATE: 26-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,689  
; FILING DATE: 27-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5837822and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32744  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-487-113D-66  
Alignment Scores: 8.75e-54 Length: 116  
Pred. No.: 8.75e-54

APPLICANT: Gallatin, W. Michael  
APPLICANT: Vazeux, Rosemay  
TITLE OF INVENTION: ICAM-RELATED PROTEIN  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive/6300 Sears Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,389  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/102,852  
FILING DATE: 05-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/009,266  
FILING DATE: 22-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/894,061  
FILING DATE: 05-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/889,724  
FILING DATE: 26-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,689  
FILING DATE: 27-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Suh, Young J.  
REGISTRATION NUMBER: P-41,337  
REFERENCE/DOCKET NUMBER: 27866/32760  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: (312) 474-6600  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-389-66  
Alignment Scores:  
Pred. No.: 8.75e-54 Length: 116  
Score: 498.00 Matches: 95  
Percent Similarity: 91.07% Conservative: 7  
Best Local Similarity: 84.82% Mismatches: 10  
Query Match: 80.45% Indels: 0  
DB: 2 Gaps: 0  
US-09-674-716B-17 (1-348) x US-08-483-389-66 (1-116)  
QY 1 GATATGTGATGACTGACTTCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 60  
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24  
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAACATACATTTGAATGG 120  
Db 25 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44  
QY 121 TCCTGTGAGAGCCAGGGAGGTCTCCACAGCTCTGATCTATTGATGTCACCCGGGCA 180  
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLysValSerAsnArgPhe 64

Score: 498.00 Matches: 95  
 Percent Similarity: 91.07% Conservative: 7  
 Best Local Similarity: 84.82% Mismatches: 10  
 Query Match: 80.45% Indels: 0  
 DB: 2 Gaps: 0

US-09-674-716B-17 (1-348) x US-08-487-113D-66 (1-116)

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QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24
QY 61 ATCTCTGCTCGCTCGAGTAAAGTCTCCTGTATAGGATGGGAAGACATCTTGAATTGG 120
Db 25 IleSerCysArgSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44
QY 121 TACCTGCAGAACCGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGGCA 180
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLysValSerAsnArgPhe 64
QY 181 TCAGGGGTCCTGACAGGTTTCAGTGCAGTGCATCAGGCACAGATTTTACACTGAAATC 240
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 85 SerArgValGluAlaGluAspValGlyValTyrCysSerGlnSerThrHisValPro 104
QY 301 TTCACGTTGGCCAGGACCAAGGTGGAGATCAA 336
Db 105 TyrThrPheGlyGlnGlyThrLysValGluLeLys 116

```

## RESULT 12

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US-08-473-503-66
; Sequence 66, Application US/08473503
; Patent No. 5869262
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,503
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,754
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689

```

```

; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5869262and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-473-503-66

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Alignment Scores:  
 Pred. No.: 8,75e-54 Length: 116  
 Score: 498.00 Matches: 95  
 Percent Similarity: 91.07% Conservative: 7  
 Best Local Similarity: 84.82% Mismatches: 10  
 Query Match: 80.45% Indels: 0  
 DB: 2 Gaps: 0

US-09-674-716B-17 (1-348) x US-08-473-503-66 (1-116)

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QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24
QY 61 ATCTCTGCTCGCTCGAGTAAAGTCTCCTGTATAGGATGGGAAGACATCTTGAATTGG 120
Db 25 IleSerCysArgSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44
QY 121 TACCTGCAGAACCGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGGCA 180
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLysValSerAsnArgPhe 64
QY 181 TCAGGGGTCCTGACAGGTTTCAGTGCAGTGCATCAGGCACAGATTTTACACTGAAATC 240
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 85 SerArgValGluAlaGluAspValGlyValTyrCysSerGlnSerThrHisValPro 104
QY 301 TTCACGTTGGCCAGGACCAAGGTGGAGATCAA 336
Db 105 TyrThrPheGlyGlnGlyThrLysValGluLeLys 116

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## RESULT 13

```

US-08-483-932-66
; Sequence 66, Application US/08483932
; Patent No. 5880268
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/483,932  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/286,754  
FILING DATE: 05-AUG-1994  
APPLICATION NUMBER: US 08/102,852  
FILING DATE: 05-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/009,266  
FILING DATE: 22-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/894,061  
FILING DATE: 05-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/889,724  
FILING DATE: 26-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,689  
FILING DATE: 27-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5880268and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32178  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856-  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-932-66

Alignment Scores:  
Pred. No.: 8,75e-54 Length: 116  
Score: 498.00 Matches: 95  
Percent Similarity: 91.07% Conservative: 7  
Best Local Similarity: 84.82% Mismatches: 10  
Query Match: 80.45% Indels: 0  
DB: 2 Gaps: 0

US-09-674-716B-17 (1-348) x US-08-483-932-66 (1-116)

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCAGCCCTGGAGAGCGGCTCC 60  
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24  
Qy 61 ATCTCTGCTGCTCGAGTAAGAGTCTCCTGTATAGGATGGAGACATATCTGAATTGG 120  
Db 25 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44  
Qy 121 TACCTGCAGAGCCAGGGAGTCTCCAGCTCCTGATCTATTGATCTCCACCGGGCA 180  
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 64  
Qy 181 TCAGGGGTCCTGACAGGTTAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84  
Qy 241 AGCAGAGTGGAGGCTCAGGATCTCGGTTTATTACTCTCAACAGCTGGTAGATCCA 300  
Db 85 SerArgValGluAlaGluAspValGlyValTyrTyrCysSerGlnSerThrHisValPro 104  
Qy 301 TTCAGGTTCCGACAGGACCAAGTGGAGATCAA 336  
Db 105 TyrThrPheGlyGlnGlyThrLysValGluIleLys 116

RESULT 14

US-08-720-420A-66

; Sequence 66, Application US/08720420A

Patent No. 5989843  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Vazeux, Rosemay  
TITLE OF INVENTION: ICAM-Related Materials and Methods  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/720,420A  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,113  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,754  
FILING DATE: 05-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/102,852  
FILING DATE: 05-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/009,266  
FILING DATE: 22-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/894,061  
FILING DATE: 05-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/889,724  
FILING DATE: 26-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,689  
FILING DATE: 27-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Joseph A., Jr.  
REGISTRATION NUMBER: 33,659  
REFERENCE/DOCKET NUMBER: 33282  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856-  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-720-420A-66

Alignment Scores:  
Pred. No.: 8,75e-54 Length: 116  
Score: 498.00 Matches: 95  
Percent Similarity: 91.07% Conservative: 7  
Best Local Similarity: 84.82% Mismatches: 10  
Query Match: 80.45% Indels: 0  
DB: 2 Gaps: 0

US-09-674-716B-17 (1-348) x US-08-720-420A-66 (1-116)

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCAGCCCTGGAGAGCGGCTCC 60  
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24

QY 61 ATCTCTGTCGCTCAGTAAAGTCTCCTGTATAGGATGGGAACACATACCTGTAATGG 120  
Db 25 IleSerCysArgSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44  
QY 121 TACCTCAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCCGGCA 180  
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 64  
QY 181 TCAGGGGTCCCTGACAGGTTCTAGTGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84  
QY 241 AGCAGAGTGGAGCTGAGGATGTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
Db 85 SerArgValGluAlaGluAspValGlyValTyrTyrCysSerGlnSerThrHisValPro 104  
QY 301 TTCACGTTCCGCAAGGACCAAGTGGAGATCAAA 336  
Db 105 TyrThrPheGlyGlnGlyThrLysValGluIleLys 116

## RESULT 15

US-08-714-017-66  
; Sequence 66, Application US/08714017  
; Patent No. 6040176  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Vazeux, Rosemay  
; TITLE OF INVENTION: ICAM-Related Materials and Methods  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/714,017  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/286,754  
; FILING DATE:  
; APPLICATION NUMBER: US 08/102,852  
; FILING DATE: 05-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/009,266  
; FILING DATE: 22-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/894,061  
; FILING DATE: 05-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/899,724  
; FILING DATE: 26-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,689  
; FILING DATE: 27-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6040176and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32178  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-714-017-66  
Alignment Scores:  
Pred. No.: 8,75e-54 Length: 116  
Score: 498.00 Matches: 95  
Percent Similarity: 91.07% Conservative: 7  
Best Local Similarity: 84.82% Mismatches: 10  
Query Match: 80.45% Indels: 0  
DB: 3 Gaps: 0  
US-09-674-716B-17 (1-348) x US-08-714-017-66 (1-116)  
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGCACCCCTCGAGAGCGGCTCC 60  
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24  
QY 61 ATCTCTGTCGCTCAGTAAAGTCTCCTGTATAGGATGGGAAGACATACCTGTAATGG 120  
Db 25 IleSerCysArgSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44  
QY 121 TACCTCAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCCGGCA 180  
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 64  
QY 181 TCAGGGGTCCCTGACAGGTTCTAGTGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84  
QY 241 AGCAGAGTGGAGCTGAGGATGTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
Db 85 SerArgValGluAlaGluAspValGlyValTyrTyrCysSerGlnSerThrHisValPro 104  
QY 301 TTCACGTTCCGCAAGGACCAAGTGGAGATCAAA 336  
Db 105 TyrThrPheGlyGlnGlyThrLysValGluIleLys 116  
Search completed: September 30, 2004, 09:31:38  
Job time : 11.5112 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: September 30, 2004, 08:29:27 ; Search time 52.926 Seconds  
(without alignments)  
4852.647 Million cell updates/sec

Title: US-09-674-716B-18  
Perfect score: 2405  
Sequence: 1 gaggtcagctggtagtc.....ccctgtctcgggtaaatga 1335

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+n2p.model -DEV=xlp  
-Q=/cgn2/USPFC\_spool\_p/US09674716/runat\_30092004\_070259\_25882/app\_query.fasta\_1.3164  
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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09674716.scgn 1 152 @runat\_30092004\_070259\_25882 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THRESH=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 78:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1756	73.0	330	1 GHU	Ig gamma-1 chain C
2	1619.5	67.3	377	2 A23511	Ig gamma-3 chain C
3	1617.5	67.3	377	2 A60764	Ig gamma-3 chain C
4	1608	66.9	326	1 G2HU	Ig gamma-2 chain C
5	1579.5	65.7	327	1 G4HU	Ig gamma-4 chain C
6	1563	65.0	444	2 PC4436	monoclonal antibody
7	1450.5	60.3	470	2 S22080	Ig heavy chain V r
8	1430.5	59.5	374	2 S69339	Ig heavy chain V r
9	1419	58.0	469	2 S37483	Ig gamma-2a chain
10	1415.5	58.9	472	2 S31459	Ig gamma-1 chain -
11	1400.5	58.2	446	2 S40295	Ig gamma-2a chain
12	1361.5	56.6	474	1 G2MS11	Ig gamma-2b chain
13	1351	56.2	475	2 S01321	Ig gamma-2b chain
14	1259	52.3	328	2 I47159	Ig gamma 2a chain

# ALIGNMENTS

## RESULT 1

GHU

Ig gamma-1 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999

C/Accession: A93433; S33887; B90563; A90564; B91668; A31723; A02146

R/Elison J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A/Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.

A/Reference number: A93433; MUID:82274238; PMID:6287432

A/Accession: A93433

A/Molecule type: DNA

A/Residues: 1-330 <ELL>

A/Cross-references: EMBL:Z17370

A/Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers, 1

R/Harris, L.J.

submitted to the EMBL Data Library, October 1992

A/Reference number: S33904

A/Accession: S36861

A/Molecule type: DNA

A/Residues: 2-330 <HAR>

A/Cross-references: EMBL:Z17370

R/Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A/Reference number: S33887; MUID:83001943; PMID:6811139

A/Accession: S33887

A/Molecule type: DNA

A/Residues: 88-113;235-330 <TAK>

A/Cross-references: EMBL:Z17370

R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A/Reference number: A90563; MUID:71064024; PMID:5489771

A/Contents: myeloma protein Eu

A/Accession: B90563

A/Molecule type: protein

Ig gamma 2b chain  
Ig gamma-1 chain C  
Ig gamma chain C r  
Ig gamma 1 chain c  
Ig gamma 3 chain c  
Ig gamma chain C r  
Ig gamma-2 chain C  
Ig heavy chain C r  
Ig gamma-1 chain C  
Ig gamma-3 heavy C  
Ig gamma-1 chain C  
Ig gamma-1 chain C  
Ig gamma-2b chain  
Ig gamma-3 chain C  
Ig gamma-3 chain C  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2b chain  
Ig gamma-2b chain  
Ig gamma 4 chain C  
Ig epsilon chain C  
Ig heavy chain pre  
Ig heavy chain VHI  
Ig y heavy chain (r  
Ig heavy chain V-I  
Ig gamma-1 heavy c  
Ig heavy chain (UO  
Ig heavy chain (Ma

A;Residues: 1-96, 'R', 98-135 <CUN>  
A;Note: this sequence has the Gln(3) marker, 97-Arg  
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequence  
A;Reference number: A90564; MUID:71064025; PMID:5530842  
A;Contents: Eu

A;Accession: A90564  
A;Molecule type: protein  
A;Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,  
A;Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met  
R;Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
igen Primärstruktur.  
A;Reference number: A91668; MUID:77070269; PMID:826475  
A;Contents: myeloma protein Nie  
A;Accession: B91668

A;Molecule type: protein  
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27,  
A;Note: this sequence has the Gln(17) and Gln(1) markers  
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A;Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL  
A;Reference number: A91723; MUID:83289131; PMID:6884994  
A;Contents: myeloma protein KOL; disulfide bonds  
A;Accession: A91723

A;Molecule type: protein  
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A;Note: this sequence has the Gln(3) and Gln(non-1) markers  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide  
A;Reference number: A90565; MUID:71064027; PMID:4923144  
A;Contents: annotation; disulfide bonds

R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enamide cleavage products, and the disulfide bridges.  
A;Reference number: A91667; MUID:77070267; PMID:1002129  
A;Contents: annotation; disulfide bonds  
C;Genetics:

A;Gene: GDB:IGHG1  
A;Cross-references: GDB:120085; OMIM:147100  
A;Map position: 14Q32.33-14Q32.33  
A;Introns: 99/1; 114/1; 224/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar  
tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin c region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;243-310/Domain: immunoglobulin homology <IM2>  
F;27-83/Domain: immunoglobulin homology <IM3>  
F;103/Disulfide bonds: interchain (to light chain) #status experimental  
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment Scores:  
Pred. No.: 4,73e-89 Length: 330  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 73.01% Indels: 0  
DB: 1 Gaps: 0

US-09-674-716b-18 (1-1335) x GHU (1-330)

QY 343 GCCTCCACAGGGCCCATCGGTCTTCCCTGGCACCCTCCACAGACACCTCTGGG 402  
Db 1 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSergly 20  
QY 403 GGCACAGCGCCCTGGGCTGCCTGCTCAAGACTACTTCCCGGACCGGTGACGGTGTGC 462

Db 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
QY 463 TGGAACTCAGGCGCCCTGACCAAGCGCGTGCACACCTTCCCGGCTGTCTCAGACTCCTCA 522  
Db 41 TrpAsnSerGlyAlaLeuThrSerglyValHisThrPheProAlaValLeuGlnSerSer 60  
QY 523 GGACTCTACTCCCTCAGCAGCGGTGGTGCCTCCAGCAGCTTGGGACCACGACC 582  
Db 61 GlyLeuTyrSerLeuSerValThrValProSerSerSerLeuGlyThrGlnThr 80  
QY 583 TACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGCACAAGAAAGTGGAGCC 642  
Db 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100  
QY 643 AAATCTGTGCAAAAACCTCACATGCCACCGTGCACACCTGCAGCTCCGCGGGGCA 702  
Db 101 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuGlyGly 120  
QY 703 CGGTCACTTCTCTTCCCTCCCAACCCAGGACACCTCATGATCTCCCGGACCCCT 762  
Db 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerglyThrPro 140  
QY 763 GAGGTCACTGCTGTGTGGTGCAGTGCACGACGACGACCCCTGAGGTCAAGTTCACCTGG 822  
Db 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160  
QY 823 TAGCTGGAGCGGTGGAGTGTGATATCCACAGACAAAGCCGCGGAGGAGCAGTACAC 882  
Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnThrAsn 180  
QY 883 AGCACCTACCGTGTGTGTGCAGCTCTCCACCGTCTGCACAGACTGGGTGAATGGCAAG 942  
Db 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200  
QY 943 GAGTCAAGTGAAGTCTTCAACAAAGCCCTCCAGCGCCCATCGAGAAACCATCTCC 1002  
Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 220  
QY 1003 AAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTCCCGCCCATCCCGGATGAG 1062  
Db 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProSerArgAspGlu 240  
QY 1063 CTGACCAAGAACCGGTTCAGCTGACCTGCCTGGTCAAGGCTTCTATCCAGCGACATC 1122  
Db 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260  
QY 1123 GCCGTGGAGTGGAGAGCAATGGCAGCGGAGACACTACAGACCGCTCCCGTCC 1182  
Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 280  
QY 1183 CTGGACTCCGAGCGGTCTCTTCTCTACACAGACTCACCGTGCACAAGACGAGGTGG 1242  
Db 281 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300  
QY 1243 CAGCAGGGGAAAGTCTTCTCATGCTCCGTGATGATGAGGTCTGCACACACCTACAG 1302  
Db 301 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 320  
QY 1303 CAGAAGAGCTCTCCCTGTCTCCGGTAAA 1332  
Db 321 GlnLysSerLeuSerLeuSerProGlyLys 330

RESULT 2  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C;Accession: A23511  
R;Huck, S.; Forc, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con  
A;Reference number: A23511; MUID:86148507; PMID:3081877

A:Accession: A23511  
 A:Molecule type: DNA  
 A:Residues: 1-377 <HUC>  
 A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056  
 C:Genetics:  
 A:Gene: GDB:IGHG3  
 A:Cross-references: GDB:119339; OMIM:147120  
 A:Map position: 14q32.33-14q32.33  
 A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Superfamily: immunoglobulin  
 C:Keywords: immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 1,39e-81 Length: 377  
 Score: 1619.50 Matches: 307  
 Percent Similarity: 84.08% Conservative: 10  
 Best Local Similarity: 81.43% Mismatches: 13  
 Query Match: 67.34% Indels: 47  
 DB: 2 Gaps: 1

US-09-674-716B-18 (1-1335) x A23511 (1-377)

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QY 343 GCCTCCACCAAGGGCCCATCGTCTTCCCTGGGCACTCTCTCAAGAGCACCTCTGGG 402
DB 1 AlaserThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGly 20
QY 403 GGCACAGCGGCTCGGCTGGTCTCAAGGACTACTTCCCGAACCGGTGACGGTGTG 462
DB 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 463 TGGAACTGAGCGGCTCGACAGCGGCTGCACACCTTCCCGGCTGCTCAGTCTCA 522
DB 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 523 GGACTCTACTCTCCAGCAGCGTGTGACCGTGGCTCCAGCAGTTCGGGACCCAGACC 582
DB 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80
QY 583 TACATCTGCAAGTGAATCACAAGCCGACACACACAGGTGGACAAAGTG----- 636
DB 81 TyrThrCysAsnValAsnHisLysProSerAnThrLysValAspLysArgValGluLeu 100
QY 636 ----- 636
DB 101 LysThrProLeuGlyAspThrThrHisThrCysProArgCysProGluProLysSerCys 120
QY 636 ----- 636
DB 121 AspThrProProCysProArgCysProGluProLysSerCysAspThrProProPro 140
QY 637 -----GAGCCCAATCTGTGACAAACTCACACATGCCCGCGGCCA 681
DB 141 CysProArgCysProGluProLysSerCysAspThrProProCysProArgCysPro 160
QY 682 GCACCTGAACTCGCGGGGCACCGTCAGTCTTCTCTTCCCGCCAAAACCCAGGACACC 741
DB 161 AlaProGluLeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThr 180
QY 742 CTCATGATCTCCGACCCCTGAGTCACATCGGTGGTGGAGTGGAGTGGACACCAAGAC 801
DB 181 LeuMetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAsp 200
QY 802 CTGAGGTCAAGTCAACTGAGTACGTGGACGCGGTGGAGGTGCATAATGCCAAGACAAAG 861
DB 201 ProGluValGlnPheLysTyrTyrValAspGlyValGluValHisAsnAlaLysThrLys 220
QY 862 CCGCGGGAGAGCAGTACAAACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 921
DB 221 ProArgGluGluGlnTyrAsnSerThrPheArgValValSerValLeuThrValLeuHis 240
QY 922 CAGGACTGCTGAATGGCAGGAGTCAAGTGCAGAGTCTCCAAAGACCCCTCCAGCC 981

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DB 241 GlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAla 260
QY 982 CCATCGAGAAAACCATCTCCAAAAGCCAAAGGCGCCCGGAGAACACACAGGTGTACACC 1041
DB 261 ProIleGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValTyrThr 280
QY 1042 CTCGCCCATCCCGGATGAGTGCACCAAGACACAGGTGAGCTGACCTGCTGCTGCTGCT 1101
DB 281 LeuProProSerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLys 300
QY 1102 GGTCTTATCCCAAGCACATCGCCGTGGAGTGGAGAGCAATGGGAGCGGAGAGACAAC 1161
DB 301 GlyPheTyrProSerAspIleAlaValGluTyrGluSerSerGlyGlnProGluAsnAsn 320
QY 1162 TACAAGACACGCTCCCGTGTGACTCCGAGCGGCTCTTCTTCTCTACAGCAAGCTC 1221
DB 321 TyrAsnThrThrProProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeu 340
QY 1222 ACCGTGCACAAGAGCAGGTGGGAGCAGGGAACGTCTTCTCATGCTCCGCTGATGATGAG 1281
DB 341 ThrValAspLysSerArgTrpGlnGlnGlyAsnIlePheSerCysSerValMetHisGlu 360
QY 1282 GCTCTGCACAACCATACACGACAGAGCGCTCTCCCTGTCTCCGGGTAAA 1332
DB 361 AlaLeuHisAsnArgPheThrGlnLysSerLeuSerLeuSerProGlyLys 377

```

# RESULT 3

A60764  
 Ig gamma-3 chain C region, form IAT - human  
 C:Species: Homo sapiens (man)  
 C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 16-Jul-1999  
 C:Accession: A60764  
 R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
 Immunogenetics 30, 250-257, 1989  
 A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert  
 A:Reference number: A60764; MUID:90007613; PMID:2571587  
 A:Accession: A60764  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-377 <HUC>  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 1,79e-81 Length: 377  
 Score: 1617.50 Matches: 307  
 Percent Similarity: 84.08% Conservative: 10  
 Best Local Similarity: 81.43% Mismatches: 13  
 Query Match: 67.26% Indels: 47  
 DB: 2 Gaps: 1

US-09-674-716B-18 (1-1335) x A60764 (1-377)

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QY 343 GCCTCCACCAAGGGCCCATCGTCTTCCCGTGGCACCCTCTCCCAAGAGCACCTCTGGG 402
DB 1 AlaserThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGly 20
QY 403 GGCACAGCGGCTCGGCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTG 462
DB 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 463 TGGAACTGAGCGGCTCGACAGCGGCTGCACACCTTCCCGGCTGCTCAGTCTCA 522
DB 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 523 GGACTCTACTCTCCAGCAGCGTGTGACCGTGGCTCCAGCAGTTCGGGACCCAGACC 582
DB 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80
QY 583 TACATCTGCAAGTGAATCACAAGCCGACACACCAAGTGGACAAAGTG----- 636
DB 81 TyrThrCysAsnValAsnHisLysProSerAnThrLysValAspLysArgValGluLeu 100

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636 ----- 636  
 101 LysThrProLeuGlyAspThrThrHisThrCysProArgCysProGluProLysSerCys 120  
 636 ----- 636  
 121 AspThrProProCysProArgCysProGluProLysSerCysAspThrProPro 140  
 637 ----- 637  
 141 CysProArgCysProGluProLysSerCysAspThrProProCysProArgCysPro 160  
 682 GCACCTGAATCCGGGGGACCGTCAGTCTCTCCCTCCCAAAACCCAGGACACC 741  
 161 AlaProGluLeuLeuGlyGlyProSerValPheLeuPheProLysPheProLysAspThr 180  
 742 CTGATGATCTCCGGACCCCTGAGTCAATCGTGGTGGAGCTGAGCCAGCAAGAC 801  
 181 LeuMetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAsp 200  
 802 CCGTGGTCAAGTCAACTGCTGAGTGGAGCGGCGTGGAGTGCATATGCCAAGACAAAG 861  
 201 ProGluValGlnPheLysIleThrValAspGlyValGluValHisAsnAlaLysThrLys 220  
 862 CCGCGGGAGGAGTACACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 921  
 221 ProArgGluGluGlnIleThrAsnSerThrPheArgValValSerValLeuThrValLeuHis 240  
 922 CAGGACTGGCTGAATGGCAGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 981  
 241 GlnAspTrpLeuAsnGlyLysGluTrpLysCysLysValSerAsnLysAlaLeuProAla 260  
 982 CCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCCAGGTGTACACC 1041  
 261 ProIleGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValThr 280  
 1042 CTGCCCCCATCCCGGATGAGTGGTACCAAGACCGAGTGGTGGTGGTGGTGGTGGTGGT 1101  
 281 LeuProProSerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLys 300  
 1102 GCGTCTATCCAGCAGCATCCCGTGGAGTGGAGCAATGGCGAGCAATGGCGAGCAAC 1161  
 301 GlyPheTrpProSerAspIleAlaValGluTrpGluSerGlyGluProGluAsn 320  
 1162 TACAAGACACCGCTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1221  
 321 TyrAsnThrThrProProValLeuAspSerAspGlySerPhePheLeuTySerArgLeu 340  
 1222 ACCGTGGCAAGAGAGGTTGGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1281  
 341 ThrValAspLysSerArgTrpGlnGluGlyAsnValPheSerCysSerValMethisGlu 360  
 1282 GCTCTCAACACCTACACGAGAGAGCGCTCTCCCTGCTCCCGGTAAG 1332  
 361 AlaLeuHisAsnArgPheThrGlnLysSerLeuSerLeuSerProGlyLys 377

RESULT 4

G2HU  
 Ig gamma-2 chain C region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text\_change 21-Jul-2000  
 C:Accession: A93906; A92809; A90752; A93132; A02148  
 R:Ellison, J.; Hood, L.  
 Proc.Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
 A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
 A:Reference number: A93906; MUID:182197621; PMID:6804948  
 A:Accession: A93906  
 A:Molecule type: DNA  
 A:Residues: 1-326 <ELL>  
 A:Cross-references: GB:V00554; GB:J00230; NID:q32759; PIDN:CA58438.1; PID:g6066056  
 A:Note: Lys-326 is probably removed posttranslationally  
 R:Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980  
 A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fu  
 A:Reference number: A92809; MUID:81007873; PMID:6774012  
 A:Contents: myeloma protein T11  
 A:Accession: A92809  
 A:Molecule type: protein  
 A:Residues: 1-19, 'Q', '21-57', 'Z', '59', 'A', '61-193', 'D', '195-325 <WAN>  
 A:Note: Trp-156 is at or near the complement-binding site  
 R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
 Can. J. Biochem. 57, 758-767, 1979  
 A:Title: The amino acid sequences of the three heavy chain constant region domains of a l  
 A:Reference number: A90752; MUID:80001357; PMID:113060  
 A:Contents: myeloma protein Zie  
 A:Accession: A90752  
 A:Molecule type: protein  
 A:Residues: 1-24, 'E', '26-57', 'EV', '60-85', '132-171', 'ZZZ', '175', 'B', '177-193', 'D', '195-196', 'Q', '198-2  
 A:Note: this sequence has since been revised  
 R:Hofmann, T.; Parr, D.M.  
 Mol. Immunol. 16, 923-925, 1979  
 A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin ga  
 A:Reference number: A93132; MUID:80114419; PMID:118920  
 A:Contents: Zie  
 A:Accession: A93132  
 A:Molecule type: protein  
 A:Residues: 238-275 <HOP>  
 R:Hofmann, T.; Parr, D.M.  
 submitted to the Atlas, March 1980  
 A:Reference number: A94591  
 A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
 A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic  
 red  
 R:Milstein, C.; Frangione, B.  
 Biochem. J. 121, 217-225, 1971  
 A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.  
 A:Reference number: A90253; MUID:72033500; PMID:4940472  
 A:Contents: annotation; myeloma protein Sa, disulfide bonds  
 R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
 Nature 221, 145-148, 1969  
 A:Title: Structural studies of immunoglobulin G.  
 A:Reference number: A93157; MUID:69064124; PMID:5782707  
 A:Contents: annotation; Sa, disulfide bonds  
 C:Genetics:  
 A:Gene: GDB:IGHG2  
 A:Cross-references: GDB:119338; OMIM:147110  
 A:Map position: 14q32.33-14q32.33  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IM1>  
 F:133-202/Domain: immunoglobulin homology <IM2>  
 F:239-306/Domain: immunoglobulin homology <IM3>  
 F:14/Disulfide bonds: interchain (to light chain) #status experimental  
 F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
 F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:	6.07e-81	Length:	326
Pred. No.:	1608.00	Matches:	302
Score:	95.15%	Conservative:	12
Percent Similarity:	91.52%	Mismatches:	12
Best Local Similarity:	66.86%	Indels:	4
Query Match:	1	Gaps:	2
DB:			

US-09-674-716B-18 (1-1335) x G2HU (1-326)

Qy 343 GCCTCCACCAAGGCCCATCGGTCTTCCCTCCGAGCCCTCTCCACAGACACCTCTGGG 402  
 Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20  
 Qy 403 GGCACAGCGCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 462

Db 21 SerThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
QY 463 TGGAACTCAGGGCCCTGACAGGGCGTGCACACCTTCCCGGCTGCTCCACAGTCTCA 522  
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 60  
QY 523 GGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAGACC 582  
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGlyThrGlnThr 80  
QY 583 TACATCTGCAACGTGAATCAAGCCCAAGCAACCAAGGTGGACAGAAAGTGGAGCCC 642  
Db 81 TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLysThrValGluArg 100  
QY 643 AAATCTTGTGACAAAACACTCACATGCCACCGTCCAGCAGCTGAACCTCGCGGGGCA 702  
Db 101 LysCysCysValGlu-----CysProProCysProAlaProProValAlaGly--- 116  
QY 703 CGCTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 762  
Db 117 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 136  
QY 763 GAGTTCATCGTGGTGGTGGACGTGACCGACGACGACGACGACGACGACGACGACG 822  
Db 137 GluValThrCysValValAspValSerHisGluAspProGluValGlnPheAsnTrp 156  
QY 823 TACGTGGACGGCGTGGAGGTGCATATGCCAAGCAAAAGCCCGCGGAGGACGATACAC 882  
Db 157 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnPheAsn 176  
QY 883 AGCAGTACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 942  
Db 177 SerThrPheArgValValSerValLeuThrValValHisGlnAspTrpLeuAsnGlyLys 196  
QY 943 GAGTCAAGTGAAGTGTCTCCAAAGACCCCTCCAGCAGCCCATCGAGAAACCATCTCC 1002  
Db 197 GluTyrLysCysLysValSerAsnLysGlyLeuProAlaProLysThrLysSer 216  
QY 1003 AAAGCCAAAGGACGCCCGAGAACACACAGTGTATACCCCTGCGCCCTCCCGGATAG 1062  
Db 217 LysThrLysGlyGlnProArgLysProGlnValTyrThrLeuProProSerArgGluGlu 236  
QY 1063 CTGACCAAGAACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1122  
Db 237 MetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 256  
QY 1123 GCCGTGGAGTGGAGCAATCGGAGCGGAGAACAACTCAAGACCAACGCTCCCGGTG 1182  
Db 257 AlaValGluTyrGlnLysAsnGlyGlnProGluAsnAsnTyrLysThrThrProProMet 276  
QY 1183 CTGGACTCGGCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1242  
Db 277 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 296  
QY 1243 CAGCAGGGGAAGCTTCTTCATGCTCCGCTGATGATGAGCTTCTGCACAAACCATACAC 1302  
Db 297 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 316  
QY 1303 CAGAGAGCGCTTCGCTGCTCCGGGTAAA 1332  
Db 317 GlnLysSerLeuSerLeuSerProGlyLys 326

RESULT 5  
G4HU  
Ig gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 16-Jul-1999  
C:Accession: A90933; A90249; A02150  
R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83157104; PMID:6299662  
A:Accession: A90933

A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A:Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant re  
A:Reference number: A90249; MUID:70207560; PMID:4192699  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30,81-326 <PIN>  
C:Genetics:  
A:Gene: GDB:IGHG4  
A:Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa)  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores: 2,21e-79 Length: 327  
Pred. No.: 1579.50 Matches: 298  
Score: 93.94% Conservative: 12  
Best Local Similarity: 90.30% Mismatches: 17  
Query Match: 65.68% Indels: 3  
DB: 1 Gaps: 1

US-09-674-716B-18 (1-1335) x G4HU (1-327)

QY 343 GCCTCCACCAAGGGCCCATCGTCTTCCCTCCGACCCCTCCACAGACCACTCTGGG 402  
Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20  
QY 403 GGACACGCGCCCTCGGCTCCCTGGTCAAGGACTACTTCCCGAAACCGGTGACGGTGTG 462  
Db 21 SerThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
QY 463 TGGAACTCAGGGCCCTGACAGGGCGTGCACACCTTCCCGGCTGCTCCACAGTCTCA 522  
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
QY 523 GGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAGACC 582  
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrLysThr 80  
QY 583 TACATCTGCAACGTGAATCAAGCCCAAGCAACCAAGGTGGACAGAAAGTGGAGCCC 642  
Db 81 TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLysArgValGluSer 100  
QY 643 AAATCTTGTGACAAAACACTCACATGCCACCGTCCAGCAGCTGAACCTCGCGGGGCA 702  
Db 101 Lys-----TyrGlyProProCysProSerCysProAlaProGluPheLeuGlyGly 117  
QY 703 CGCTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 762  
Db 118 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 137  
QY 763 GAGTTCATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 822  
Db 138 GluValThrCysValValAspValSerGlnGluAspProGluValGlnPheAsnTrp 157  
QY 823 TACGTGGACGGCGTGGAGGTGCATATGCCAAGCAAAAGCCCGGAGGAGGACGATACAC 882  
Db 158 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnPheAsn 177

Qy	883	AGCAGTACCGTGTGGTCAGCGTCTCACCGTCTGTGCACCAGGACTGGCTGAATGCAAG	942
Db	178	SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys	197
Qy	943	GAGTACAGTGCAGGTCCTCAACAAAGCCCTCCACGCCCCATCGAGAAACCATCTCC	1002
Db	198	GluTyrLysCysLysValSerAsnLysGlyLeuProSerSerLeuGluYsThrIleSer	217
Qy	1003	AAAGCCAAAGCGCACGCCCGAGAACACACAGGTGTACACCTGTGCCCTCCCGGATGAG	1062
Db	218	LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerGlnGluGlu	237
Qy	1063	CTGACCAAGAACAGGTCAGCCTGACCTGCTGGTCAAGGCTCTATCCAGCGACATC	1122
Db	238	MetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle	257
Qy	1123	GCCTGTGAGTGGGAGACCAATGGCGACCCGGAGAACAACTACAAGACACCGCTCCCGTG	1182
Db	258	AlaValGluTrpGluSerAsnGlyGlnProGluAsnTyrLysThrThrProProVal	277
Qy	1183	CTGGACTCCACCGGCTCCTTCTCTACAGCAAGCTCACCGTGGAGACAGACAGGTGG	1242
Db	278	LeuAspSerAspGlySerPhePheLeuTyrSerArgLeuThrValAspLysSerArgTrp	297
Qy	1243	CAGCAGGGGAACGTTCTCTCATGTCCTCGTGATGATGAGGCTGTGCACCAACCACTACAG	1302
Db	298	GlnGluLysAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr	317
Qy	1303	CAGAAGAGCTCTCCCTGTCTCCGGGTAAA	1332
Db	318	GlnLysSerLeuSerLeuSerLeuGlyLys	327

## RESULT 6

monoclonal antibody 13-1 heavy chain - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
C/Accession: PC4436  
R/Axashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A/Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin  
A/Reference number: JC5810; MUID:98063277; PMID:9398605  
A/Accession: PC4436  
A/Molecule type: protein  
A/Residues: 1-444 <AKA>  
C/Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
F/251-320/Domain: immunoglobulin homology <IMM>  
F/22/Disulfide bonds: interchain (to 98) #status Predicted  
F/99/Disulfide bonds: interchain (to 109) #status Predicted

Alignment Scores:	1.69e-78	Length:	444
Pred. No.:	1563.00	Matches:	288
Score:	78.76%	Conservative:	68
Percent Similarity:	63.72%	Mismatches:	80
Best Local Similarity:	64.99%	Indels:	16
Query Match:		Gaps:	6
DB:	2		

US-09-674-716B-18 (1-1335) x PC4436 (1-444)

1	GAGGTGACGCTGGTGA	CTCGGGAGAGCCTGTG	TAAAGCCCGGGGGT	CCCTTAGACTC	60
1	GluValGln**ValGlu	ThrGlyGlyLeuValArg	ProGlyAsnSerLeu	LysLeu	20
61	TCTGTGCAGCTAGCG	ATTCACTTTCAGTGG	CTACTCGGATGCTCT	CGGTCCGCCAGGCT	120
21	SerCysLeuThr-Ser	GlyPheThrPheSer	AsnTyrArgMetHis	TrpLeuAsnGlnPro	40
121	CCAGGGAAGGGGCT	CGAGTGGGTTCCTCA	AATTAGATGAAATCT	GTGATAATTATGCAACA	180
41	ProGlyLysArgLeu	GluTrpIlealaVal	lleThrValLysSerAsp	AsnTyrGlyIle	60

QY 1237 AGGTGGCAGCGGGAGAGCTCTCTCAGCTCCCTGATGCTGATGAGGCTTGACACACAC 1296  
 Db 413 AsnTrpGluAlaGlyAsnThrPheThrCysSerValLeuHisGluGlyLeuHisAsnHis 432  
 QY 1297 TACACGACAGAGAGCTCTCCTCTCTCCGGGTAAA 1332  
 Db 433 HisThrGluLysSerLeuSerHisSerProGlyLys 444

RESULT 7  
 S22080  
 Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine  
 N:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text\_change 23-Jul-1999  
 C:Accession: S22080; S06610; A31303  
 R:Sanders, P.G.  
 submitted to the EMBL Data Library, November 1991  
 A:Reference number: S22080  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-470 <SAN>  
 A:Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440  
 R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
 Mol. Immunol. 26, 841-850, 1989  
 A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2  
 A:Reference number: S06610; MUID:90097956; PMID:2513487  
 A:Accession: S06610  
 A:Molecule type: DNA  
 A:Residues: 142-470 <SYM>  
 A:Cross-references: EMBL:X16701  
 A:Note: the sequence was determined from the germline gene  
 C:Genetics:  
 A:Gene: IG CH gamma-1  
 A:Introns: 98/1; 111/1; 221/1  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
 F:161-225/Domain: immunoglobulin homology <IMW>  
 F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
 Pred. No.: 2,45e-72 Length: 470  
 Score: 1450.50 Matches: 280  
 Percent Similarity: 73.52% Conservative: 56  
 Best Local Similarity: 61.27% Mismatches: 102  
 Query Match: 60.31% Indels: 19  
 DB: 2 Gaps: 6

US-09-674-716B-18 (1-1335) x S22080 (1-470)

QY 1 GAGGTGCAGCTGGTGGAGCTCTGGGGAGGCTTGTAAGCCCGGGGGTCCCTTAGACTC 60  
 Db 20 GlnValGlnLeuArgGluSerGlyProSerLeuValLysProSerGlnThrLeuSerLeu 39  
 QY 61 TCCTGTGAGCTAGCGGATTCATCTTCAGTGCTACTGATGCTCTGGTGGCGGAGCT 120  
 Db 40 ThrCysThrValSerGlyPheSerLeuSerSerValAlaLeuThrTrpValArgGlnAla 59  
 QY 121 CCAGGAGAGGGCTCGAGTGGGTTCGTAATAGATTGAAATCTGATAATTATGCAACA 180  
 Db 60 ProGlyLysAlaLeuGluTrpValGlyGlyLe-----ThrSerGlyGlyThrThr 76  
 QY 181 CATTTAGCGGACTGTGAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240  
 Db 77 TyrTyrAsnProAlaLeuLysSerArgLeuSerIleThrLysGluAsnSerLysSerGln 96  
 QY 241 CNGTATCTGCAATGAACAGCTGAAACCGAGGACACAGCGGTCTATTACTGTACAGAT 300  
 Db 97 ValSerLeuSerValSerSerValThrProGluAspThrAlaThrTyrTyrCysAlaArg 116  
 QY 301 TTCATA-----GACTGGGGCCAGGACACTA 327  
 Db 117 SerThrTyrGlyGluValGlyAspGlyAlaIleAlaAspAlaTrpGlyGlnGlyLeuLeu 136

QY 328 GTCACCGCTCTCTCAGCTCTCCACCAAGGGCCCATCGGTCTTCCCTCTGCACACCTCTCC 387  
 Db 137 ValThrValSerSerAlaSerThrThrAlaProLysValTyrProLeuSerSerCysCys 156  
 QY 388 AAGAGCAGCTCTGGGGGCACAGCGGCCCTGGCTGCTGCTCAAGGACACTTCCCGCAA 447  
 Db 157 GlyAspLysSerSerSerThrValThrLeuGlyCysLeuValSerSerTyrMetProGlu 176  
 QY 448 CCGGTGACGGTGTGCGGAACCTCAGCGGCCCTGACAGCGGGGTGACACCTTCCCGGT 507  
 Db 177 ProValThrValThrTrpAsnSerGlyAlaLeuLysSerGlyValHisThrPheProAla 196  
 QY 508 GTCCTACAGTCTCAGGACTCTACCTCCCTCAGCAGGTGTGTCAGCGTCCCTCCAGCAGC 567  
 Db 197 ValLeuGlnSerSerGlyLeuTyrSerLeuSerSerMetValThrValProGlySerThr 216  
 QY 568 TTGGGCACCCAGACCTACATCTGCAACGTGAATCAACAGCCCAAGCAACCAAGGTGGAC 627  
 Db 217 SerGly---GlnThrPheThrCysAsnValAlaHisProAlaSerSerThrLysValAsp 235  
 QY 628 AAGAAAGTGGAGCCCAAAATCTGTGACAAACTCACACATGCCACCGTCCCGGCGCACCT 687  
 Db 236 LysAlaValAspPro---ThrCys---LysProSerProCysAspCysCysProPro 253  
 QY 688 GAACTCGCGGGGCACCGCTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 747  
 Db 254 GluLeuProGlyGlyProSerValPheIlePheProProLysProLysAspThrLeuThr 273  
 QY 748 ATCTCCGGACCCCTGAGGTACATCGCTGGTGGTGGAGCTGAGCCACCAAGACCTCTGAG 807  
 Db 274 IleSerGlyThrProGluValThrCysValValValAspValGlyHisAspAspProGlu 293  
 QY 808 GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGTGCATAATGCCAAGCAAAAGCGCGG 867  
 Db 294 ValLysPheSerTrpPheValAspValGluValAsnThrAlaThrThrLysProArg 313  
 QY 868 GAGGACAGTACAAACAGACGCTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 927  
 Db 314 GluGluGlnPheAsnSerThrTyrArgValValSerAlaLeuArgIleGlnHisGlnAsp 333  
 QY 928 TGGCTGAATGGCAAGAGTACAGTCAAGGTCTCCAAAGAGCCCTCCCGAGCCCGCATC 987  
 Db 334 TrpThrGlyGlyLysGluPheLysCysLysValHisAsnGluGlyLeuProAlaProIle 353  
 QY 988 GAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCCACAGGTGTACACCTGCCC 1047  
 Db 354 ValArgThrIleSerArgThrLysGlyProAlaArgGluProGlnValTyrValLeuAla 373  
 QY 1048 CMTCCCGGATGAGTGCACCAAGACAGGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1107  
 Db 374 ProProGlnGluGluLeuSerLysSerThrValSerLeuThrCysMetValThrSerPhe 393  
 QY 1108 TATCCAGCAGCATCGCGTGGAGTGGAGCAATGGGCGAGCGG-----GAGAACAA 1161  
 Db 394 TyrProAspTyrIleAlaValGluTrpGlnArgAsnGlyGlnProGluSerGluAspLys 413  
 QY 1162 TACAAGACCAAGCTCCCGTGGCTGAGCTCGAGCGGTCTCTCTCTCTCTCTCTCTCTCT 1221  
 Db 414 TyrGlyThrThrProGlnLeuAspAlaAspSerSerTyrPheLeuTyrSerLysLeu 433  
 QY 1222 ACCTGGACCAAGAGCAGGTGCGCAGCGAGGAAAGCTCTTCATGCTCCGCTGATGCTGAG 1281  
 Db 434 ArgValAspArgAsnSerTrpGlnGluLysThrThrCysValValMetHisGlu 453  
 QY 1282 GCTCTGCACAAACCATACACGACAGAGAGCTCTCCCTGTCTCCGGGTAAA 1332  
 Db 454 AlaLeuHisAsnHisTyrThrGlnLysSerThrSerLysSerAlaGlyLys 470

RESULT 8  
 S69339  
 Ig heavy chain V region precursor - human  
 C:Species: Homo sapiens (man)

C; Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text\_change 01-Dec-2000  
C; Accession: S69339; S72664  
R; Khamlichi, A.A.; Aconturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition  
A; Reference number: S69339; MUID:95263687; PMID:7744049

Alignment Scores:		
Pred. No.:	3,15e-71	Length:
Score:	1430.50	Matches:
Percent Similarity:	66.67%	Mismatches:
Best Local Similarity:	61.84%	Gaps:
Query Match:	59.48%	Indels:
DB:	2	4

US-09-674-716B-18 (1-1335) x S69339 (1-374)

1	QY	1	GAGGTGACAGCTGGTGGAGCTCTGGGGAGAGCTTGTAAGAAGCCCGGGGGTCCCTTAGACTC	60
20	Db	20	GINIIeThrLeuLysGluSerGlyProThrLeuValLysProThrGlnThrLeuThrIleu	39
61	QY	61	TCCTGTGTGAGCTAGCGGATTCACATTTC-----AGTGGCTACTGGATGTCCTGGGTCCGC	114
40	Db	40	ThrCysThrPheSerGlyPheSerLeuSerLysSerGlyValGlyValGlyTrpIleArg	59
115	QY	115	CAGGCTCCAGGAAGGGGCTCGAGTGGTTGCTGAATTAGATTGAAATCTCATATAT	174
60	Db	60	GlnProProGlyGlnAlaLeuGluTrpLeuAlaLeuIlePheTrpAspAspLys---	78
175	QY	175	GCACACACATTATCGGAGCTCTGTAAGGGGAATTACCATCTCAAGAGATGATTCAAA	234
79	Db	79	-----ArgTyrSerProSerLeuArgThrArgLeuThrIleThrLysAspThrSerLys	96
235	QY	235	TCTAGACTGTATCTGCAAAATCAACAGGCTGAAACCCGAGGACACAGCCGTGATTACTGT	294
97	Db	97	AsnGlnValValLeuThrMetThrAsnValAspProAlaaspThrAlaThrTyrTyrCys	116
295	QY	295	-----ACGATTTTCATGACTTGGGGCCAGGGGAACA	324
117	Db	117	GlyTyrSerValGluGlyTyrGlyGlnGlyTyrArgPheHisSerTrpGlyGlnGlyThr	136
325	QY	325	CTAGTCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCTCCGGCACCCCTCC	384
137	Db	137	LeuValThrValSerSer-----	142
385	QY	385	TCCAAGAGACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGACTACTTCCCC	444
142	Db	142	-----	142
445	QY	445	GAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTCAGCACGGCGGTGCACACCTTCCGG	504
142	Db	142	-----	142
505	QY	505	GCTGTCTACAGTCTCTCAGGACTCTACTCTCCTCAGCAGCGTGTGTGACCGTGCCTCCAGC	564
142	Db	142	-----	142
565	QY	565	AGCTTGGGCAACCCAGACCTACATCTGCAACGTGAATCAAGGCCACAGCAACCAAGGTG	624

[illegible]

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RESULT 9
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Rudencel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

```

Alignment Scores:	
Pred. No.:	1.3e-70
Score:	1419.00
Percent Similarity:	74.45%
Best Local Similarity:	59.25%
Length:	469
Matches:	269
Conservative:	69
Mismatches:	102



Query Match:	59.00%	Indels:	14
DB:	2	Gaps:	6
US-09-674-716B-18 (1-1335) x S37483 (1-469)			
QY	1	GAGGTGACGTGGTGGAGTCTGGGGAGGCCTTGTTAAGCCCGGGGGTCCTTAGACTC	60
Db	20	GlInleGlnLeuGlnSerGlyProGluLeuVallysProGlyAlaSerValysIle	39
QY	61	TCTGTGCAGTAGCGGATTCACATTTCAGTGCTACTGGATGTCCTGGGTCCGCCAGGCT	120
Db	40	SerCysLysAlaSerGlyTyThrPheThrAspTyTrileAsnTpVallysGlnLys	59
QY	121	CCAGGGAAGGGCTCGAGTGGGTTCGTGAATTAGATTGAATCTGATAATTATGCACA	180
Db	60	ProGlyGlnGlyLeuLysTrpIleGlyTrpIleTyProAlaSerGlyAsn-----Thr	77
QY	181	CATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATCAAATACTAGA	240
Db	78	LysTyRasnGluAenPheLysGlyLysAlaThrLeuThrValAspThrSerSerSerTh	97
QY	241	CTGTATCTGAAATGAACAGCTGAAACCCAGAGACACAGCCGTGTATTACTGT-----	294
Db	98	AlaTyMetGlnLeuSerSerLeuThrSerGluAspThrAlaValTyPheCysAlaArg	117
QY	295	-----ACAGATTTTCATAGAC--TGGGGCCAGGAAACAACACTAGTCACCGTC	336
Db	118	AlaMetGlyAlaThrAlaThrLeuLeuAspTyTrpGlyGlnGlyThrThrLeuThrVal	137
QY	337	TCTTCAGCCTTCACAAAGGCCCATCGGTCTTCCCCTTGGCACCTCTCCAAGAGCACC	396
Db	138	SerSerAlaLysThrThrAlaProSerValTyProLeuAlaProValCysGlyAspThr	157
QY	397	TCTGGGGCACAGGGCCCTGGCTGCTGTGCAAGNACTACTTCCCGRACCCGTGACG	456
Db	158	ThrGlySerServalThrLeuGlyCysLeuVallysGlyTyPheProgluProvalThr	177
QY	457	GTGTCGTGGAACTCAGGCGCCCTCACCAGCGCGCTGCACACTTCCCGCTGTCTCAG	516
Db	178	LeuThrTrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGln	197
QY	517	TCCTCAGACCTACTCCTCCTCAGACGCTGTGTACCGTCGCCCTCCAGCAGCTTGGGACC	576
Db	198	SerAsp---LeuTyThrLeuSerSerServalThrValThrValThrSerSerThrTrpSer	216
QY	577	CAGACCTACATCTCAACGTCAATCACAGGCCAGCACACCAAGTGGACAGAAGATGTG	636
Db	217	GlnSerlleThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysIle	236
QY	637	GAGCCCCAAATCTGTGACAAAACCTCACATGCCACC-----TGCCCCAGCACTGAA	690
Db	237	GluProArgGly---ProThrIleLysProCysProProCysLysCysProAlaProAsn	255
QY	691	CTCGGGGGGACCGTCACTCTTCTCTTCCCCCAAAACCCAGGACACCTCATGATC	750
Db	256	LeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeuMetIle	275
QY	751	TCCCGGACCCCTGAGGTCACATGCGTGTGTGGACGTGAGCCACGACAGACCTCAGGTC	810
Db	276	SerLeuSerProIleValThrCysValValValAspValSerGluAspAspProaspVal	295
QY	811	AAGTTCAACTGTGACGTGGACGCGTGTGAGGTGCATATGCCAACAAAGCCCGGGAG	870
Db	296	GlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArg	315
QY	871	GAGCAGTACAACAGCACGTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	930
Db	316	GluAspTyRasnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrp	335
QY	931	CTGAATGCAAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAG	990
Db	336	MetSerGlyLysGluPhelysCysLysValAsnAsnLysAspLeuProAlaProIleGlu	355

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Db      115 ValAspTyrAspSerSerHisAlaPheAlaTyrAlaSerTyrAspPhe-----TrpGly 132
QY      316 CAGGAACTAGTACCGTCTCTCAGCCTCCACCAAGGGCCCATCGCTCTTCCCGCTG 375
Db      133 ProGlyLeuLeuLeuSerValLeuSerAlaSerThrThrProProlysValTyrProLeu 152
QY      376 GCACCCCTCTCCAGAGACCTCTGGGGCCACAGCGCCCTGGCTGCTGTCTCAAGAC 435
Db      153 ThrSerCysCysGlyAspThrSerSerSerIleValThrLeuGlyCysLeuValSerSer 172
QY      436 TACTTCCCGCAACCGGTGCGTGTCTGGAACCTCAGCGCCCTCACCAGCGCGCTGCAC 495
Db      173 TyrMetProGluProValThrTrpAsnSerGlyAlaLeuThrSerGlyValHis 192
QY      496 ACCTTCCCGCTCTCAGTACCTCAGTCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTG 555
Db      193 ThrPheProAlaIleLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrVal 212
QY      556 CCTCCAGCAGCTTGGCCACCCAGACCTACATCTGCAACGTCAATCAACAAGCCCAAGCAAC 615
Db      213 ProAlaSerThrSerGlyAlaGlnThrPheIleCysAsnValAlaHisProAlaSerSer 232
QY      616 ACAAGGTGACAGAAAGTGGAGCCCAAAATCTGTGACAAACTCACACATGCCCAACG 675
Db      233 ThrLysValAspLysArgValGluProGlyCysProAspProCysLysHisCys---Arg 251
QY      676 TGCCAGCACCTGAACCTCGCGGGGACCGCTCAGTCTCTCTTCCCGCCCAAAACCCCAAG 735
Db      252 CysProProProGluLeuProGlyGlyProSerValPheIlePheProProlysProlys 271
QY      736 GACACCTCATGATCTCCCGGACCCCTCAGGTGACATCGTGTGGTGGTGGAGCTGAGCCAC 795
Db      272 AspThrLeuThrIleSerGlyThrProGluValThrCysValValValAspValGlyGln 291
QY      796 GAAGACCTGAGTCAAGTCAACTGGTACGTGGAGCGCGTGGAGTGCATAATGCCAAG 855
Db      292 AspAspProGluValGlnPheSerTrpPheValAspAsnValGluValArgThrAlaArg 311
QY      856 ACAAGCCCGGAGAGCAGTACACAGCAGTACCTGCTGTGGTGGTGGTGGTGGTGGTGGTGG 915
Db      312 ThrLysProArgGluGlnPheAsnSerThrPheArgValValSerAlaLeuProIle 331
QY      916 CTGCACCGAGTGGTGAATGGAGAGTACAGTCAAGTCAAGTCTCCAAAGCCCGCTC 975
Db      332 GlnHisGlnAspTrpThrGlyGlyLysGluPheLysCysLysValHisAsnGluAlaLeu 351
QY      976 CCAGCCCGCCATCGAAGAACCATCTCCAAAGCCAAAGCCGAGCCCGGAGACACCAAGTG 1035
Db      352 ProAlaProIleValArgThrIleSerArgThrLysGlyGlnAlaArgGluProGlnVal 371
QY      1036 TACACCTGCCCCATCCCGGATGAGTGCACCAAGACCAAGTCAAGTCAAGTCAAGTCAAGT 1095
Db      372 TyrValLeuAlaProGlnGluLeuSerLysSerThrLeuSerValThrCysLeu 391
QY      1096 GTCAAAGGCTTCTATCCAGACATCCCGTGGAGTGGAGGAGCAATGGGACCGC--- 1152
Db      392 ValThrGlyPheTyrProAspTyrIleAlaValGluTrpGlnLysAsnGlyGlnProGlu 411
QY      1153 ---GAGAACAACTACAGACCAACCGCTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1209
Db      412 SerGluAspLysTyrGlyThrThrThrSerGlnLeuAspAlaAspGlySerTyrPheLeu 431
QY      1210 TACACCAAGTCCACGTGACAGAGCAGTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1269
Db      432 TyrSerArgLeuArgValAspLysAsnSerTrpGlnGluGlyAspThrTyrAlaCysVal 451
QY      1270 GTGATGATAGGCTCTCACAAACCACTACACGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1329
Db      452 ValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerIleSerLysProGlyGly 471
QY      1330 AAA 1332

```

```

Db      472 Lys 472
RESULT 11
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bit
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446<KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C3 region <CH3>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:237/binding site: carboxylate (Asn) (covalent) #status experimental
Alignment Scores:
Pred. No.: 1 35e-69 Length: 446
Score: 1400.50 Matches: 267
Percent Similarity: 73.89% Conservative: 67
Best Local Similarity: 59.07% Mismatches: 103
Query Match: 58.23% Indels: 15
DB: 2 Gaps: 6
US-09-674-716B-18 (1-1335) x S40295 (1-446)

```

```

QY      1 GAGTGCAGCTGTGGAGTCTGGGGAGCGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db      1 GlnIleGlnLeuGlnSerGlyProGluLeuValArgProGlyAlaSerValLysile 20
QY      61 TCCTGTGACGTAGCGGATTCATCTTCAGTGTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db      21 SerCysLysAlaSerGlyTyrThrPheThrAspTyrTyrIleHisTrpValLysGlnArg 40
QY      121 CCAGGAAAGGGCTCGAGTGGTGTCTGCTGAAATAGATTGAAATCTGATAATTATGCAACA 180
Db      41 ProGlyGluGlyLeuGluTrpIleGlyTrpIleTyrProGlySerGlyAsn-----Thr 58
QY      181 CATTATGCCGAGTCTGTGAGGGGAAATTCACCATCTCAAGAGATGATTCAAAAATCTAGA 240
Db      59 LysTyrAsnGlnLysPheLysGlyLysAlaThrLeuThrValAspThrSerSerThr 78
QY      241 CTGTATCTCAAAATGAACCGCTGAAACCCAGGACACAGCCGCTGTATTACTGTGTACA--- 297
Db      79 AlaTyrMetGlnLeuSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArg 98
QY      298 -----CATTTTCATAGCTGGGCGCAGGAGAACACTAGTACCGCTCTCC 339
Db      99 GlyGlyLysPheAlaMetAspTyr-----TrpGlyGlnGlyThrSerValThrValSer 116
QY      340 TCAGCCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCCTCTCCCAAGAGCACCTCT 399
Db      117 SerAlaLysThrThrAlaProSerValTyrProLeuAlaProValCysGlyAspThrThr 136
QY      400 GGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGGACCGGTGACGGTG 459

```

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-474 <F15>  
A:Cross-references: ENBL:X67210; NID:954826; PIDN:CAA47649.1; PID:G54827  
A:Ri:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Horjo, T.  
Nature 283, 786-789, 1980  
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from ne  
A:Reference number: A02157; MUID:80120716; PMID:6766534  
A:Contents: a allele  
A:Accession: A02157  
A:Molecule type: DNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <YAM>  
A:Cross-references: GB:J00461  
A:Note: the sequence was determined from the germline gene  
Ri:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979  
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heav  
A:Reference number: A26235; MUID:80081501; PMID:117548  
A:Contents: MPC 11  
A:Accession: A26235  
A:Molecule type: mRNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>  
A:Note: Lys-474 is probably removed posttranslationally  
Ri:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob  
A:Reference number: A26232; MUID:80081502; PMID:117549  
A:Accession: A26232  
A:Molecule type: DNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>  
Ri:Ollo, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma  
A:Reference number: A26233; MUID:82173203; PMID:6803173  
A:Contents: b allele  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>  
A:Cross-references: GB:J00461  
A:Ri:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi  
J. Biol. Chem. 269, 12345-12350, 1994  
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A:Reference number: A33598; MUID:94216359; PMID:7512967  
A:Accession: A33598  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 234-251 <KIM>  
C:Comment: The a allele sequence is shown.  
C:Genetics:  
A:Introns: 138/1; 236/1; 258/1; 368/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into lar  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul  
F:157-222/Domain: immunoglobulin homology <IM1>  
F:236-257/Region: hinge  
F:281-350/Domain: immunoglobulin homology <IM2>  
F:387-454/Domain: immunoglobulin homology <IM3>  
F:152/Disulfide bonds: interchain (to light chain) #status predicted  
F:164-220, 288-394-452/Disulfide bonds: #status predicted  
F:247, 250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
Pred. No.: 1.83e-67 Length: 474  
Score: 1361.50 Matches: 259  
Percent Similarity: 71.33% Conservative: 67  
Best Local Similarity: 56.67% Mismatches: 116  
Query Match: 56.61% Indels: 15  
DB: 1 Gaps: 4

US-09-674-716B-18 (1-1335) x G2MS11 (1-474)

US-09-674-716B-18 (1-1335) x G2MS11 (1-474)

[illegible]

Db	378	LeuProProAlaGluGlnLeuSerArgLysAspValSerLeuThrCysLeuVal	397
Qy	1102	GGCTTCATCCAGCGACATCGCGGTGGAGTGGGAGCAATGGCAGCCGGAGAACAC	1161
Db	398	GlyPheAsnProGlyAspIleSerValGluTrpThrSerAsnGlyHisThrGluGluAsn	417
Qy	1162	TACAAGACCAAGCGCTCCCGTGTGGACTCGAGCGTCTCTTCTCTACACAAGCTC	1221
Db	418	TyrLysAspThrAlaProValLeuAspSerAspGlySerTyrPheIleTyrSerLysLeu	437
Qy	1222	ACGTGGACAGACAGGTGGCGACAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG	1281
Db	438	AsnMetLysThrSerLysTrpGluLysThrAspSerPheSerCysAsnValArgHisGlu	457
Qy	1282	GCTCTGCACAACCACTACACGACAGAGAGCGCTCTCCCTGTCCTCCGGGTAAA	1332
Db	458	GlyLeuLysAsnTyrTyrLeuLysLysThrIleSerArgSerProGlyLys	474
RESULT 13			
S01321			
Ig gamma-2b chain precursor - mouse			
C/Species: Mus musculus (house mouse)			
C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999			
C/Accession: S01321			
R/de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.			
Eur. J. Biochem. 176: 287-295, 1988			

RESULT 13

S01321  
Ig gamma-2b chain precursor - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1  
C/Accession: S01321  
R/de Waele, P.; Rye, V.; van de Voorde, A.; Molemans, F.; Piers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A/Title: Expression in non-lymphoid cells of mouse recombinant immunoglob  
A/Reference number: S01320; MUID:88329081; PMID:3138116  
A/Accession: S01321  
A/Molecule type: mRNA  
A/Residues: 1-475 <DEL>  
A/Cross-references: EMBL:X13188; NID:G51780; PID:CAA31580.1; PID:G51781  
A/Note: this sequence was determined from the differentiated gene  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F/1-19/Domain: signal sequence #status predicted <SIG>  
F/20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
F/159-223/Domain: immunoglobulin homology <IMW>

US-09-674-716B-18 (1-1335) x S01321 (1-475)

QY	1	GAGGTGAGCTGTGTGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC	60
Db	20	GlnValGlnLeuGlnSerGlyAlaGluLeuAlaArgProGlyAlaSerValValLeu	39
QY	61	TCCTGTGCAGCTAGCGGATTCACTTTTCAGTGGCTACTGGATGTCCTGGGTCGCCCAAGGCT	120
Db	40	SerCysLysAlaSerGlyTyrThrLeuThrSerTyrGlyLeuSerTrpValLysGlnArg	59
QY	121	CGAGGAAGGGCTCGAGTGGGTGCTGAAATAGATTTGAAATCTGATATATATGCAACA	180
Db	60	ThrGlyGlnGlyLeuGluTrpIleGlyGluIleTyrProGlySerGlyAsn-----Ser	77
QY	181	CATTATCGCGAGTCTGTGAAGGGGAAATTCCACCATCTCAAGAGATGATTCAAAATCTAGA	240
Db	78	TyrPheAsnGluLysPheLysGlyLysAlaThrLeuThrValAspLysSerSerSerThr	97
QY	241	CTGTATCTCGAATGAACAGCGCTGAAACCGAGGACACAGCCGTGTATTACTGTACA----	297
Db	98	AlaTyrLeuHisLeuSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaGly	117
QY	298	-----GATTTTCATAGCTGGGGCCAGGGAACACTAGTACCCGCTC	336
Db	118	ProArgGlnValGlyLeuLeuProPheGlyTyrTrpGlyGlnGlyThrLeuValThrAla	137

337 TCCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTGGACCCCTCTCTCAAGAGCACC 396  
|||||  
138 SerAlaAlaLysThrThrProSerValThrProLeuAlaProGlyCysGlyAspThr 157  
|||||  
397 TCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACG 456  
|||||  
158 ThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPheProGluSerValThr 177  
|||||  
457 GTGTCGTGAAGTCAAGCGCCCTGACCAAGCGGTGACACCTTCCCGGTGCTCTCAAG 516  
|||||  
178 ValThrTrpAsnSerGlySerLeuSerSerValHisThrPheProAlaLeuLeuGln 197  
|||||  
517 TCCTCAGACCTACTCTCCCTCAGCAGCGTGTGACCGTGCCTCCACGAGCTTGGGACC 576  
|||||  
198 ---SerGlyLeuTyrThrMetSerSerValThrValProSerSerThrTrpProSer 216  
|||||  
577 CAGACCTACATCTGCAAGTGAATCACAAGCCGACCAACCAAGGTGGACAAGAAAGTG 636  
|||||  
217 GlnThrValThrCysSerValAlaHisProAlaSerSerThrValAspLysLysLeu 236  
|||||  
637 GAGCCCAATCTGTGACAAACT---CACATGCCCCACCG----- 675  
|||||  
237 GluProSerGlyProThrSerThrIleAsnProCysProCysLysGluCysHisLys 256  
|||||  
676 TGCCCAAGCAGCTGAATCGCGGGGCACCGTCAGTCTTCTCTTCCCGCCCAAAACCCAAAG 735  
|||||  
257 CysProAlaProAsnLeuGluGlyGlyProSerValPheIlePheProProAsnIleLys 276  
|||||  
736 GACACCTCATGATCTCCGGACCCCTGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 795  
|||||  
277 AspValLeuMetIleSerLeuThrProLysValThrCysValValValAspValSerGlu 296  
|||||  
796 GAAGACCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 855  
|||||  
297 AspAspProAspValGlnIleSerTrpPheValAsnAsnValGluValLeuThrAlaGln 316  
|||||  
856 ACAAGCCCGGGAGGAGCAGTACACAGCAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTG 915  
|||||  
317 ThrGlnThrHisArgGluAspTyrAsnSerThrIleArgValValSerAlaLeuProIle 336  
|||||  
916 CTGACACGAGGCTGCTGAATGGCAGGAGTACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 975  
|||||  
337 GlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeu 356  
|||||  
976 CCAGCCCGCATCGAAGAACCATCTCCAAAGCCAAAGGGCAGCGCCCGAGAACCCAGAGTG 1035  
|||||  
357 ProAlaProIleGluArgThrIleSerLysIleLysGlyIleValArgAlaProGlnVal 376  
|||||  
1036 TACACCCCTGCCCATCCCGGATGAGTACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1095  
|||||  
377 TyrIleLeuSerProProGluGlnLeuSerArgLysAspValSerLeuThrCysLeu 396  
|||||  
1096 GTCAAAGGCTTCTATCCCAAGCAGATCCCGTGGAGTGGGAGCAATGGGCGAGCGGAG 1155  
|||||  
397 AlaValGlyPheSerProGluAspIleSerValGluTrpThrSerAsnGlyHisThrGlu 416  
|||||  
1156 AACAACTCAAGACCAAGCCTCCCGTGTGACTCCGACCGCTCTCTCTCTCTCTCTCTCTCTCT 1215  
|||||  
417 GluAsnTyrLysAspThrAlaProValLeuAspSerAspGlySerTyrPheIleTyrSer 436  
|||||  
1216 AGCTCACCCTGGACAAGCAGGTTGGCAGGAGGAGGACCTCTCTCTCTCTCTCTCTCTCTCTCT 1275  
|||||  
437 LysLeuAsnMetLysThrSerLysTrpGluLysThrAspSerPheSerCysAsnValArg 456  
|||||  
1276 CATGAGGCTCTGCACAAACCATACAGCAGGAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCT 1332  
|||||  
457 HisGluGlyLeuLysAsnTyrThrLeuLysLysThrIleSerArgSerProGlyLys 475  
|||||

## RESULT 14

147159

Ig gamma 2a chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IGH identified from the cDNA sequences of a si  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DBAJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03779; NID:G433123; PID:AAA52217.1; PID:G433124  
C:Genetics:  
A:Gene: IGG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin.homology  
F:133-202/Domain: immunoglobulin homology <IM>

## Alignment Scores:

Pred. No.:	7,966-62	Length:	328
Score:	1259.00	Matches:	233
Percent Similarity:	82.83%	Conservative:	42
Best Local Similarity:	70.18%	Mismatches:	51
Query Match:	52.35%	Indels:	6
DB:	2	Gaps:	3

US-09-674-716B-18 (1-1335) x I47159 (1-328)

QY 343 GCCTCCACCAAGGGCCCATCGGTCTTCCCTGGACCCCTCTCTCAAGAGCACCCTCTGGG 402  
|||||  
Db 1 AlaProLysThrAlaProSerValTyrProLeuAlaProCysSerArgAspThrSerGly 20  
|||||  
QY 403 GGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACGCTGTCG 462  
|||||  
Db 21 ProAsnValAlaLeuGlyCysLeuAlaSerSerTyrPheProGluProValThrValThr 40  
|||||  
QY 463 TGAACCTCAGGCGCCCTGACCGCGCGTGCACACCTTCCCGCTCTCTACAGTCTCTCA 522  
|||||  
Db 41 TrpAsnSerGlyAlaLeuSerSerGlyValHisThrPheProSerValLeuGlnProSer 60  
|||||  
QY 523 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACC 582  
|||||  
Db 61 GlyLeuTyrSerLeuSerSerMetValThrValProAlaSerSerLeuSerSerLysSer 80  
|||||  
QY 583 TACATCTGCAAGTGAATCACAAGCCCGACCAACCAAGTGGACAGCAAGAGTGGAGCCCC 642  
|||||  
Db 81 TyrThrCysAsnValAsnHisProAlaThrThrLysValAspLysArgValGlyThr 100  
|||||  
QY 643 AAATCTGTGACAAAACACTCACATGCCACCCCGTCCCGACCGCTGAACCTCGCGGGGCA 702  
|||||  
Db 101 LysThr-----LysProProCysProIleCysProAlaCysGluSerProGly--- 116  
|||||  
QY 703 CGGTCAAGTCTTCTCTCTTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 762  
|||||  
Db 117 ProSerValPheIlePheProLysProLysAspThrLeuMetIleSerArgThrPro 136  
|||||  
QY 763 GAGTCACATGCTGCTGCTGGTGGACGTCAGCCAGCAAGACCTGAGGTCAAGTTCAACTGG 822  
|||||  
Db 137 GlnValThrCysValValValAspValSerGlnGluAsnProGluValGlnPheSerTrp 156  
|||||  
QY 823 TACGTGACCGCTGAGGTGCATATGCAAGCAAAAGCCGCGGAGGAGGAGTCAAC 882  
|||||  
Db 157 TyrValAspGlyValGluValHisThrAlaGlnThrArgProLysGluGluGlnPheAsn 176  
|||||  
QY 883 AGCAGCTACCGTGTGCTCAGCTCCTCACCGTCTCCACCGAGGAGTGGCTGAATGCAAG 942  
|||||  
Db 177 SerThrTyrArgValValSerValLeuProIleGlnHisGlnAspTrpLeuAsnGlyLys 196  
|||||  
QY 943 GAGTCAAGTGCAGGTCTCCAAACAAAGCCCTCCCGAGCCCGCCATCGAGAAACCATCTCC 1002  
|||||  
Db 197 GluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleThrArgIleIleSer 216  
|||||  
QY 1003 AAGCCAAAGGAGCGCCCGAGAACACACAGTGTACACCTGCCCCCCTCCCGGATGAG 1062  
|||||  
Db 217 LysAlaLysGlyGlnThrArgGluProGlnValTyrThrLeuProHisAlaGluGlu 236  
|||||



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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:20:22 ; Search time 28.9645 Seconds  
(without alignments)  
4799.922 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 2405  
Sequence: 1 gaggtgcagctgtgagtc.....ccctgtctccgggtaataatga 1335

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool\_p/US09674716/runat\_30092004\_070257\_25855/app\_query.fasta\_1.3.64  
-DB=SwissProt 42 -OFMT=fastan -SUFFIX=rs -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=EPC -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09674716 -CGEN 1 1 82 @runat\_30092004\_070257\_25855 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1756	73.0	330	1	GC1_HUMAN
2	1608	66.9	326	1	GC2_HUMAN
3	1579.5	65.7	327	1	GC4_HUMAN
4	1219.5	50.7	323	1	GC_RABIT
5	1205.5	50.1	329	1	GC2_CAVO
6	1154	48.0	326	1	GC1_RAT
7	1153.5	48.0	290	1	GC3_HUMAN
8	1144	47.6	324	1	GC1_MOUSE
9	1139	47.4	333	1	GC1_MOUSE
10	1135.5	47.2	393	1	GC1_MOUSE
11	1130	47.0	329	1	GC3_MOUSE
12	1119	46.5	398	1	GC3_MOUSE
13	1115	46.4	330	1	GC3_MOUSE
14	1114.5	46.3	329	1	GCA_RAT
15	1114	46.3	322	1	GCA_RAT
16	1112.5	46.3	335	1	GCA_MOUSE
17	1110	46.2	399	1	GCA_MOUSE
18	1083	45.0	336	1	GCB_MOUSE
1	1756	73.0	330	1	GC1_HUMAN
2	1608	66.9	326	1	GC2_HUMAN
3	1579.5	65.7	327	1	GC4_HUMAN
4	1219.5	50.7	323	1	GC_RABIT
5	1205.5	50.1	329	1	GC2_CAVO
6	1154	48.0	326	1	GC1_RAT
7	1153.5	48.0	290	1	GC3_HUMAN
8	1144	47.6	324	1	GC1_MOUSE
9	1139	47.4	333	1	GC1_MOUSE
10	1135.5	47.2	393	1	GC1_MOUSE
11	1130	47.0	329	1	GC3_MOUSE
12	1119	46.5	398	1	GC3_MOUSE
13	1115	46.4	330	1	GC3_MOUSE
14	1114.5	46.3	329	1	GCA_RAT
15	1114	46.3	322	1	GCA_RAT
16	1112.5	46.3	335	1	GCA_MOUSE
17	1110	46.2	399	1	GCA_MOUSE
18	1083	45.0	336	1	GCB_MOUSE

## ALIGNMENTS

RESULT 1

ID	GCL_HUMAN	STANDARD	PRT	330 AA
AC	P01857			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	IG gamma-1 chain C region.			
GN	IGHG1			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=82274238; PubMed=6287432;			
RA	Edlison J.W.; Berson B.J.; Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RP	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A.; Rutishauser U.; Gall W.E.; Gottlieb P.D.;			
RA	Waxdal M.J.; Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RP	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U.; Cunningham B.A.; Bennett C.; Konigsberg W.H.;			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RP	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H.; Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). iii. The chymotryptic peptides of the H-chain, alignment of the tryptic			

P01867	mus musculus
P01801	mus musculus
P01854	homo sapien
P01799	mus musculus
P01855	rattus norv
P01796	mus musculus
P01802	mus musculus
P01797	mus musculus
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P01798	mus musculus
P06336	mus musculus
P01803	mus musculus
P01804	mus musculus
P01805	rattus norv
P01871	homo sapien
P03988	oryctolagus
P01872	mus musculus
P04221	oryctolagus
P01873	mus musculus
P20768	suncus muri
P01874	canis famil
P01876	mus musculus
P06337	mesocricetu
P01768	homo sapien
P01770	homo sapien
P01791	mus musculus
P01790	mus musculus

peptides and discussion of the complete structure.";  
 Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
 [5]  
 RN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
 RP MEDLINE=83289131; PubMed=6884994;  
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
 RX "Three-dimensional structure determination of antibodies. Primary  
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
 [6]  
 RN DISULFIDE BONDS.  
 RP MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RX "The covalent structure of a human gamma G-immunoglobulin. X.  
 RT Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 [7]  
 RN DISULFIDE BONDS.  
 RP MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RX "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie). I: Purification and  
 RL characterization of the protein, the L- and H-chains, the  
 RT cyanogen bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 [8]  
 RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RP MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RX "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RL aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the  
 CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the  
 CC G1M(3) marker and the G1M (non-1) markers.  
 CC -!- MISCELLANEOUS: Nie also differs in the amidation states of  
 CC 35, 116, 198, 269 and 272.  
 CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues  
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
 CC 268-272.  
 CC -!- MISCELLANEOUS: KOL also differs in the amidation states of  
 CC residues 198, 267 and 272.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; J00228; AAC82527.1; ALT\_INIT.  
 CC FIR; A83433; GHVU.  
 CC PDB; 1FC1; 15-JUL-92.  
 CC PDB; 1FC2; 15-JUL-92.  
 CC PDB; 1A77; 12-NOV-97.  
 CC PDB; 1D5B; 09-FEB-00.  
 CC PDB; 1D5I; 09-FEB-00.  
 CC PDB; 1D6V; 04-OCT-00.  
 CC PDB; 1DN2; 16-JUN-00.  
 CC PDB; 1E4K; 06-JUN-01.  
 CC PDB; 1FCC; 20-JUL-95.  
 CC PDB; 1H2H; 12-JUN-02.  
 CC PDB; 1H2I; 08-AUG-01.  
 CC PDB; 1IIS; 16-MAY-01.  
 CC PDB; 1IIX; 16-MAY-01.  
 CC PDB; 1L6X; 10-APR-02.  
 CC PDB; 2RCS; 12-NOV-97.  
 CC Genew; HGNC:5525; IGHG1.  
 CC MIM; 147100; -.  
 CC GO; GO:0005624; C:membrane fraction; NAS.  
 CC GO; GO:0003823; F:antigen binding; TAS.

GO; GO:0006955; P:immune response; NAS.  
 InterPro; IPR007110; Ig-like.  
 InterPro; IPR003597; Ig CL.  
 InterPro; IPR003006; Ig\_MHC.  
 Pfam; PF00047; Ig; 3.  
 SMART; SM00407; IGG1; 2.  
 PROSITE; PS00835; IG LIKE; 3.  
 PROSITE; PS00290; IG\_MHC; 2.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 3D-structure.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98 CHI.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 223 CH2.  
 FT DOMAIN 224 330 CH3.  
 FT DISULFID 27 83  
 FT DISULFID 103 103  
 FT DISULFID 109 109 INTERCHAIN (WITH LIGHT CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 144 204 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 250 308 N-LINKED (GLCNAC...).  
 FT CARBOHYD 180 180 REMOVED POST-TRANSLATIONALLY.  
 FT MOD\_RES 330 330 /FTID=VAR\_003886.  
 FT VARIANT 97 97 K -> R (IN G1M(3) MARKER).  
 FT VARIANT 239 239 D -> E (IN G1M(NON-1) MARKER).  
 FT VARIANT 241 241 L -> M (IN G1M(NON-1) MARKER).  
 FT VARIANT 241 241 /FTID=VAR\_003888.  
 FT STRAND 122 126  
 FT HELIX 130 134  
 FT TURN 136 137  
 FT STRAND 141 147  
 FT STRAND 157 162  
 FT TURN 163 164  
 FT STRAND 165 166  
 FT TURN 168 171  
 FT STRAND 176 179  
 FT TURN 180 181  
 FT STRAND 182 190  
 FT HELIX 193 197  
 FT TURN 198 199  
 FT STRAND 202 207  
 FT TURN 209 210  
 FT STRAND 215 219  
 FT STRAND 227 227  
 FT STRAND 230 234  
 FT HELIX 238 242  
 FT STRAND 245 256  
 FT STRAND 260 265  
 FT STRAND 270 270  
 FT STRAND 274 276  
 FT STRAND 280 281  
 FT TURN 283 284  
 FT STRAND 287 296  
 FT HELIX 297 301  
 FT TURN 302 303  
 FT STRAND 305 312  
 FT TURN 313 314  
 FT TURN 316 317  
 FT STRAND 320 325  
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Alignment Scores:  
 Pred. No.: 3,89e-100 Length: 330  
 Score: 1756.00 Matches: 328  
 Percent Similarity: 99.39% Conservative: 0  
 Best Local Similarity: 99.39% Mismatches: 2  
 Query Match: 73.01% Indels: 0  
 DB: 1 Gaps: 0

US-09-674-716B-18 (1-1335) x GCL\_HUMAN (1-330)



QY 343 GCCTCCACCAAGGGCCCATCGTCTTCCCGCTGGCACCTCTCTCCAAAGACACCTCTGGG 402  
 Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 20  
 QY 403 GGCACAGCGGCGCTGGCTGCTGCTCAGGACTACTTCCCGAACCGGTGACGGTCTCG 462  
 Db 21 GlyThrAlaLeuGlyCysLeuValLysAspThrPheProGluProValThrValSer 40  
 QY 463 TGGAACTCAGCGCGCTGACCAAGCGGCGTGCACACCTTCCCGGTCTCTACAGTCTCTCA 522  
 Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
 QY 523 GGACTTACTCTCCACAGAGCGGTGGTACCGTGGCTCCAGCAGCTGGGGACCCAGACC 582  
 Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80  
 QY 593 TACATCTCAACGCTGAATCAAGCCCAAGCAACCAAGGTGGCAAGAAAGTGGAGCC 642  
 Db 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100  
 QY 643 AAATCTTGTCACAAACTCACAATGCCACCGTGGCCAGCACCTGAATCGCGGGGCA 702  
 Db 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuGlyGly 120  
 QY 703 CCGTCAGTCTTCTCTCCCGCCCAACCCCAAGGACACCTCATGATCTCCCGGACCCCT 762  
 Db 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 140  
 QY 763 GAGTTCACATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 822  
 Db 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160  
 QY 823 TACGTGGAGCGGTGGAGTGCATATCCAGACACCAAGCCCGGGAGGACGACATCAAC 882  
 Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnThrAsn 180  
 QY 893 AGCAGTACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 942  
 Db 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200  
 QY 943 GAGTCAAGTCAAGTCTCAACAAAGCCCTCCAGCCCGCCCATCGAGAAACCATCTCC 1002  
 Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 220  
 QY 1003 AAAGCCAAAGGCGCCCGGAGAACACAGGTGTACACCTGCCCGCCATCCCGGATGAG 1062  
 Db 221 LysAlaLysGlyGlnProArgGluProGlnValThrLeuProProSerArgAspGlu 240  
 QY 1063 CTGACCAAGAACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1122  
 Db 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260  
 QY 1123 GCCGTGGAGTGGAGCAATGGCGGAGCGGAGCAACTACAGACCAAGCCCTCCCGTG 1182  
 Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 280  
 QY 1183 CTGGACTCCGCGCT 1242  
 Db 281 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300  
 QY 1243 CAGCAGGGGAAGTCTTCT 1302  
 Db 301 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 320  
 QY 1303 CAGAAGAGCT 1332  
 Db 321 GlnLysSerLeuSerLeuSerProGlyLys 330  
 RESULT 2  
 ID GC2\_HUMAN  
 AC P01859;  
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DN Ig gamma-2 chain C region.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 2-326 FROM N.A.  
 RA MEDLINE=82197521; PubMed=6804948;  
 RX Ellison J.W., Hood L.E.;  
 RT "Linkage and sequence homology of two human immunoglobulin gamma  
 heavy chain constant region genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
 RN [2]  
 RP SEQUENCE OF 88-115 FROM N.A.  
 RA TISSUE=Fetal liver;  
 RX MEDLINE=83001943; PubMed=6811139;  
 RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;  
 RT "Structure of human immunoglobulin gamma genes: implications for  
 evolution of a gene family.";  
 RL Cell 29:671-679(1982).  
 RN [3]  
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
 RA TISSUE=Fetal liver;  
 RX MEDLINE=84235992; PubMed=6329676;  
 RA Krawinkel U., Rabbitts T.H.;  
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
 genes.";  
 RL EMBO J. 1:403-407(1982).  
 RN [4]  
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
 RA MEDLINE=81007873; PubMed=6774042;  
 RA Wang A.-C., Tung E., Fudenberg H.H.;  
 RT "The primary structure of a human IgG2 heavy chain: genetic,  
 evolutionary, and functional implications.";  
 RL J. Immunol. 125:1048-1054(1980).  
 RN [5]  
 RP SEQUENCE OF 1-95 AND 132-325 (MYELOMA PROTEIN ZIE).  
 RA MEDLINE=80001357; PubMed=113060;  
 RA Connell G.E., Farr D.M., Hofmann T.;  
 RT "The amino acid sequences of the three heavy chain constant region  
 domains of a human IgG2 myeloma protein.";  
 RL Can. J. Biochem. 57:758-767(1979).  
 RN [6]  
 RP SEQUENCE OF 238-275 (ZIE).  
 RA MEDLINE=80114419; PubMed=118920;  
 RA Hofmann T., Farr D.M.;  
 RT "A note of the amino acid sequence of residues 381-391 of human  
 immunoglobulins gamma chains.";  
 RL Mol. Immunol. 16:923-925(1979).  
 RN [7]  
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
 RA Hofmann T., Farr D.M.;  
 RT Submitted (MAR-1980) to the PIR data bank.  
 RN [8]  
 RP SEQUENCE OF 1-121 (DOT).  
 RA MEDLINE=95255298; PubMed=7737190;  
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
 RT "Characterization of the two unique human anti-flavin monoclonal  
 immunoglobulins.";  
 RL Eur. J. Biochem. 228:886-893(1995).  
 RN [9]  
 RP DISULFIDE BONDS.  
 RA MEDLINE=72033500; PubMed=4940472;  
 RA Milstein C., Frangione B.;  
 RT "Disulfide bridges of the heavy chain of human immunoglobulin G2.";  
 RL Biochem. J. 121:217-225(1971).  
 RN [10]  
 RP DISULFIDE BONDS.  
 RA MEDLINE=69064124; PubMed=5782707;  
 RX

RA Frangione B., Milstein C., Pink J.R.L.;  
 RT "Structural studies of immunoglobulin G.";  
 RL Nature 221:145-148(1969).  
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 CC -----  
 DR EMBL; J00230; AAB59393.1; -.  
 DR PIR; A93906; G2HU.  
 DR HSP; P01857; 1FC1.  
 DR Genew; HGNC:5526; IGHG2.  
 DR MIM; 147110; -.  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding; TAS.  
 DR GO; GO:0005955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00407; IGH1; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1  
 FT DOMAIN 1 98  
 FT CH1.  
 FT HINGE.  
 FT DOMAIN 99 110  
 FT CH2.  
 FT DOMAIN 111 219  
 FT CH3.  
 FT DOMAIN 220 326  
 FT INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 14 14  
 FT DISULFID 27 83  
 FT INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 102 102  
 FT DISULFID 103 103  
 FT INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106  
 FT INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109  
 FT INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 140 200  
 FT DISULFID 246 304  
 FT SITE 156 156  
 FT SITE 156 156  
 FT MOD\_RES 326 326  
 FT VARIANT 60 60  
 FT AT OR NEAR THE COMPLEMENT-BINDING SITE.  
 FT REMOVED POST-TRANSLATIONALLY (PROBABLE).  
 FT S->A (IN MYELOMA PROTEINS TIL & ZIE).  
 FT /FTIG=VAR 003889.  
 FT C->S (IN REF. 3).  
 FT SQ SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

## Alignment Scores:

Pred. No.: 4,25e-91 Length: 326  
 Score: 1608.00 Matches: 302  
 Percent Similarity: 95.1% Conservative: 12  
 Best Local Similarity: 91.52% Mismatches: 12  
 Query Match: 66.86% Indels: 4  
 DB: 1 Gaps: 2

US-09-674-716B-18 (1-1335) x GC2\_HUMAN (1-326)

QY 343 GCCTCACCAGGGCCCAATCGTCTTCCCTGGACCTCTCTCAAGACACCTCTGGG 402  
 Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20  
 QY 403 GCACAGCGGCCCTGGCTGCTGCTCAAGACTACTTCCCGAACCGGTACAGGTGTCG 462  
 Db 21 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
 QY 463 TGGAACTCAGGGCCCTGACACAGCGGTGACACACTTCCCGGCTGTCTACAGTCTCA 522  
 Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
 QY 523 GGACTCTACTCCTCAGCAGCGTGTGACCTGCCCTCCAGCAGTGTGGGCACCCAGACC 582  
 Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGlyThrGlnThr 80

QY 583 TACATCTGCAACGTGAATCAACAGCCCGACCAACAGAGGTGGACAAAGAGTGGAGCCC 642  
 Db 81 TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLysThrValGluArg 100  
 QY 643 AAATCTTGTCACAAACTCACATGCGCCACCTGCGCCAGCACTGAATCTCGCGGGGCA 702  
 Db 101 LysCysCysValGlu-----CysProProCysProAlaProProValAlaGly--- 116  
 QY 703 CGGTGAGTCTTCTCTTCTCCCGCCCAACCAAGACACCTCTCATGATCTCCCGAGCCCT 762  
 Db 117 ProSerValPheLeuPheProLysProLysProLysAspThrLeuMetIleSerArgThrPro 136  
 QY 763 GAGTGCATGCGTGGTGGAGCGTGAGCCAGCAAGACCCCTGAGGTCAAGTTCACACTGG 822  
 Db 137 GluValThrCysValValValAspValSerHisGluAspProGluValGlnPheAsnTrp 156  
 QY 823 TAGCTGGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAC 882  
 Db 157 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnPheAsn 176  
 QY 883 AGCAGTACCGTGGTGGTGGAGCGTGGAGCGTGGAGCGTGGAGCGTGGAGCGTGGAG 942  
 Db 177 SerThrPheArgValValSerValLeuThrValValHisGlnAspTrpLeuAsnGlyLys 196  
 QY 943 GAGTACAAAGTGAAGTCTCCAAAGAGCCCTCCAGCGCCCGATCGAGAAACCATCTCC 1002  
 Db 197 GluTyrLysCysLysValSerAsnLysGlyLeuProAlaProIleGluLysThrIleSer 216  
 QY 1003 AAAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCGCCCGATCGCGGATGAG 1062  
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 QY 1063 CTGACCAAGAACACCGTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1122  
 Db 237 MetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 256  
 QY 1123 GCGTGGAGTGGAGCAATGGCAGCGGAGCAACAACTACAAAGACCGCTCCCGTGG 1182  
 Db 257 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAspTyrLysThrThrProMet 276  
 QY 1183 CTGAGTCTCGAGCGCTCTTCT 1242  
 Db 277 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 296  
 QY 1243 CAGCAGGGGAACGTCTTCT 1302  
 Db 297 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 316  
 QY 1303 CAGAAAGAGCT 1332  
 Db 317 GlnLysSerLeuSerLeuSerProGlyLys 326

## RESULT 3

GC4\_HUMAN

ID GC4 HUMAN

AC P01861;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE IG gamma-4 chain C region.

GN IGHG4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83157104; PubMed=6299662;

RA Ellison J.W., Buxbaum J.N., Hood L.E.;

RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";

RN DNA 1:11-18 (1981). [2]

RP SEQUENCE OF 1-30 AND 81-326.  
RX MEDLINE=70207560; PubMed=4192699;  
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;  
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the  
RL Biochem. J. 117:33-47(1970).  
CC -----  
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CC -----  
CC EMBL; K01316; AAB59394.1; ALT\_INIT.  
DR PIR; A90933; G4HU.  
DR PDB; 1ADO; 16-SEP-98.  
DR Genew; HGNC:5528; IGH4.  
DR MIM; 147130; ..  
DR GO; GO:0005624; C:membrane fraction; NAS.  
DR GO; GO:0003823; F:antigen binding; TAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF0047; IG\_3.  
DR SMART; SM00407; IGc1; 2.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.  
FT NON\_TER 1 98  
FT DOMAIN 1 98  
FT CH1.  
FT HINGE.  
FT DOMAIN 99 110  
FT DOMAIN 111 220  
FT DOMAIN 221 327  
FT CH3.  
FT INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 14 14  
FT DISULFID 27 83  
FT DISULFID 106 106  
FT DISULFID 109 109  
FT DISULFID 141 201  
FT DISULFID 247 305  
SQ SEQUENCE 327 AA; 35940 MW; 3EBD811EF208E7A CRC64;

Alignment Scores:  
Pred. No.: 2,348-89 Length: 327  
Score: 1579.50 Matches: 298  
Percent Similarity: 93.94% Conservative: 12  
Best Local Similarity: 90.30% Mismatches: 17  
Query Match: 65.68% Indels: 3  
DB: 1 Gaps: 1  
US-09-674-716B-18 (1-1335) x GC4\_HUMAN (1-327)  
QY 343 GCCTCACCAAGGGCCATCGCTTCCCTGGCACCTCTCCACAGAGACCTCTGGG 402  
Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20  
QY 403 GGCACAGCGCCCTGGGCTGCTGCTCAGGACTACTCCCGAACCGGTGACGGTGTG 462  
Db 21 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
QY 463 TGGAACTCAGCGCCCTGACACCGCGGTGACACCTTCCCGGCTGTCTACAGTCCTCA 522  
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
QY 523 GGACTCTACTCTCAGCAGCGGTGTGACCGGCTCCAGCAGGTGGGACCCAGACC 582  
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrLysThr 80  
QY 583 TACATCTGCAAGCTGAATCACAGCCAGCAACCAAGGTGGACAAAGAAAGTGGAGGCC 642  
Db 81 TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLysArgValGluSer 100

QY 643 AAATCTTGACAAAACCTCACACATGCCACCTGCCAGCACCTGAATCTCGGGGGGCA 702  
Db 101 Lys-----TyrGlyProProCysProSerCysProAlaProGluPheLeuGlyGly 117  
QY 703 CCGTCAGTCTTCTCTTCCCCCAAAACCCAGGACACCTCATGATCTCCCGAGCCCT 762  
Db 118 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 137  
QY 763 GAGTCCATGCTGCTGGTGGAGCTGAGCCACCAAGACCTCAGGTCAAGTTCAACTGG 822  
Db 138 GluValThrCysValValValAspValSerGlnGluAspProGluValGlnPheAsnTrp 157  
QY 823 TAGGTGACCGCTGAGGTGTCATATGCCAAGCAAAAGCCGGGAGGAGAGTACAAC 882  
Db 158 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnPheAsn 177  
QY 883 AGCAGGTACCGTGTGGTTCAGCTCCTCACCGTCTCCACAGGACTGGGTGAATGCCAAG 942  
Db 178 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 197  
QY 943 GAGTACAGTCAAGGTCTCCAAAGGCTCCCGAGCCCTCCAGCCCTCCAGAAACCATCTCC 1002  
Db 198 GluTyrLysCysLysValSerAsnLysGlyLeuProSerSerIleGluLysThrIleSer 217  
QY 1003 AAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACAGCTGCCCTCCCGATGATGAG 1062  
Db 218 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProSerGlnGluGlu 237  
QY 1063 CTACCAAGAACAGGTGACCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATC 1122  
Db 238 MetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 257  
QY 1123 GCGTGGAGTGGAGAGCAATGGGCGGAGCAACACTACAGACCCAGCTCCCGTG 1182  
Db 258 AlaValGluTrpGluSerAsnGlyGlnProGluAsnTyrLysThrThrProProVal 277  
QY 1183 CTGACTCCGACGCTCTCTTCTCTCTCAGCAAGCTCACCGTGGACAAAGAGCAGTGG 1242  
Db 278 LeuAspSerAspGlySerPhePheLeuTyrSerArgLeuThrValAspLysSerArgTrp 297  
QY 1243 CAGCAGGGGAACGTCTTCTCATGCTCGTGTGATGATGAGCTCTGCAACACCTACACG 1302  
Db 298 GlnGluGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 317  
QY 1303 CAGAAGAGCTCTCTCCGTCTCCGGGTAAA 1332  
Db 318 GlnLysSerLeuSerLeuSerLeuGlyLys 327  
RESULT 4  
GC\_RABIT STANDARD; PRT; 323 AA.  
AC P01870; 1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig gamma chain C region.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84030930; PubMed=6313520;  
RA Bernstein K.E., Alexander C.B., Mage R.G.;  
RT "Nucleotide sequence of a rabbit IGG heavy chain from the recombinant  
RT F-I haplotype.";  
RL Immunogenetics 18:387-397(1983).  
RN [2]  
RP SEQUENCE OF 1-128.  
RX MEDLINE=76135469; PubMed=1243651;  
RA Pratt D.M., Mole L.E.;  
RT "Sequence studies on the constant region of the Fd sections of rabbit

immunoglobulin G of different allotype.";  
 Biochem. J. 151:337-349(1975).  
 [3]  
 RP SEQUENCE OF 88-266 FROM N.A.  
 RX MEDLINE=8329917; PubMed=6193512;  
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
 RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma  
 RT heavy chain and identification of two genomic C gamma genes.";  
 Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
 [4]  
 RN SEQUENCE OF 132-161.  
 RP MEDLINE=70110015; PubMed=5461106;  
 RA Fructer R.G., Jackson S.A., Mole L.E., Porter R.R.;  
 RT "Sequence studies of the Fd section of the heavy chain of rabbit  
 RT immunoglobulin G".  
 Biochem. J. 116:249-259(1970).  
 [5]  
 RN SEQUENCE OF 129-131 AND 155-322.  
 RP Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
 RA (in) Killander J. (eds.);  
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,  
 Stockholm (1967).  
 CC -!- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker,  
 CC 104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15  
 CC markers and Ref.5 the E15 marker.  
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.  
 CC  
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 CC  
 CC  
 DR EMBL; M16426; AAA31289.1; --  
 DR FIR; A91749; GHRB.  
 DR HSP; P01857; 1FC1.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00407; Igc1; 2.  
 DR PROSITE; PS00835; IG-LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Repeat.  
 FT NON\_TER 1 1  
 FT DOMAIN 6 96 IG-LIKE 1.  
 FT DOMAIN 114 213 IG-LIKE 2.  
 FT DOMAIN 222 318 IG-LIKE 3.  
 FT VARIANT 104 104 T -> M (IN D11 MARKER).  
 FT VARIANT 185 185 T -> A (IN E15 MARKER).  
 FT CONFLICT 48 48 N -> E (IN REF. 2).  
 FT CONFLICT 71 71 V -> VPV (IN REF. 2).  
 FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).  
 FT CONFLICT 173 173 N -> D (IN REF. 5).  
 FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).  
 FT CONFLICT 201 201 N -> D (IN REF. 5).  
 FT CONFLICT 218 218 Q -> E (IN REF. 5).  
 FT CONFLICT 233 233 E -> Q (IN REF. 5).  
 FT CONFLICT 246 246 N -> D (IN REF. 5).  
 FT CONFLICT 256 256 E -> G (IN REF. 5).  
 FT CONFLICT 260 260 N -> D (IN REF. 5).  
 FT CONFLICT 266 266 N -> D (IN REF. 5).  
 FT CONFLICT 280 280 Y -> W (IN REF. 5).  
 FT CONFLICT 284 284 N -> S (IN REF. 5).  
 SQ SEQUENCE 323 AA; 35404 MW; 69E9AA118D579A8B CRC64;

## Alignment Scores:

Pred. No.: 2-28e-67 Length: 323  
 Score: 1219.50 Matches: 227  
 Percent Similarity: 79.82% Conservatives: 34  
 Best Local Similarity: 69.42% Mismatches: 59

Query Match: 50.71% Indels: 7  
 DB: 1 Gaps: 2  
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 QY 352 AAGGGCCATCGGTCTTCCCTGGCACCCCTCCCAAGAGCACCTCTCGGGGCACAGCG 411  
 DB 4 LysAlaProSerValPheProLeuAlaProCysCysGlyAspThrProSerThrVal 23  
 QY 412 GCCCTGGGCTGCTGTCAGGACTACTCCCGAACCCGGTACGGTCTCGGGAACCTCA 471  
 DB 24 ThrLeuGlyCysLeuValLysGlyThrLeuProGluProValThrValTrpAsnSer 43  
 QY 472 GGGCCCTGACCGCGCGTGACACCTCCCGGCTGTCTACAGTCCTCAGACTCTAC 531  
 DB 44 GlyThrLeuThrAsnGlyValArgThrPheProSerValArgGlnSerSerGlyLeuTyr 63  
 QY 532 TCCTCAGACGCTGTGTCACCGTCCCTCCAGAGCTTGGGCACCCAGACCTACATCTGC 591  
 DB 64 SerLeuSerSerValValSerValThrSerSerSer-----GlnProValThrCys 80  
 QY 592 AAGCTGAATCACAAGCCCGACCAAGGTGGACAGAAAGTGGAGCCCAATCTTGT 651  
 DB 81 AsnValAlaHisProAlaThrAsnThrLysValAspLysThrValAlaProSerThrCys 100  
 QY 652 GACAAACTCACACATGCCCGCCGTCGCCAGCACCTGAATCGCGGGGACCGTCAGTC 711  
 DB 101 SerLys-----ProThrCysProProGluLeuLeuGlyGlyProSerVal 116  
 QY 712 TTCTCTTCCCCCAAAACCCAGGACCTCATCTCCCGGACCCCTGAGGTACA 771  
 DB 117 PheIlePheProLysProLysAspThrLeuMetIleSerArgThrProGluValThr 136  
 QY 772 TGGTGTGTGTGACGTGAGCCAGACACCTCGAGGTCAAGTTCAACTGGTACGTGGAC 831  
 DB 137 CysValValValAspValSerGlnAspAspProGluValGlnPheThrTrpTyrIleAsn 156  
 QY 832 GGGGTGAGGTGATTAATGCCAAGACAAAGCCCGGAGAGAGAGTACACAGCAGTAC 891  
 DB 157 AsnGluGlnValArgThrAlaArgProProLeuArgGluGlnGlnPheAsnSerThrIle 176  
 QY 892 CGTGTGTGACGTCTCTCACCGCTCGCACAGACTGGCTGAATGGCAAGAGTACAAG 951  
 DB 177 ArgValValSerThrLeuProIleThrHisGlnAspTrpLeuArgGlyLysGluPheLys 196  
 QY 952 TGCAAGGTCTCCAACAAAGCCCTCCAGGCCCCCATCGAGAAACCATCTCCAAAGCCAA 1011  
 DB 197 CysLysValHisAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaArg 216  
 QY 1012 GGGCAGCCCCGAGACACACAGGTGTACACCTCCCTCCCGGATGAGTGCACCAAG 1071  
 DB 217 GlyGlnProLeuGluProLysValThrMetGlyProProArgGluGluLeuSerSer 236  
 QY 1072 AACGAGTCACTGACCTGCTGCTGGTCAAGGCTTCTATCCAGCAGCATCGCGGTGAG 1131  
 DB 237 ArgSerValSerLeuThrCysMetIleAsnGlyPheTy:ProSerAspIleSerValGlu 256  
 QY 1132 TGGGAGAGCAATGGCAGCGGAGAACACTACAAGACCCAGCTCCCGTGGGACTCC 1191  
 DB 257 TrpGluLysAsnGlyLysAlaGluAspAsnTyrLysThrProAlaValLeuAspSer 276  
 QY 1192 GACGCTCTCTTCTCTTACCAAGAGCTCACCGTGGACAAAGAGAGGTGGCAGCAGGGG 1251  
 DB 277 AspGlySerTyrPheLeuTyrAsnLysLeuSerValProThrSerGluTrpGlnArgGly 296  
 QY 1252 AAGCTCTTCTATGCTCCGCTGATGCTAGGCTCTGCACACACCTACAGCGAGAGAC 1311  
 DB 297 AspValPheThrCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSer 316  
 QY 1312 CTCTCCCTGTCTCCGGGTAAA 1332  
 DB 317 IleSerArgSerProGlyLys 323

RESULT 5  
GC2\_CAVPO STANDARD; PRT; 329 AA.  
AC P01862;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE I9 gamma-2 chain C region.  
OC Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RN SEQUENCE OF 1-3.  
RA Trischmann T.M.;  
RL Submitted (APR-1975) to the PIR data bank.  
RN [2]  
RN SEQUENCE OF 4-68.  
RX MEDLINE=71058471; PubMed=5538606;  
RA Birenstein B.K., Hussain Q.Z., Cebra J.J.;  
RT "Structure of heavy chain from strain 13 guinea pig  
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the  
RT half-cysteine joining heavy and light chains.";  
RL Biochemistry 10:18-25(1971).  
RN [3]  
RN SEQUENCE OF 69-133 AND 312-329.  
RX MEDLINE=71058486; PubMed=5538616;  
RA Turner K.J., Cebra J.J.;  
RT "Structure of heavy chain from strain 13 guinea pig  
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal  
RT and hinge region cyanogen bromide fragments.";  
RL Biochemistry 10:9-17(1971).  
RN [4]  
RN SEQUENCE OF 134-226.  
RX MEDLINE=75036072; PubMed=4429665;  
RA Tracey D.E., Cebra J.J.;  
RT "Primary structure of the CH2 homology region from guinea pig IgG2  
RT antibodies.";  
RL Biochemistry 13:4796-4803(1974).  
RN [5]  
RN SEQUENCE OF 227-311.  
RX MEDLINE=75036073; PubMed=4609467;  
RA Trischmann T.M., Cebra J.J.;  
RT "Primary structure of the CH3 homology region from guinea pig IgG2  
RT antibodies.";  
RL Biochemistry 13:4804-4811(1974).  
RN [6]  
RN DISULFIDE BONDS.  
RX MEDLINE=71058474; PubMed=4922544;  
RA Oliveira B., Lamm M.E.;  
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";  
RL Biochemistry 10:26-31(1971).  
CC -I- MISCELLANEOUS: This chain was isolated from pooled serum of strain  
CC 13 inbred guinea pigs.  
DR PIR; A94553; G2GP.  
DR HSSP; P01842; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; I9\_MHC.  
DR Pfam; PF00047; I9; 2.  
DR SMART; SM00407; Igcl; 2.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
FT NON\_TER 1 1  
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 28 79  
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 142 202  
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).  
FT DISULFID 248 308

SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;  
Alignment Scores:  
Pred. No.: 1,64e-66 Length: 329  
Score: 1205.50 Matches: 233  
Percent Similarity: 78.14% Conservative: 28  
Best Local Similarity: 69.76% Mismatches: 64  
Query Match: 50.12% Indels: 9  
DB: 1 Gaps: 4  
US-09-674-716B-18 (1-1335) x GC2\_CAVPO (1-329)  
Qy 340 TCAGCTCCACCAAGGGCCCATCGTCTTCCCTCGCACCCCTCTCCAGACACCTCT 399  
Db 1 SerAlaArgThrThrAlaProSerValPheProLeuAlaAlaSerCysValAspThrSer 20  
Qy 400 GGGGGCACAGCGCCCTGGCTGCTCAAGGACTTCTCCCGAACCGGTGACGGTG 459  
Db 21 GlySerMetMetThrLeuGlyCysLeuValLysGlyTyPheProGluProValThrVal 40  
Qy 460 TCGTGAACATCAGCGCCCTGACAGCGGGGTGCACACCTTCCCGCTCTCTACAGTCC 519  
Db 41 LysTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGln--- 59  
Qy 520 TCAGGACTCTACTCCCTCAGCAGCGGTGGTACCGTCCCTCCAGCAGCTGGGCACCCAG 579  
Db 60 SerGlyLeuTyTrSerLeuThrSerMetValThrValProSerSerGlnLysAlaThr--- 78  
Qy 580 ACCTATATCTGCAACGTCATCAAGCCAGCACACCAAGGTGGACAGAAAGTGGAG 639  
Db 79 -----CysAsnValAlaHisProAlaSerSerThrLysValAspLysThrValGlu 95  
Qy 640 CCCAATCTTGTGACAAAACCTAC-----ACATGCCACCGTGGCCAGCACCTGAATC 693  
Db 96 ProIleArgThrPro\*\*\*ProCysThrCysProLysCysProProGluAsn 115  
Qy 694 GCGGGCAGCCGTCAGTCTTCTCTTCCCTCCCGCCAAAACCAAGCACACCTCATGATCTCC 753  
Db 116 LeuGlyGlyProSerValPheIlePheProProLysProLysAspThrLeuMetIleSer 135  
Qy 754 CGGACCCCTGAGTCAATCGTGGTGGTGGAGCGTGAGCCACGACACCTCATGATCTCAAG 813  
Db 136 LeuThrProArgValThrCysValValValAspValSerGlnAsnGluProGluValGln 155  
Qy 814 TTCAACTGGTACGTGGAGCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 873  
Db 156 PheThrTrpPheValAspAsnLysProValGlyAsnAlaGluThrLysProArgValGlu 175  
Qy 874 CAGTACAACACAGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 933  
Db 176 GlnTyAsnThrThrPheArgValGluSerValLeuProIleGlnHisGlnAspTrpLeu 195  
Qy 934 AATGGCAGGAGTACAGTCAAGTCAAGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAA 993  
Db 196 ArgGlyLysGluPheLysCysLysValTyAsnLysAlaLeuProAlaProIleGluLys 215  
Qy 994 ACCATCTCCAAAGCCAAAGGGCAGCCCGCCAGAACACACAGGTGTACACCTGCCCCCATCC 1053  
Db 216 ThrIleSerLysThrLysGlyAlaProArgMetProAspValTyThrLeuProProSer 235  
Qy 1054 CGGATAGCTGACCAAGAACCCAGTGCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113  
Db 236 ArgAspGluLeuSerLysSerLysValSerValThrCysLeuIleIleAsnPhePhePro 255  
Qy 1114 AGGCACATCCGCTGGAGTGGAGAGCAATGGCAGCG-----GAGAACAACTACAAG 1167  
Db 256 AlaAspIleHisValGluTrpAlaSerAsnArgValProValSerGluLysGluTyLys 275  
Qy 1168 ACCACGCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1227  
Db 276 AsnThrProProIleGluAspAlaAspGlySerTyPheLeuTyTrSerLysLeuThrVal 295  
Qy 1228 GACAAGAGCAGGTGGCAGCAGGGGACGCTTCTCTCATGTCCGTGATGATGAGGCTCTG 1287

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Db      296 AspLysSerAlaTrpAspGlnGlyThrValThrCysSerValMetHisGluAlaLeu 315
      1288 CACAACCATACACGAGAGAGCTCTCCCTGTCCTCCGGT 1329
      316 HisAsnHisValThrGlnLysAlaIleSerArgSerProGly 329

RESULT 6
GC1_RAT
ID      GC1_RAT      STANDARD;      PRT;      326 AA.
AC      P20759;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig gamma-1 chain C region.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89232738; PubMed=3149946;
RA      Brueggemann M.;
RT      Evolution of the rat immunoglobulin gamma heavy-chain gene family. ";
RL      Gene 74:473-482(1988).
DR      PIR; PS0017; PS0017.
DR      HSSP; P01842; 7FAB.
DR      InterPro; IPR007110; Ig-Like.
DR      InterPro; IPR003597; Ig cl.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00047; Ig; 3.
DR      SMART; SM00407; Igcl; 2.
DR      PROSITE; PS50835; IG_LIKE; 3.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT      NON_TER      1
FT      DOMAIN      1      97      CH1.
FT      DOMAIN      98      112      HINGE.
FT      DOMAIN      113      219      CH2.
FT      DOMAIN      220      326      CH3.
FT      DISULFID      27      82
FT      DISULFID      102      102      INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID      106      106      INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID      109      109      INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID      111      111      INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID      140      200
FT      DISULFID      246      304
FT      CARBOHYD      176      176      N-LINKED (GLCNAC. .) (POTENTIAL).
SQ      SEQUENCE      326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

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## Alignment Scores:

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Best Local Similarity:      63.25%      Mismatches:      60
Query Match:      47.98%      Indels:      8
DB:      1      Gaps:      4

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## US-09-674-716b-18 (1-1335) x GC1\_RAT (1-326)

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QY      343 GCTCCACCAAGGGCCATCGGTCTTCCCTCCGACCCCTCCCTCCAGACGACCTCTGGG 402
Db      1 AlaGluThrAlaProSerValThrProLeuAlaProGlyThrAlaLeuLysSerAsn 20
QY      403 GGCACAGCGCCCTGGCTGCTCCGTACAGGACTACTTCCCGAACCGGTGACGGTTCG 462
Db      21 SerMetValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThrValThr 40
QY      463 TGGAACTCAGGCGCCCTGACACGCGGTGACACCTTCCCGGCTGTCTACAGTCCTCA 522
Db      41 TrpAsnSerGlyAlaLeuSerSerGlyValHisThrPheProAlaValLeuGln---Ser 59
QY      523 GGACTCTACTCCCTCAGCAGCGTGTGTGACCGTGTGACCGTCTCCAGCAGCTTGGGCACCCAGACC 582

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Db      60 GlyLeuThrThrLeuThrSerSerValThrValProSerSerThrThrProSerGlnThr 79
QY      583 TACATCTGCAACGTGAATCAACAGCCGACCAACACCAAGGTGGAAGAAGTGGAGCC 642
Db      80 ValThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysLeuValPro 99
QY      643 AAATCTTGTCACAAAATCAACATCCACACCG-----TGCCACGACCTGAACCTCGCG 696
Db      100 ArgAsnCysGly-----GlyAspCysLysProCysIleCysThrGlySerGluValSer 117
QY      697 GGGCACCGTCAGTCTCTCTCCCTCCCAAAACCAAGACACACCTCAATCTCCCGG 756
Db      118 -----SerValPheIlePheProLysProLysAspValLeuThrIleThrLeu 134
QY      757 ACCCTGAGGTACATCGCTGGTGGAGTGCATATGCCAAGACCAAGCCGCGGAGGAGCAG 816
Db      135 ThrProLysValThrCysValValValAspIleSerGlnAspAspProGluValHisPhe 154
QY      817 AACTGTGTACGTGACCGCGTGGAGTGCATATGCCAAGACCAAGCCGCGGAGGAGCAG 876
Db      155 SerTrpPheValAspValGluValHisThrAlaGlnThrArgProGluGluGln 174
QY      877 TACACAGCAGCTACCGTGTGGTTCACGGTCTCTACCGTCTCCACGACGACTGGCTGAAT 936
Db      175 PheAsnSerThrPheArgSerValSerGluLeuProIleLeuHisGlnAspTrpLeuAsn 194
QY      937 GGCAAGGAGTACAAAGTCAAGGTCTCCAAAGACCCCTCCACGACCCCTCCAGAAAAC 996
Db      195 GlyArgThrPheArgCysLysValThrSerAlaAlaPheProSerProIleGluLysThr 214
QY      997 ATCTCCAAAGCAAGGAGCAGCCCGAGAGACACAGGTGTACACCTGCCCGCTCCCGG 1056
Db      215 IleSerLysProGluGlyArgThrGlnValProHisValThrMetSerProThrLys 234
QY      1057 GATGAGCTGACCAAGAACCAAGGTACAGCTGCTGCTGCTCAAGGCTTCTATCCAGC 1116
Db      235 GluGluMetThrGlnAsnGluValSerIleThrCysMetValLysGlyPheThrProPro 254
QY      1117 GACATCGCCCTGGAGTGGGAGCAATGGGACCGGAGCAACAACTACAGACCAAGCCT 1176
Db      255 AspiletyrValGluTrpGlnMetAsnGlyGlnProGlnGluAsnTrpLysAsnThrPro 274
QY      1177 CCGTGTGACCTCCGACGCTCTCTTCTCTCTACAGAGCTACCGTCCGTCAGCAGAGC 1236
Db      275 ProThrMetAspThrAspGlySerTyrPheLeuTrpSerLysLeuAsnValLysLysGlu 294
QY      1237 AGGTGGCAGCAGGGGAACTCTTCTCTCATGCTCGGTGATCATGATGCTGTGCAACAC 1296
Db      295 LysTrpGlnGlnGlyAsnThrPheThrCysSerValLeuHisGluGlyLeuHisAsnHis 314
QY      1297 TACACGACGAGAGCTCTCCCTGCTCCGGGTAAA 1332
Db      315 HisThrGluLysSerLeuSerHisSerProGlyLys 326

RESULT 7
GC3_HUMAN
ID      GC3_HUMAN      STANDARD;      PRT;      290 AA.
AC      P01860;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Ig gamma-3 chain C region (heavy chain disease protein) (HDC) .
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE (DISEASE PROTEIN WIS).
RX      MEDLINE=81021548; PubMed=6774747;
RA      Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT      "Primary structure of human gamma 3 immunoglobulin deletion mutant:

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QY 403 GGCACAGCGGCGCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTCTCG 462  
Db 21 SerMetValThrLeuGlyCysLeuValGlyTyrPheProGluProValThrValThr 40  
QY 463 TGGAACTCAGCGCGCTGACACAGCGGGGTGCACACCTTCCCGGTGCTTACAGTCTCTCA 522  
Db 41 TrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGlnSerAsp 60  
QY 523 GGACTTACTCTCCCTCAGCAGCGGTGGTGCCTGCTGCTCCAGCAGCTTGGGCAACCCAGCC 582  
Db 61 ---LeuTyrThrLeuSerSerValThrValProSerSerProArgProSerGluThr 79  
QY 583 TACATCTCAACGCTGAATCAACAGCCCAAGCAACCAAGGTGGAGCAAGAAGTGGAGCC 642  
Db 80 ValThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysValLeuValPro 99  
QY 643 AAATCTTGTGCAAACTCACACATGCCACG-----TCCACGACCTGACTCGCG 696  
Db 100 ArgAspCysGly-----CysLysProCysLysThrValProGluValSer 115  
QY 697 GGGGACCGCTAGTCTTCTTCCCTCCCAACCAAGGACACCTCATGCTCCCGG 756  
Db 116 -----SerValPheIlePheProLysProLysAspValLeuThrIleThrLeu 132  
QY 757 ACCCTGAGTGCATCGTGGTGGTGCAGTGCAGCCAGCAAGACCTGAGTCAAGTTC 816  
Db 133 ThrProLysValThrCysValValAspLysSerLysAspAspProGluValGlnPhe 152  
QY 817 AACTGTGACGTGGCGGTGGTGCATATGCAAGCAAGACCAAGCCGCGGAGGACG 876  
Db 153 SerTrpPheValAspValGluValHisThrAlaGlnThrGlnProArgGluGluGln 172  
QY 877 TACACACAGCAGTACCGTGTGGTGCAGCTCTCCACGCTCTGACACAGGACTGCTGAAT 936  
Db 173 PheAsnSerThrPheArgSerValSerGluLeuProIleMetHisGlnAspTrpLeuAsn 192  
QY 937 GCAAGAGTACAGTCAAGTCTCCAAAGAGCCCTCCAGCCCTCCAGCCCATCGAAGAAC 996  
Db 193 GlyLysGluPheLysCysArgValAsnSerAlaAlaPheProAlaProIleGluLysThr 212  
QY 997 ATCTCAAGCAAGCGCGCGCGGAGCAACCAAGGTGTACACCTCCCGCCCTCCCGG 1056  
Db 213 IleSerLysThrLysGlyArgProLysAlaProGlnValThrIleProProLys 232  
QY 1057 GATGAGTACCAAGAACAGCTGAGTGCCTGCTGCTGCTCAAGAGTCTTATCCAGC 1116  
Db 233 GluGlnMetAlaLysAspLysValSerLeuThrCysMetIleThrAspPheProGlu 252  
QY 1117 GACATCGCGGTGGTGGAGGAGCAATGGGAGCGGAGAACACACTACAAGACACCGCT 1176  
Db 253 AspIleThrValGluTrpGlnTrpAsnGlyGlnProAlaGluAsnTyrLysAsnThrGln 272  
QY 1177 CCGGTGCTGACTCCGAGCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGC 1236  
Db 273 ProIleMetAsnThrAsnGlySerTyrPheValTyrSerLysLeuAsnValGlnLysSer 292  
QY 1237 AGGTGGCAGCGGAGCAAGCTCTTCTTCATGCTCCGTGATGATGATGATGATGATGAT 1296  
Db 293 AsnTrpGluAlaGlyAsnThrPheThrCysSerValLeuHisGluGlyLeuHisAsnHis 312  
QY 1297 TACAGCAGAGAGCTCTCCCTGCTCCCGGTA 1332  
Db 313 HisThrGluLysSerLeuSerHisSerProGlyLys 324

RESULT 9  
GCIM MOUSE  
ID GCIM MOUSE STANDARD; PRT; 393 AA.  
AC P01869;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig gamma-1 chain C region, membrane-bound form.

Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=80045036; PubMed=115593;  
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
RA Takahashi N., Mano Y.;  
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
RT gamma 1 chain gene.";  
RL Cell 18:559-568(1979).  
RN [2]  
RP SEQUENCE OF 323-393 FROM N.A.  
RX MEDLINE=82197626; PubMed=6804950;  
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;  
RT "cDNA for surface immunoglobulin gamma chains encodes a highly  
RT conserved transmembrane sequence and a 28-residue intracellular  
RT domain.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).  
RN [3]  
RP SEQUENCE OF 323-366 FROM N.A.  
RX MEDLINE=82115295; PubMed=6799207;  
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,  
RA Eisenberg D., Wall R.;  
RT "Gene segments encoding transmembrane carboxyl termini of  
RT immunoglobulin gamma chains.";  
RL Cell 26:19-27(1981).  
RN [4]  
RP SEQUENCE OF 1-44 FROM N.A.  
RX MEDLINE=82222190; PubMed=6283537;  
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;  
RT "Nucleotide sequences of gene segments encoding membrane domains of  
RT immunoglobulin gamma chains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
CC -I- ALTERNATIVE PRODUCTS;  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Membrane-bound;  
CC IsoId=P01869-1; Sequence=Displayed;  
CC Name=Secreted;  
CC IsoId=P01868-1; Sequence=External;  
CC Note=May be the major isoform;  
CC -----  
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CC -----  
DR EMBL; V00793; CAA24172.1; -;  
DR EMBL; V00793; CAA24173.1; -;  
DR EMBL; V00793; CAA24174.1; -;  
DR PIR; B02159; GIMSM.  
DR PDB; 15C8; 23-MAR-98.  
DR PDB; 1AE6; 18-MAR-99.  
DR PDB; 1CL7; 12-JAN-00.  
DR PDB; 1F11; 06-FEB-01.  
DR PDB; 1F58; 29-DEC-99.  
DR PDB; 1KCS; 24-JUL-02.  
DR PDB; 1KCR; 11-MAY-02.  
DR PDB; 25C8; 09-JUL-99.  
DR MGD; MGI:96446; Igh-4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00407; IGcl; 2.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Alternative splicing; Transmembrane; 3D-structure.



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AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
DE OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RX Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.,
RA "Structural analysis of the murine IgG3 constant region gene.";
RT EMBO J. 3:2041-2046(1984).
RL -----CC
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CC or send an email to license@isb-sib.ch).
CC -----CC
CC EMBL; J00451; -; NOT ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT FT_NTER 1 1
FT FT_DOMAIN 1 97 CH1.
FT FT_DOMAIN 98 113 HINGE.
FT FT_DOMAIN 114 223 CH2.
FT FT_DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Alignment Scores:
Pred. No.: 6.69e-62 Length: 329
Score: 1130.00 Matches: 210
Percent Similarity: 77.64% Conservative: 47
Best Local Similarity: 63.44% Mismatches: 70
Query Match: 46.99% Indels: 4
DB: 1 Caps: 3

US-09-674-716B-18 (1-1335) x GC3_MOUSE (1-329)
QY 346 TCCACCAAGGGCCATCGGTCTTCCCGCTGGCACCCCTCTCCACAGAGCACCTCTGGGGG 405
DB 1 ThrThrThralaProSerValTyProLeuValProGlyCysSerAspThrSerGlySer 20
QY 406 ACAGCGGCCCTGGCTGCTGTCGTCAGAGACTACTTCCCGAACCGGTGACGGTGTCTGTG 465
DB 21 SerValThrLeuGlyCysLeuValLysGlyTyPheProGluProValThrValLysTrp 40
QY 466 AACTCAGGCGCCTGACCGACCGACGCGGTGCACACCTTCCCGGCTCTCTCTACAGTCTCAGGA 525
DB 41 AsnTyGlyAlaLeuSerSerGlyValArgThrValSerSerValLeuGln---SerGly 59
QY 526 CTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGACGACTTGGGCACCCAGACCTAC 585
DB 60 PheTySerLeuSerSerLeuValThrValProSerSerThrThrTrpProSerGlnThrVal 79
QY 586 ATCTGCAAGCTGAATCACAGCCCGACCAACCAAGGTGCACGAAGAAGTGGAGCCCAAA 645
DB 80 IleCysAsnValAlaHisProAlaSerLysThrGluLeuLeuLysArgIleGluProArg 99

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646 TCTGTGACAAACTCACATGCCCCA-----CGTGCCTCCAGCACCTGAACCTCGCGGG 699
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      ---IleProLysProSerThrProProGlySerSerCysProProGlyAsnIleLeuGly 118

700 GCACGCTGAGTCTCTCTCCCTCCCAACCAAGGACACCTCATCATCTCCCGGACC 759
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      |||||ProSerValPheIlePheProProLysProLysAspAlaLeuMetIleSerLeuThr 138

760 CTGAGGTCACATGCTGTGTGTGAGCTGAGCCAGACACCTGAGGTCAAGTTCAAC 819
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      |||||ProLysValThrCysValValValAspValSerGluAspProAspValHisValSer 158

820 TGTGCTGAGCGGCTGAGTGCATATGCAAGACCAAGCCCGGAGGAGGAGTAC 879
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      |||||TrpPheValAspAsnLysGluValHisThrAlaTrpThrGlnProArgGluAlaGlnTrp 178

880 AACAGCAGCTACGCTGTGTGTGAGCTGAGCCAGACACCTGAGGTCAAGTTCAAC 939
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      |||||AnSerThrPheArgValValSerAlaLeuProlIleGlnHisGlnAspTrpMetArgGly 198

940 AAGAGTACAAGTGAAGTCTCCAAAGCCCTCCAGCCCGGAGGAGGAGTAC 999
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      |||||LysGluPheLysCysLysValAsnAsnLysAlaLeuProAlaProIleGluArgThrIle 218

1000 TCCAAAGCCAAAGGAGCGCCGAGAACACACAGGTGTACACCTGCCCGGAT 1059
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      |||||SerLysProLysGlyArgAlaGlnThrProGlnValThrIleProProArgGlu 238

1060 GAGCTGACCAAGAACAGTACGCTGAGCTGCTCCCTGCTCAAGGCTTCTATCCCGGAC 1119
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      |||||GlnMetSerLysLysLysValSerLeuThrCysLeuValThrAsnPheSerGluAla 258

1120 ATCCGCTGAGTGGAGAGCAATGGGAGCGGAGAGCACTACAGACACCGCTCC 1179
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      |||||IleSerValGluTrpGluArgGlnGlyGluLeuGluGlnAspTyrLysAsnThrProPro 278

1180 GTGCTGAGCTGAGGCTCTCTCTTCTTCTACAGCAAGCTCACCGTGGAGCAAGAGCAGG 1239
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      |||||IleLeuAspSerAspGlyThrThrPheLeuTyrSerLysLeuThrValAspThrAspSer 298

1240 TGGCAGCAGGGAAGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1299
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      |||||TrpLeuGlnGlyGluIlePheThrCysSerValValHisGluAlaLeuHisAsnHis 318

1300 AGCGAAGAGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
QY      |||      |||      |||      |||      |||      |||      |||      |||
Db      |||||ThrGlnLysAsnLeuSerArgSerProGlyLys 329

RESULT 12
GC3M MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041493; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;

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RT      "The structure of the mouse immunoglobulin in gamma 3 membrane gene
RL      segment.";
CC      Nucleic Acids Res. 11:6775-6785(1983).
CC      -----
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CC      -----
DR      EMBL; J00451; AAB59655.1; --
DR      EMBL; V01526; CAA24767.1; ALT_SEQ.
DR      PIR; A01556; G3MSM.
DR      HSP; P01857; IFC1.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00047; ig; 3.
DR      SMART; SM00407; Igcl; 2.
DR      PROSITE; PSS0835; IG_LIKE; 3.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW      Transmembrane; Alternative splicing.
FT      NON_TER 1 1
FT      DOMAIN 1 97 CHI.
FT      DOMAIN 98 113 HINGE.
FT      DOMAIN 114 223 CH2.
FT      DOMAIN 224 327 CH3.
FT      TRANSMEM 346 362 POTENTIAL.
FT      DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT      CONFLICT 333 333 E -> G (IN REF. 2).
FT      CONFLICT 342 342 E -> Q (IN REF. 2).
FT      CONFLICT 388 388 F -> F (IN REF. 2).
SQ      SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Alignment Scores:
Pred. No.: 3-22e-61 Length: 398
Score: 1119.00 Matches: 208
Percent Similarity: 77.51% Conservative: 47
Best Local Similarity: 63.22% Mismatches: 70
Query Match: 46.53% Indels: 4
DB: 1 Gaps: 3

US-09-674-716B-18 (1-1335) x GC3M_MOUSE (1-398)

QY      346 TCCACCAAGGCGCCATCGCTCTCCCGCTGGACACCTCTCCAGAGCACCTCTGGGGGC 405
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      406 ACAGCGCGCCCTGGCGCTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTCTGG 465
Db      :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      466 AACTAGGCGCCCTGACACGCGGTGACACCTTCCCGGCTGCTCTACAGTCTCTCAGGA 525
Db      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      41 AsnTyrGlyAlaLeuSerSerGlyValArgThrValSerSerValLeuGln---SerGly 59
Db      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      526 CTCTACTCTCCCTACAGCGTGTGTGACCGTGCCTCTCCAGCAGCTTGGGCAACCGACCTTAC 585
Db      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      60 PheTyrSerLeuSerSerLeuValThrValProSerSerThrTrpProSerGlnThrVal 79
Db      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      586 ATCTGCAAGTGAATCAAGCCACCAAGCCACCAAGTGTGCAAGAAAGTGAAGCCCAA 645
Db      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      80 IleCysAsnValAlaHisProAlaSerLysThrGluLeuLeuLysArgIleGluProArg 99
Db      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      646 TCTTGTGACAAACTCACATGCCCCA-----CGTGCCTCCAGCACCTGAACCTCGCGGG 699
Db      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      100 ---IleProLysProSerThrProProGlySerSerCysProProGlyAsnIleLeuGly 118
Db      ---:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      700 GCACCGTGAAGTCTCTCTCCCTCCCAACCAAGGACACCTCATCATCTCCCGGACC 759
Db      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 463 TGAAGTACAGGCGCCCTGACACAGCGCGGTGCACACCTTCCGGCTGTCTCTACAGTCTGCA 522
Db 41 TrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGlnSerAsp 60
QY 523 GCAGTCTACTCCCTCAGCAGCGTGTGACCGCTCCAGCAGCTTGGGACCCAGCCAGCC 582
Db 61 LeuThrLeuSerSerSerValThrValThrSerSerThrTrpProSerGlnSer 79
QY 583 TACATCTGCAAGTGAATCACAAGCCCAAGCAACCAAGGTGGACAAGAGTGGAGCC 642
Db 80 IleThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysIleGluPro 99
QY 643 AAATCTGTGACAAACTCACATGCCCCACCG-----TGCCAGCAGCTGAATCGCG 696
Db 100 ArgGly---ProThrIleLysProCysProProCysLysCysProAlaProAsnLeu 118
QY 697 GGGGACCGCTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGG 756
Db 119 GlyGlyProSerValPheIlePheProProLysIleLysAspValLeuValIleSerLeu 138
QY 757 ACCCTGAGGTACATGCGTGTGTGAGTGTGAGCAGCAGCAGCAGCAGTCAAGTTC 816
Db 139 SerProIleValThrCysValValValAspValSerGluAspAspProAspValGlnIle 158
QY 817 AACTGTGAGTGGAGCGGTGAGGTGCATATGCAAGACAAAGCCGCGGAGGAGCAG 876
Db 159 SerTrpPheValAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAsp 178
QY 877 TACAACAGCAGCTACCGTGTGTGTGAGTGTCTCAGCTGCTCCTGACAGGATGCTGAAT 936
Db 179 TyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSer 198
QY 937 GCAAGGAGTACAAGTGAAGTCTCCAAAGAGCCCTCCAGCCCGCCATCGAAGAAC 996
Db 199 GlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThr 218
QY 997 ATCTCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1056
Db 219 IleSerLysProLysGlySerValArgAlaProGlnValTyrValLeuProProGlu 238
QY 1057 GATGAGTCAACAAGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1116
Db 239 GluGluMetThrLysLysGlnValThrLysThrCysMetValThrAspPheMetProGlu 258
QY 1117 GACATCGCGCTGAGTGGAGAGCAATGGGAGCGAGGAGGAGGAGGAGGAGGAGGAG 1176
Db 259 AspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGlu 278
QY 1177 CCGTGTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1236
Db 279 ProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLys 298
QY 1237 AGGTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1296
Db 299 AsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHis 318
QY 1297 TACAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1332
Db 319 HisThrThrLysSerPheSerArgThrProGlyLys 330

```

## RESULT 14

```

GCC_RAT ID GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC NCBI_TaxID=10116;

```

```

RN RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi P.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RL region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X07189; CAA30169.1; -.
DR PIR; S00847; S00847.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGL1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

```

## Alignment Scores:

```

Pred. No.: 5 91e-61 Length: 329
Score: 1114.50 Matches: 205
Percent Similarity: 77.78% Conservative: 54
Best Local Similarity: 61.56% Mismatches: 67
Query Match: 46.34% Indels: 7
DB: 1 Gaps: 3

```

US-09-674-716B-18 (1-1335) x GCC\_RAT (1-329)

```

QY 343 GCCTCACCAGGGGCCATCGGTCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCG 402
Db 1 AlaArgThrAlaProSerValTyrProLeuValProGlyCysSerGlyThrSerGly 20
QY 403 GGCACAGCGCCCTGGCTCGCTGCTCAAGGACTACTTCCCGAACCCGGTGAAGTGTGCG 462
Db 21 SerLeuValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThrVallys 40
QY 463 TGAATCTAGGCGCCTGACCGCGGTGACACCTTCCCGGTGTCTCTCAGTCTCA 522
Db 41 TrpAsnSerGlyAlaLeuSerSerGlyValHisThrPheProAlaValLeuGln---Ser 59
QY 523 GGAATCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAGCCAGCC 582
Db 60 GlyLeuThrLeuSerSerSerValThrValProSerSerThrTrpSerSerGlnThr 79
QY 583 TACATCTGCAAGTGAATCACAAGCCCAAGCAACCAAGGTGGACAAGAGTGGAGCC 642
Db 80 ValThrCysSerValAlaHisProAlaThrLysSerAsnLeuIleLysArgIleGluPro 99
QY 643 AAATCTGTGACAAACTCACATGCCCCACCG-----TGCCAGCAGCTGAATC 693
Db 100 Arg-----ArgProLysProArgProProThrAspIleCysSerCysAspAsn 116

```







GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:27:18 ; Search time 169.047 Seconds  
(without alignments)  
4983.418 Million cell updates/sec

Title: US-09-674-716b-18

Perfect score: 2405

Sequence: 1 gaggtgagctgggtggagtc.....ccctgtctcgggtaaatga 1335

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODBL=frame+n2p\_model -DEV=xlp  
-Q=/sgn2\_1/USPTO\_spool\_p/US09674716/runat\_30092004\_070258\_25867/app\_query.fasta\_1.3164  
-DB=SPTRMBL\_25 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEL=0 -LOOPEX=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09674716 @CGN 1.1.499 @runat\_30092004\_070258\_25867 -NCPU=6 -ICPU=3  
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=5  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2139.5	89.0	470	4 Q7Z5W1	Q7Z5W1 homo sapien

RESULT 1

Q7Z5W1 ID Q7Z5W1 PRELIMINARY; PRT; 470 AA.

AC Q7Z5W1; 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=2238257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

ALIGNMENTS

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzyzinski M.I., Skalska U., Schmutz J., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC053984; AAH53984.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 470 AA, 51204 MW; 778CF34521483E1A CRC64;

## Alignment Scores:

Pred. No.: 4,088-162 Length: 470  
 Score: 2139.50 Matches: 407  
 Percent Similarity: 91.85% Conservative: 10  
 Best Local Similarity: 89.65% Mismatches: 24  
 Query Match: 88.96% Indels: 13  
 DB: 2 Gaps: 4

US-09-674-716B-18 (1-1335) x Q725W1 (1-470)

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGAGGCTTGTAAAGCCGGGGGTCCCTTAGACTC 60  
 DB 20 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39  
 QY 61 TCCTGTGAGCTAGCGGATTCATCTTCTAGTGGCTACTGGATGCTCTGGTCCGCGAGCT 120  
 DB 40 SerCysValAlaSerGlyPheThrLeuAsnAspMetHisTrpValArgGlnGly 59  
 QY 121 CCAGGGAAGGGCTCGAGTGGTCTCTGAAATAGATTGAAATCTGTAATATGCAACA 180  
 DB 60 IleGlyLeuGlyLeuGlnTrpValSerLysIleGlyThrAlaGlyAspArgTyr----- 77  
 QY 181 CATTATCGGAGCTCTGTGAAGGGGAATTCACCAATCTCAAGAGATGATCAAAATCTAGA 240  
 DB 78 ---TyrAlaGlySerValIysGlyArgPheThrIleSerArgGluAsnAlaLysAspSer 96  
 QY 241 CTGTATCTGCAATGCAAGCTGTAACCGGTAACCGGACAGCGCTGTATTACTGTACA--- 297  
 DB 97 LeuTyrLeuGlnMetAsnSerLeuArgValGlyAspAlaAlaValTyrTyrCysAlaArg 116  
 QY 298 -----GATTTTCATAGACTGGGGCCAGGGAACACTAGTC 330  
 DB 117 GlyAlaGlyArgTrpAlaProLeuGlyAlaPheAspIleTrpGlyGlnGlyThrMetVal 136  
 QY 331 ACCGTCTCTAGCTCTCAACGAGGCGCATCGTCTTCCCGCTGGACCTCTCCAG 390  
 DB 137 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 156  
 QY 391 AGCACTCTGGGGCACAGCGCCCTCGGCTGCTCCCTGGTCAAGGACTACTTCCCGAACCG 450  
 DB 157 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 176  
 QY 451 GTGAGGTGCTGTGAACTCAGCGCCCTCAGCAGCGCGGTGCACACCTTCCCGGTGTC 510  
 DB 177 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 196  
 QY 511 CTACAGTCTCTCAGGACTCTACTCTCCCTCAGCAGCGGTGGTGGCTCCCTCAGAGCTTG 570  
 DB 197 LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeu 216  
 QY 571 GGCACCCAGACCTACATCTGCAACGTGAATCAAGCCGACCAACCAAGGTGGACAG 630  
 DB 217 GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 236

QY 631 AAAGTCGAGCCCAAAATCTTGTGACAAAATCAATGCCCCACCGTGGCCAGCACTGAA 690  
 DB 237 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 256  
 QY 691 CTCGGGGGGCACCGTCAGTCTCTCTTCCCCCAAAACCCCAAGGACACCTCATGTC 750  
 DB 257 LeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIle 276  
 QY 751 TCCCGGACCCCTGAGGTCAATCGCTGGTGGAGCTGAGCCACCAAGACCTCAGGTC 810  
 DB 277 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 296  
 QY 811 AGTTCAACTGGTACGTGACCGCGTGGAGGTGCAATATGCCAAGACAAAGCCGGGAG 870  
 DB 297 LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 316  
 QY 871 GAGCAGTACAAACAGCAGCTACCGCTGTGTGTCAGCGCTCTCACCGTCTGACACGACTGG 930  
 DB 317 GluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrp 336  
 QY 931 CTGAATGGCAAGAGTACAAAGTCAAGTCTCCAAAGACCTCCAGCCCTCCAGCTCGAG 990  
 DB 337 LeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 356  
 QY 991 AAAACCATCTCCAAAGCCAAAGCGGAGCCCGGAGAACCAACAGGTGTACACCTGCCCCA 1050  
 DB 357 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro 376  
 QY 1051 TCCCGGATGAGTACCAAGAACAGGTCAACCTGACCTGCTGCTGCTCAAGGCTCTAT 1110  
 DB 377 SerArgAspGluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 396  
 QY 1111 CCAGGAGCATCGCGTGGAGTGGAGACATGGCAGCGGAGAACCAACCTACAGGACC 1170  
 DB 397 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnThrLysThr 416  
 QY 1171 ACCTCTCCGCTGTGACTCCGACCGCTCTTCTTCTTCTTCTACAGCAAGCTCACCTGAGC 1230  
 DB 417 ThrProProValLeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAsp 436  
 QY 1231 AGAGCAGTGGCAGCAGGAGACGCTCTTCTCATGCTCCGTCATGCTGAGCTCTGAC 1290  
 DB 437 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 456  
 QY 1291 AACCACTACAGCAGGAAGACCTCTCCCTGTCTCCGGGTAAA 1332  
 DB 457 AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 470

## RESULT 2

Q72351 PRELIMINARY; PRT; 482 AA.  
 ID Q72351  
 AC Q72351;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein DKFZP686N02209.  
 GN DKFZP686N02209.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RA Bloembergen H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX538118; CAD98026.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 482 AA; 52852 MW; ED475F1901D1A034 CRC64;

Alignment Scores:

Pred. No.: 5,8e-158 Length: 482  
 Score: 2087.50 Matches: 400  
 Percent Similarity: 89.46% Conservative: 16  
 Best Local Similarity: 86.02% Mismatches: 26  
 Query Match: 86.80% Indels: 23  
 DB: 4 Gaps: 4

US-09-674-716b-18 (1-1335) x Q72351 (1-482)

QY	1	GAGTGCAGCTGGAGTCTGGGGAGGCTGTGTAAGCCCGGGGGTCCCTTAGACTC	60
DB	20	GlnAlaGlnValValGlnSerGlyGlySerValValGlnProGlyArgSerLeuArgLeu	39
QY	61	TCCTGTGCAGTACGGGATTCACCTTTCAGTGGCTACTGGATGCTCTGGTCCGCCAGGCT	120
DB	40	SerCysIleAlaSerGlyPheSerPheSerGlySerAlaMetHisThrLeuArgGlnIle	59
QY	121	CCAGGAAAGGGCTCGAGTGGTGTCTGAAATAGATTGAATCTGATAATTATGCAACA	180
DB	60	ProGlyLysGlyLeuGluTrpValAlaValIle-----SerTyrAspGlyAsnHisLys	77
QY	181	CATTATGGGAGTCTGTAAGGGGNAATTCACCATCTCAAGAGATGATTCAAATCTAGA	240
DB	78	LeuTyrSerAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysSerLeu	97
QY	241	CTGTATCTGCAATGAACAGAGCTGAAACCCAGGACACAGCGCTGATTACTGTACA---	297
DB	98	LeuPheLeuHisValAsnSerLeuThrSerAlaAspThrAlaIleTyrTyrCysAlaArg	117
QY	298	GATTTCT-----	303
DB	118	AspPheHisSerLysThrThrSerIlePheGlyLeuIleProLeuTyrPheTyrTyrSer	137
QY	304	---ATAGAC---TGGGGCGAGGAACTAGTCAAGCTCTCTCAGCGCTCCACCAAGGGC	357
DB	138	AlaMetAspThrTrpGlyArgGlyThrThrValIleValSerSerAlaSerThrLysGly	157
QY	358	CCATCGGCTTCCCTCGCCACCTCTCCAGAGACACTCTGGGGGACACGCGCCCTG	417
DB	158	ProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeu	177
QY	418	GGCTGCTGGTCAAGGACTATCTCCGAGCGGTGACGGTGTCTGGTGAAGTCAAGGCGC	477
DB	178	GlyCysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAla	197
QY	478	CTGACGAGCGGCTGCACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTC	537
DB	198	LeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeu	217
QY	538	AGCAGCGTGGTACCGTCCCTCCAGAGTGGGACCCAGACCTACATCTGCAAGCTG	597
DB	218	SerSerValValThrValProSerSerLeuGlyThrGlnThrTyrIleCysAsnVal	237
QY	598	AATCAAGCCCGCAGCAACACCAAGTGGACAAAGTGGAGCCCAAAATCTTGTGACAAA	657
DB	238	AsnHisLysProSerAsnThrLysValAspLysLysValGluProLysSerCysAspLys	257
QY	658	ACTCACATGCCCACCGTCCAGACCTGACCTGCGGGGGGACCGCTGAGTCTTCTCTC	717
DB	258	ThrHisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSerValPheLeu	277
QY	718	TTCCCCCAACCAAGCACCTCTGATCTCTCCCGGACCCCTGAGTCAATGGGTG	777
DB	278	PheProProLysProGlyAspThrLeuMetIleSerArgThrProGluValThrCysVal	297
QY	778	GTGGTGGAGCTGAGCCAGAGACCTGAGTTCAGTTCAGTTCAGTGGAGCGGCTG	837
DB	298	ValValAspValSerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyVal	317
QY	838	GAGGTGCATATGCCAAGCAAGCCGGGGAGGAGGAGTACACAGCAGCTACCGGTG	897
DB	318	GluValHisAlaLysThrLysProArgLeuGluGlnTyrAsnSerThrTyrArgVal	337

QY	898	GTCCAGCGTCTCACCGTCTCCACAGGACTGGCTGAATGGCAAGAGTACAGTGCAG	957
DB	338	ValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysIleLysCysLys	357
QY	958	GTCTCCAAACAAAGCCCTCCACAGCCCTCATCGAGAAACCATCTCCAAAGCCAG	1017
DB	358	ValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGln	377
QY	1018	CCCCGAGAACCAAGTGTACACCTGCCCTGCCATCCCGGATGAGTGTACCAAGACCAG	1077
DB	378	ProArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGln	397
QY	1078	GTCCAGCTCACCTCGCTCAAGAGCTTCTATCCACAGCAGCATCCCTGGAGTGGGAG	1137
DB	398	ValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGlu	417
QY	1138	AGCAATGGGCGAGGAGAACAACTCAAGACACACCCCTCCCTGCTGTGACTCCGACGGC	1197
DB	418	SerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProValLeuAspSerAspGly	437
QY	1198	TCCTTCTTCTCTACACAGAGCTCACCGTGGCAAGAGCAGGTGGCAGAGGGAACGTC	1257
DB	438	SerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnVal	457
QY	1258	TTCTCATGCTCCGTGATGATGAGCTGTGCACACCATCACGAGAGACCTCTCTCC	1317
DB	458	PheSerCysSerValMetHisGlyLeuHisAsnHisTyrThrGlnLysSerLeuSer	477
QY	1318	CTGCTCTCCGGTAAA	1332
DB	478	LeuSerProGlyLys	482

RESULT 3  
 Q727P5 PRELIMINARY; PRT; 469 AA.  
 AC Q727P5;  
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 MDLINE=22388257; PubMed=12477932;  
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toohyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Boak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,  
 RA Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Srausberg R.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC051328; AAHS1328.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Alignment Scores:  
 Pred. No.: 3,26e-155 Length: 469  
 Score: 2053.00 Matches: 386  
 Percent Similarity: 90.2% Conservative: 22  
 Best Local Similarity: 85.40% Mismatches: 34  
 Query Match: 85.36% Indels: 10  
 DB: 4 Gaps: 2

US-09-674-716B-18 (1-1335) x Q727P5 (1-469)

QY	1	GAGGTGACGCTGGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC	60
Db	20	GINVALHISLEUVALGINSERGLYALAGLUVALLYSProGLYALASerVallylsLeu	39
QY	61	TCCTGTGACGCTAGCGGATTCACCTTCAGTGGCTACTGGATCTCCGGTCCGCCAGCT	120
Db	40	SerCysLysThrSerGlyTyrAsnPheSerSerTyrAspLeuIleTyrValArgGlnAla	59
QY	121	CCAGGAGAGGGCTCGAGTGGGTTCGTAATAGATTGAAATCTGATAATTATGCAACA	180
Db	60	ProGLYGLNGLYLeuGLUTrpMetGlyTrpIle-----SerAlaHisAsnGLYAspThr	77
QY	181	CATTATGCGGAGTCTGTGAGGGGAATTCACCATCTCAAGAGATGATCAAAATCTAGA	240
Db	78	LysTyrAlaArgLysPheGlnGlyArgValThrMetThrThrAspThrSerAlaThrThr	97
QY	241	CTGTATCTCAATGAACAGCTGAAACCCGAGGACACAGCGCTGTATTACTGTACA---	297
Db	98	SerTyrMetGluPheArgSerLeuArgSerAspThrAlaLeuPheTyrCysAlaThr	117
QY	298	-----GATTCATAGACTGGGCGCCAGGGAACACTAGTCACCGTC	336
Db	118	LysSerArgGlyGlnValGlyAspPheAspSerTrpGlyGlnGlyThrLeuValThrVal	137
QY	337	TCCTCAGCTCCACCAAGGGCCATCGCTCTCCCTCGGACCTCTCCCAAGAGGACCC	396
Db	138	SerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThr	157
QY	397	TCTGGGGCACGCGCCCTCGGCTGCTGTCAGAGCACTATCTCCCGAACCCGCTGACG	456
Db	158	SerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThr	177
QY	457	GTGTGTGGAACCTCAGGCGCCCTGACCGGCGTGCACACCTTCCCGCTGCTCTACAG	516
Db	178	ValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGln	197
QY	517	TCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACC	576
Db	198	SerSerGlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThr	217
QY	577	CAGACTACATCTGAACTGGAATCACAGCCCAACACCAAGTGGGACAAAGAGTG	636
Db	218	GlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysVal	237
QY	637	GAGCCCAAACTTTGTACAAAACCTCACATCCCGCCAGCGTCCCGCCAGCCTGAACTCGC	696
Db	238	GluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeu	257
QY	697	GGGGCACCTCTAGTCT	756
Db	258	GlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArg	277
QY	757	ACCCCTGAGTCCACATCGT	816
Db	278	ThrProGluValThrCysValValValAspValSerHisGluAspProGluValLysPhe	297
QY	817	AACTGGTACGTCGCGGCTGGAGTGCATATATGCAAGCAAAAGCCCGCGGAGGACAG	876
Db	298	AsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGln	317

QY	877	TACAACAGCAGCTACCGTGTGGTTCAGCGTCTCTACCGTCTCTCACAGGACTGGTGAAT	936
Db	318	TyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsn	337
QY	937	GGCAAGAGTACAAAGTCCCAAGGCTCCCAACAAGCCCTCCAGCCCTCGAGAAACC	996
Db	338	GlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThr	357
QY	997	ATCTCCAAAGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1056
Db	358	IleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProSerArg	377
QY	1057	GATGAGCTGACCAAGAACCAAGGTCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT	1116
Db	378	AspGluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSer	397
QY	1117	GACATCGCGTGGAGTGGGAGGAGCAATGGCGAGCGGAGAGCAAACTTACAAAGCAGCCT	1176
Db	398	AspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrPro	417
QY	1177	CCGCTGCTGACTCCGACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1236
Db	418	ProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSer	437
QY	1237	AGTGGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1296
Db	438	ArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHis	457
QY	1297	TACACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1332
Db	458	TyrThrGlnLysSerLeuSerLeuSerProGlyLys	469

RESULT 4

Q8N4Y9	Q8N4Y9	PRELIMINARY;	PRT;	521 AA.
AC	Q8N4Y9;	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RA	Strausberg R.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC031178; AAH31178.1; -			
DR	PIR; A60764; A60764.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig_cl.			
DR	InterPro; IPR00306; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig; 4.			
DR	SMART; SM00407; Igc1; 3.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS00835; IG_LIKE; 4.			
DR	PROSITE; PS00290; IG_MHC; 2.			
KW	Hypothetical protein.			
SQ	SEQUENCE 521 AA; 57156 MW; 2AC7D2E72D6CAA2 CRC64;			

Alignment Scores:  
 Pred. No.: 5,22e-152 Length: 521  
 Score: 2013.00 Matches: 385  
 Percent Similarity: 81.67% Conservative: 25  
 Best Local Similarity: 76.69% Mismatches: 34  
 Query Match: 83.70% Indels: 58  
 DB: 4 Gaps: 2

US-09-674-716B-18 (1-1335) x Q8N4Y9 (1-521)





Db 103 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 122  
Qy 520 TCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGGACACCCAG 579  
Db 123 SerGlyLeuThrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGln 142  
Qy 580 ACCTACATCTGCAACGCGAATCAACAAGCCAGCAACACCAAGGTGGCAAGAAGTG--- 636  
Db 143 ThrTyrThrCysAsnValAsnHisCysProSerAsnThrLysValAspLysArgValGlu 162  
Qy 636 ----- 636  
Db 163 LeuLysThrProLeuGlyAspThrThrHisThrCysProArgCysProGluProLysSer 182  
Qy 636 ----- 636  
Db 183 CysAspThrProProProCysProArgCysProGluProLysSerCysAspThrProPro 202  
Qy 637 -----GACCCCAAAATCTTGTGACAAACTCACACATGCCACCCCTGTC 678  
Db 203 ProCysProArgCysProGluProLysSerCysAspThrProProCysProArgCys 222  
Qy 679 CCAGACCTGAACCTCGCGGGGGGCGACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 738  
Db 223 ProAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAsp 242  
Qy 739 ACCCTCATGATCTCCGACCCCTGAGGTACATCGGTGGTGGTGGTGGTGGTGGTGGTGGT 798  
Db 243 ThrLeuMetIleSerArgThrProGluValThrCysValValValAspValSerHisGlu 262  
Qy 799 GACCTGAGGTCAAGTTCAACTGCTGAGTGGACGCGGTGGAGGTGCATATATGCCAAGACA 858  
Db 263 AspProGluValGlnPheLysTyrTyrValAspGlyValGluValHisAsnAlaLysThr 282  
Qy 859 AAGCCGGGGAGGAGCAGTCAACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 918  
Db 283 LysProArgGluGluGlnPheAsnSerThrPheArgValValSerValLeuThrValLeu 302  
Qy 919 CACCAGGACTGGCTGAATGGCAAGAGTACAAAGTCAAGTCTCCAAAGAGCCCTCCCA 978  
Db 303 HisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuPro 322  
Qy 979 GCCCCCATCGAAMAAACCATCTCCAAAGCCAAAGGGGAGCCCGAGAACCCAGAGTGTAC 1038  
Db 323 AlaProIleGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValTyr 342  
Qy 1039 ACCCTGCCCATCCCGGATGAGTGCACCAAGAACCAAGGTGCAGCTGACCTGCTGCTC 1098  
Db 343 ThrLeuProProSerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuVal 362  
Qy 1099 AAAGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGCAGCCGAGAAC 1158  
Db 363 LysGlyPheTyrProSerAspIleAlaValGluTrpGluSerSerGlyGlnProGluAsn 382  
Qy 1159 AACTACAAGACACCGCTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1218  
Db 383 AsnTyrAsnThrThrProMetLeuAspSerAspGlySerPhePheLeuTyrSerLys 402  
Qy 1219 CTCACCGTGGCAAGAGCAGGTGGCAGCAGGGGAACTTCTCTCATGCTCCGTGATGCAT 1278  
Db 403 LeuThrValAspLysSerArgTrpGlnGlnGlyAsnIlePheSerCysSerValMetHis 422  
Qy 1279 GAGGCTCTGCACACCACTACAGCAGAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCCG 1326  
Db 423 GluAlaLeuHisAsnArgPheThrGlnLysSerLeuSerLeuSerPro 438

RESULT 7  
Q8R3V9 PRELIMINARY; PRT; 469 AA.  
ID Q8R3V9  
AC Q8R3V9  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.  
GN IGH-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC024405; AAH24405.1; -.  
DR PIR; B45837; B45837.  
DR MGI; MG1:96446; Igh-4.  
DR InterPro; IPR007110; Igh-4.  
DR InterPro; IPR003006; Igh-MHC.  
DR InterPro; IPR003596; Igh\_v.  
DR Pfam; PF00047; Igh\_3.  
DR SMART; SM00406; Ighv; 1.  
DR PROSITE; PS00835; IGH\_LIKE; 4.  
DR PROSITE; PS00290; IGH\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;  
  
Alignment Scores:  
Pred. No.: 2,41e-118 Length: 469  
Score: 1591.00 Matches: 293  
Percent Similarity: 78.82% Conservative: 68  
Best Local Similarity: 63.97% Mismatches: 75  
Query Match: 66.15% Indels: 22  
Gaps: 5  
DB:  
  
US-09-674-716b-18 (1-1335) x Q8R3V9 (1-469)  
Qy 1 GAGGTGACGTGGTGGAGTCTGGGGAGCTTGGTAAAGCCCGGGGGTCCCTTAGATC 60  
Db 20 GluValAsnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39  
Qy 61 TCCTGTGACGTACCGGATTCACCTTCAGTGGCTACTGATGCTCCTGGTCCGCCAGGCT 120  
Db 40 SerCysAlaAlaSerGlyPheThrAspTyrTyrMetSerTrpValArgGlnPro 59  
Qy 121 CCAGGGAAGGGCTCCAGTGGGTGCTGAAATAGATTGAAATCTGATTAATTCGAACA 180  
Db 60 ProGlyLysAlaLeuGluTrpLeuGlyPheIleArgAsnLysAlaAsnGlyTyrThr 79  
Qy 181 CATTATCGGAGTCTGTGAAGGGGAAATTCACATCTCAAGAGATGATTCAAATCTAGA 240  
Db 80 GluTyrSerAlaSerValLysGlyArgPheThrIleSerArgAspAsnSerGlnSer 99  
Qy 241 CTGTATCTGCAATGAACAGCCTGAAACCCGAGGACACAGCCGCTGTATTACTGT----- 294  
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Qy 295 -----ACAGATTTCATAGACTGGGGCCAGGGAACA 324  
Db 120 AspArgArgSerSerTyrTyrSerGlyThrSerPheAlaTyrTrpGlyGlnGlyThr 139  
Qy 325 CTAGTCACCGTCTCCCTCAGCTCCACAGGGCCCATCGTCTTCCCTCCCTGGCACCTCC 384  
Db 140 LeuValThrValSerAlaLysThrThrProSerValTyrProLeuAlaProGly 159  
Qy 385 TCCAAGAGCACCTCTCGGGGCACAGCGCCCTCGGCTGCTGCTCAAGGACTACTTCCCC 444  
Db 160 SerAlaAlaGlnThrAsnSerMetValThrLeuGlyCysLeuValLysGlyTyrPhePro 179  
Qy 445 GAACCGGTGACGGTGTGCTGGAACCTAGGCGCCCTGACAGCGCGCTGACACCTTCCCG 504  
Db 180 GluProValThrValThrTrpAsnSerGlySerLeuSerSerGlyValHisThrPhePro 199  
Qy 505 GCTGCTCTCAGTCTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGGTGGTGGTGGTGGT 564  
Db 200 AlaValLeuGlnSerAsp---LeuTyrThrLeuSerSerSerValThrValProSerSer 218









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138 SerAlaAlaLysThrThrProProSerValTyrProLeuAlaProGlySerAlaAlaGln 157
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158 ThrAsnSerMetValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThr 177
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178 ValThrTrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGln 197
517 TCCCTCAGGAATCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTGGGCACC 576
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198 SerAsp--LeuTyrThrLeuSerSerSerValThrValProSerSerThrTrpProSer 216
577 CAGACCTACATCTGCACAGTGAATCACAGCCCGACACACCAAGGTGGCAAGAAAGTG 636
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217 GluThrValThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysLe 236
637 GAGCCCAAAATCTGTGCACAAAATCACACATGCCACCG-----TGCCACGACCTGAA 690
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237 ValProArgAspCysGly-----CysLysProCysLysThrValProGlu 252
691 CTCGGGGGGACCGTCAGTCTTCCTCTTCCCGCCGAAACCAAGGACACCTCATGATC 750
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253 ValSer-----SerValPheIlePheProLysProLysAspValLeuThrIle 269
751 TCCCGGACCCCTGAGGTTCATCGCTGGTGGACGTGAGCCAGCACAGACCCCTGAGTCT 810
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270 ThrLeuThrProLysValThrCysValValValAspIleSerLysAspAspProGluVal 289
811 AAGTTCAACTGTACGTGGAGCGCGTGGAGGTGCATAATGCCAAGAACAAAGCCGGGAG 870
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290 GlnPheSerTrpPheValAspAspValGluValHisThrAlaGlnThrGlnProArgGlu 309
871 GAGCAGTACACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 930
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310 GluGlnPheAsnSerThrPheArgSerValSerGluLeuProIleValHisGlnAspTrp 329
931 CTGAATGCGAAGGAGTACAAAGTCCAAAGTCTCCAAAGACCCCTCCAGCCCCCATCGAG 990
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330 LeuAsnGlyLysGluPheLysCysArgValAsnSerAlaAlaPheProAlaProIleGlu 349
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430 LysSerAsnTrpGluAlaGlyAsnThrPheThrCysSerValLeuHisGlyLeuHis 449
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450 AsnHisHisThrGluLysSerLeuSerHisSerProGlyLys 463

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DE 181060009Rik protein.  
GN IGH-1 OR 181060009RIK.  
OC Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CS7BL/6J; TISSUE=Pancreas;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Akaiwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Asburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL; AK007918; BAB25349.1; -;  
DR PIR; S26746; S26746.  
DR HSSP; P01842; 7FAB.  
DR MGD; MG1:96443; Igh-1.  
DR InterPro; IPR007110; Igh-like.  
DR InterPro; IPR003006; Igh.MHC.  
DR InterPro; IPR003596; Igh.V.  
DR Pfam; PF00047; Igh; 3.  
DR SMART; SM00406; Igh; 1.  
DR PROSITE; PS50835; IGH LIKE; 4.  
DR PROSITE; PS00290; IGH.MHC; 1.  
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FB8 CRC64;

Alignment Scores:  
Pred. No.: 1.3e-106 Length: 473  
Score: 1444.00 Matches: 267  
Percent Similarity: 75.49% Conservative: 78  
Best Local Similarity: 58.42% Mismatches: 96  
Query Match: 60.04% Indels: 16  
DB: 11 Gaps: 4

US-09-674-716B-18 (1-1335) x Q9D8L4 (1-473)

QY 1 GAGGTGACGTGTCGAGTCTGGGGAGGCTGTGTAAGCCGGGGGTCCTTAGATC 60  
Db .....  
QY 20 GlnValGlnLeuLysGlnSerGlyAlaGluLeuValLysProGlyAlaSerValLysIle 39  
Db .....  
QY 61 TCTGTGACGTAGCGGATTCATCTTCACTGAGTGGCTACTGAGTCTCTGGGTCGGCAGGCT 120  
Db .....  
QY 40 SerCysLysAlaSerGlyTyrThrPheThrAspTyrTyrIleAsnTrpValLysGlnArg 59  
Db .....  
QY 121 CCAGGGAAGGGCTGAGTGGGCTGCTGAAATAGATTGAATCTGAAATATTATGCACA 180  
Db .....  
QY 60 ProGlyGlnGluLeuTrpIleGlyLysIleGlyProGlySerGly-----SerThr 77  
Db .....  
QY 181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGA 240  
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QY 78 TyrTyrAsnGluLysPheLysGlyLysAlaThrLeuThrAlaAspLysSerSerThr 97  
Db .....  
QY 241 CTGATCTCAATGACAGCTGAAACCGAGGACACAGCGGTATATCTGATGACAGAT 300  
Db .....  
QY 98 AlaTyrMetGlnLeuSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArg 117  
Db .....

QY 301 -----TTCTATAGACTGGGGCAGGGAAACACTAGTACCGTCTCC 339  
Db .....  
QY 118 SerGlyTyrAspTyrAspTrpPheAlaValTyrTrpGlyGlnGlyThrLeuValThrValSer 137  
Db .....  
QY 340 TCAGCCTCCACCAAGGGCCATCGGTCTTCCCTGGCACCTCTCCTCCAAGACACCTCT 399  
Db .....  
QY 138 AlaAlaLysThrThrAlaProSerValTyrProLeuAlaProValCysGlyGlyThrThr 157  
Db .....  
QY 400 GGGGGCACAGCGCCCTCGGTCAAGGACTACTTCCCGAAACCGGTGACGGTG 459  
Db .....  
QY 158 GlySerSerValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThrLeu 177  
Db .....  
QY 460 TCGTGGAACTCAGCGCCCTGACCGGGCGGTGCACACCTTCCCGGTCTCTACAGTCC 519  
Db .....  
QY 178 ThrTrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaLeuLeuGln--- 196  
Db .....  
QY 520 TCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAG 579  
Db .....  
QY 197 SerGlyLeuTyrThrLeuSerSerSerValThrValThrSerAsnThrTrpProSerGln 216  
Db .....  
QY 580 ACCTACATCTGCAACGTGAATCAAGCCGACACACCAAGGTGACAGAAAGTGGAG 639  
Db .....  
QY 217 ThrIleThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysIleGlu 236  
Db .....  
QY 640 CCCAAA-----TCTTGTGACAAAACCTCACACATGCCCCACCGTCCCA 681  
Db .....  
QY 237 ProArgValProIleThrGlnAsnProCysProProLeuLysGluCysProProCysAla 256  
Db .....  
QY 682 GCACCTGAATCGCGGGGACCGTCACTTCTTCTTCCCGCCAAAACCCAGGACACC 741  
Db .....  
QY 257 AlaProAspLeuLeuGlyGlyProSerValPheIlePheProLysIleLysAspVal 276  
Db .....  
QY 742 CTGATGATCTCCCGGACCCCTGAGGTACATGCTGTGGTGGACGTGACGACGACGAGAC 801  
Db .....  
QY 277 LeuMetIleSerLeuSerProMetValThrCysValValValAspValSerGluAspAsp 296  
Db .....  
QY 802 CTTGAGTCAAGTTCACTGGTACGTGGAGCGGTGGAGTGCATATATCCCAAGACAAAG 861  
Db .....  
QY 297 ProAspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGln 316  
Db .....  
QY 862 CCGGGGAGGAGCAGTACACAGCAGTACCTGCTGTGTGCTGAGCTCCTACCGTCTGTCAC 921  
Db .....  
QY 317 ThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHis 336  
Db .....  
QY 922 CAGGACTGGCTGAATGCAAGGAGTACAAAGTCAAGGTCTCCAACAAAGCCCTCCAGCC 981  
Db .....  
QY 337 GlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnArgAlaLeuProSer 356  
Db .....  
QY 982 CCATCGAGAAACCATCTTCCAAAGCCAAAGGGCAGCCCGGAGACCAACAGGTGTACACC 1041  
Db .....  
QY 357 ProIleGluLysThrIleSerLysProArgGlyProValArgAlaProGlnValTrpVal 376  
Db .....  
QY 1042 CTGCCCCCATCCCGGATGAGTGCACCAAGAACCCAGTCAAGTCAAGTCAAGTCAAGTCAAA 1101  
Db .....  
QY 377 LeuProProProAlaGluGluMetThrLysLysGluPheSerLeuThrCysMetIleThr 396  
Db .....  
QY 1102 GGTTTCTATCCAGCAGCATTCGCGGTGGAGTGGAGAGCAATGGGCGAGCCGAGAACAC 1161  
Db .....  
QY 397 GlyPheLeuProAlaGluIleAlaValAspTrpThrSerAsnGlyArgThrGluGlnAsn 416  
Db .....  
QY 1162 TACAAGACCAAGCTCCCGTGTGGACTCCGAGGCTCTCTTCTCTCTACAGCAAGCTC 1221  
Db .....  
QY 417 TyrLysAsnThrAlaThrValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeu 436  
Db .....  
QY 1222 ACCGTGGACAGAGCAGGTGGCAGAGGGGAAACGTCTTCTCATGTCTCGTATGATGATG 1281  
Db .....  
QY 437 ArgValGlnLysSerThrTrpGluArgGlySerLeuPheAlaCysSerValValHisGlu 456  
Db .....  
QY 1282 GCTCTGCACACCACTACAGCAGAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332  
Db .....  
QY 457 GlyLeuHisAsnHisLeuThrThrLysThrIleSerArgSerLeuGlyLys 473  
Db .....

Q7TMK1  
 ID Q7TMK1 PRELIMINARY; PRT; 470 AA.  
 AC Q7TMK1.  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CZECH II; TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loguillano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CZECH II; TISSUE=Breast tumor;  
 RA Strausberg R.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC055910; AAH55910.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;

Alignment Scores:  
 Pred. No.: 6,2e-106 Length: 470  
 Score: 1435.50 Matches: 272  
 Percent Similarity: 74.29% Conservative: 66  
 Best Local Similarity: 59.78% Mismatches: 102  
 Query Match: 59.69% Indels: 15  
 DB: 11 Gaps: 5

US-09-674-716b-18 (1-1335) x Q7TMK1 (1-470)

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
 Db 20 GluValGlnLeuGlnSerGlyProGluLeuValValysProGlyAlaSerValysile 39  
 QY 61 TCCTGTGACGTAGCGGATCACTTTCAGTGCTACTGCTGCTGCTGGTCCGCCAGGCT 120  
 Db 40 SerCysLysAlaSerGlyThrPheThrGlyTyrThrMetHisTrpValysGlnSer 59  
 QY 121 CCAGGGAAGGGCTCGAGTGGGTGTGCTGAAATAGATTGAAATCTCATTAATATGCAACA 180  
 Db 60 HisGlyLysSerLeuGluTrpIleGlyLeuVal-----AsnProSerAsnGlyAspThr 77  
 QY 181 CATATTGCGGAGTCTGTGAAGGGAAATTCACATCTCAAGAGATGATTCAAATCTAGA 240  
 Db 78 SerTyrAsnGlnLysPheLysGlyLysAlaThrLeuThrValAspLysSerSerThr 97  
 QY 241 CTGTATCTCAATGAACAGCTGAAACCGAGGACACAGCGGTGTATTACTGTACAGAT 300  
 Db 98 AlaTyrMetGluLeuAsnSerLeuThrSerGluAspSerAlaValTyrTyrCysalaarg 117

QY 301 -----TTCATAGACTGGGGCCAGGGAACACACTAGTCACC 333  
 Db 118 TyrTyrTyrSerGlySerTyrTrpTyrPheAspValTrpGlyAlaGlyThrThrValThr 137  
 QY 334 GTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCTCGCACCCTCTCCACAGAGC 393  
 Db 138 ValSerSerAlaThrThrAlaProSerValTyrProLeuValProGlyCysGlyAsp 157  
 QY 394 ACCTCTGGGGGCACAGCGGCGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTG 453  
 Db 158 ThrSerGlySerSerValThrLeuGlyCysLeuValysGlyTyrPheProGluProVal 177  
 QY 454 ACGGTGCTGTGAACACTCAGGCGCCCTGACGAGCGGGGTGCACACTTCCCGGCTGCTTA 513  
 Db 178 ThrValysTrpAsnTyrGlyAlaLeuSerSerGlyValArgThrValSerSerValLeu 197  
 QY 514 CAGTCTCAGAGCTACTCTCCCTCAGCAGCGTGGTACCGTGCCTCCACAGCACTTGGGC 573  
 Db 198 Gln---SerGlyPheTyrSerLeuSerSerLeuValThrValProSerSerThrTrpPro 216  
 QY 574 ACCCAGACCTACATCTGCAACGTAATCAACGCCGACCAACCAAGGTTGGACAGAAA 633  
 Db 217 SerGlnThrValIleCysAsnValAlaHisProAlaSerLysThrGluLeuIleLysArg 236  
 QY 634 GTGAGGCCAAATCTTGTGACAAACTCACACATGCCCA-----CCGTGCCAGCACCT 687  
 Db 237 IleGluProArg---IleProLysProSerThrProProGlySerSerCysProProGly 255  
 QY 688 GAATCTCGCGGGGCACCGTCACTCTCTCTCTCCCTCCCAAAACCAAGGACACCTCATG 747  
 Db 256 AsnIleLeuGlyGlyProSerValPheIlePheProLysProLysAspAlaLeuMet 275  
 QY 748 ATCTCCCGGACCTCAGGTACATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 807  
 Db 276 IleSerLeuThrProLysValThrCysValValValAspValSerGluAspAspProAsp 295  
 QY 808 GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGTGCATTAATGCCAAGACAAAGCCCGG 867  
 Db 296 ValHisValSerTrpPheValAspAsnLysGluValHisThrAlaTrpThrGlnProArg 315  
 QY 868 GAGGAGCAGTACACACACACGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 927  
 Db 316 GluAlaGlnTyrAsnSerThrPheArgValValSerAlaLeuProIleGlnHisGlnAsp 335  
 QY 928 TGGCTGATGCAAGGAGTACAGTCAAGTCTCCAACAAAGCCCTCCAGCCGCCCATC 987  
 Db 336 TrpMetArgGlyLysGluPheLysCysLysValAsnAsnLysAlaLeuProAlaProIle 355  
 QY 988 GAGAAAACCATCTCCAAAGCCAAAGGCGACGCCCGGAGAACACACAGTGTACACCTGCC 1047  
 Db 356 GluArgThrIleSerLysProLysGlyArgAlaGlnThrProGlnValTyrThrIlePro 375  
 QY 1048 CCATCCCGGATGAGTGCACCAAGACACCGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1107  
 Db 376 ProProArgGluGlnMetSerLysLysValSerLeuThrCysLeuValThrAsnPhe 395  
 QY 1108 TATCCAGCGACATCGCCGTGGAGTGGAGCAATGGGCGAGCGGAGAGAACAACTACAAG 1167  
 Db 396 PheSerGluAlaIleSerValGluTrpGluArgAsnGlyGluLeuGluGlnAspTyrLys 415  
 QY 1168 ACCAGCGCTCCCGTGTGGAGCTCCGACGGCTCTTCTCTCTACACCAAGCTCACCGT 1227  
 Db 416 AsnThrProIleLeuAspSerAspGlyThrTyrPheLeuTyrSerLysLeuThrVal 435  
 QY 1228 GACAAGACGAGTGGCAGCGGGGAACGTCTCTCATGCTCCGATGATGATGAGGCTCTG 1287  
 Db 436 AspThrAspSerTrpLeuGlnGlyGluIlePheThrCysSerValValHisGluAlaLeu 455  
 QY 1288 CACAACCACTACACGCAAGAGCTCTCCCTGTCTCCGGGTAAA 1332  
 Db 456 HisAsnHisThrGlnLysAsnLeuSerArgSerProGlyLys 470

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RESULT 14
Q99L31 PRELIMINARY; PRT; 468 AA.
ID Q99L31
AC Q99L31;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC003878; AA03878.1; -.
DR PDB; 2AP2; 24-NOV-99.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Alignment Scores:
Pred. No.: 4,2e-102 Length: 468
Score: 1387.50 Matches: 267
Percent Similarity: 72.63% Conservative: 62
Best Local Similarity: 58.94% Mismatches: 111
Query Match: 57.69% Indels: 13
DB: 11 Gaps: 6

US-09-674-716B-18 (1-1335) x Q99L31 (1-468)
QY 1 GAGGTGACCTGGTGGAGCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGATC 60
Db 20 GluValGlnGlnSerGlyAlaGluLeuValArgProGlyAlaSerValIysLeu 39
QY 61 TCCTGTGCACTAGCGAGTTCATCTTCACTGGGTCTGATGCTGCTGGGTCCGCCAGGCT 120
Db 40 SerCysThrAlaSerGlyPheAsnIleLysAspSerLeuMetHisTrpValIysGlnArg 59
QY 121 CAGGGAAGGGCTCGAGTGGGTGCTGAAATAGATTGAATCTGATAATTATCAACA 180
Db 60 ProGluGlnGlyLeuGluTrpIleGlyTrpIle-----AspProGluAspGlyGluThr 77
QY 181 CATTATCGGAGTCTGTGAAGGGGAATTCACATCTCAAGAGATGATTCAAAATCTAGA 240
Db 78 LysTyrAlaProLysPheGlnAspIysAlaThrIleThrAlaAspThrSerSerAsnThr 97
QY 241 CTGTATCTGCAATGAACAGCTGAAACCGAGGACACAGCGGTATTAATCTGTACA--- 297
Db 98 AlaTyrLeuGlnLeuSerSerLeuThrSerGluAspThrAlaIleTyrTyrCysAlaArg 117
QY 298 -----GATTTCATAGAC---TGGGGCCGAGGACACTAGTACCGTCTCC 339
Db 118 AsnLeuLeuTyrGlyTyrTyrAspTyrTrpGlyGlnGlyThrIleThrValSer 137
QY 340 TCAGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCTCTCCCAAGACACCTCT 399
Db 138 SerAlaLysThrThrAlaProSerValTyrProLeuAlaProValCysGlyAspThrThr 157
QY 400 GGGGGCACAGCGGCTGGCTGGCTGGCTCAGGACTCTTCCCGAACCGGTGACGGTG 459
Db 158 GlySerSerValThrLeuGlyCysLeuValIysGlyTyrPheProGluProValThrLeu 177
QY 460 TCGTGAATCTAGGCGCCCTACGACGCGGCTGCACACCTTCCCGGCTGTCTACAGTCC 519
Db 178 ThrTrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGlnSer 197

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QY 520 TCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGACCCAG 579
Db 198 Asp---LeuTyrThrLeuSerSerValThrValThrSerSerThrTrpProSerGln 216
QY 580 ACCTACATCTGCAACGTGAATCAAGCCAGCCAGCAACACCAAGGTGACCAAGAAAGTGGAG 639
Db 217 SerIleThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysIleGlu 236
QY 640 CCAGAACTTGTGACAAACTCACACATGCCACCG-----TGCCAGCACCTGAATC 693
Db 237 ProArgGly--ProThrIleLysProCysProProCysLysCysProAlaProAsnLeu 255
QY 694 GCGGGGACACCGTCAGTCTTCTTCCCGCCCAAAACCCCAAGGACACCTCATGATCTCC 753
Db 256 LeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeuMetIleSer 275
QY 754 CGGACCCCTGAGTCCATCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 813
Db 276 LeuSerProMetValThrCysValValValAspValSerGluAspAspProAspValGln 295
QY 814 TTCAACTGGTACGTGGACGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAG 873
Db 296 IleSerTrpPheValAsnAsnValGluValLeuThrAlaGlnThrGlnThrHisArgGlu 315
QY 874 CAGTACAAAGCAGGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 933
Db 316 AspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMet 335
QY 934 AATGGCAAGGAGTCAAGTCAAGGTCTCCAAAGCCCTCCAGCCCGCCCATCCGAGAAA 993
Db 336 SerGlyLysGluPheLysCysLysValAsnAsnLysAlaLeuProIleGluArg 355
QY 994 ACCATCTCAAAGCCAAAGGCGAGCCCGAGAACCCAGAGTGTACACCTGCCCGCCATCC 1053
Db 356 ThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeuProProPro 375
QY 1054 CGGATGAGTGTGACCAAGAACCAAGGTCAAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 1113
Db 376 GluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetPro 395
QY 1114 AGCGACATCCCGTGGAGTGGGAGAGCAATGGGACGCGGAGAACCACTACAGACCCAG 1173
Db 396 GluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThr 415
QY 1174 CTCCCGTGTGCACTCCGAGCGGTCTTCTTCTCTCTACAGCAAGCTCAGCGTGGACAG 1233
Db 416 GluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLys 435
QY 1234 AGCAGTGGCAGCAGGGGACGCTTCTTCTCATGTCCGTGATGATGATGATGATGATGAT 1293
Db 436 LysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsn 455
QY 1294 CACTACCGCAGAGACCGCTCTCCCTGCTCCCGGTAAA 1332
Db 456 HisHisThrThrLysSerPheSerArgThrProGlyLys 468

RESULT 15
Q8R3H6 PRELIMINARY; PRT; 474 AA.
ID Q8R3H6
AC Q8R3H6;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AU04919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC025447; AAH25447.1; -.  
DR MGD; MGI:2144967; A044919.  
DR GO; GO:0005489; F:electron transporter activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR000345; Cytochrome\_BS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_3.  
DR SMART; SM00406; IGV.1.  
DR PROSITE; PS00190; CYTOCHROME\_C; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6D2874A CRC64;

Alignment Scores:  
Pred. No.: 1,06e-101 Length: 474  
Score: 1382.50 Matches: 262  
Percent Similarity: 72.71% Conservative: 71  
Best Local Similarity: 57.21% Mismatches: 108  
Query Match: 57.48% Indels: 17  
DB: 11 Gaps: 5

US-09-674-716B-18 (1-1335) x Q8R3H6 (1-474)

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QY 61 TCCTGTGACGTAGGGGATTCACTTTCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
DB 40 SerCysArgAlaSerGlyAlaPheSerLysSerLysSerLysSerLysSerLysSer 59  
QY 121 CCAGGGAAGGGCTCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180  
DB 60 ProGlyLysGlyLeuGluTrpIleGly-----ArgIlePheProGlyAspGlyThr 77  
QY 191 CATATGGGGAGTCTGTGAAGGGGAAATTCACCTCTCAAGAGATGATTCAAAATCTAGA 240  
DB 78 HisTyrSerGlyLysPheGlnGlyLysAlaLysLeuThrAlaAspLysSerValThr 97  
QY 241 CTGTATCTGCAAAATGAACAGCTGAAACCCAGAGACACAGCCGTGTTACTGTACAGAT 300  
DB 98 AlaPheLeuGlnLeuThrSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArg 117  
QY 301 -----TTCTATGACTGGGGCCAGGGAAACACATAGTACCGTCTCC 339  
DB 118 AspSerAspTyrGlyAspTyrPheAspAspTrpGlyGlnGlyAlaThrValThrValSer 137  
QY 340 TCAGCTCCACCAAGGCCCTCGGTCTCCCTCGGCACCTCTCCCAAGAGCACCTCT 399  
DB 138 SerAlaLysThrProProSerValTyrProLeuAlaProGlyCysGlyAspThrThr 157  
QY 400 GGGGGCACAGCGCCCTGGGTGCTGTGCTCAAGGACTACTTCCCGGAACCGGTGACGGTG 459  
DB 158 GlySerSerValThrLeuGlyCysLeuValLysGlyTyrPheProGluSerValThrVal 177  
QY 460 TCGTGGAACTCAGCGCCCTGACAGCGCGGTGACACCTTCCCGGTGCTCTACAGTCC 519  
DB 178 ThrTrpAsnSerGlySerLeuSerSerSerValHisThrPheProAlaLeuLeuGln--- 196  
QY 520 TCAGACTCTACTCCTCAGACCGTGTGTGACCGCTCCAGCAGCTTGGGACCCAG 579  
DB 197 SerGlyLeuTyrThrMetSerSerSerValThrValProSerSerThrTrpProSerGln 216  
QY 580 ACCTACATCTGCAAGCTGAATCACAAGCCCGACACACACAGGTGGAGCAAGAAGTGGAG 639  
DB 217 ThrValThrCysSerValAlaHisProAlaSerSerThrThrValAspLysLysLeuGlu 236  
QY 640 CCCAAATCTGTGCAAAACT---CACACATGCCACCG-----TGC 678  
DB 237 ProSerGlyProIleAsnThrIleAsnProCysProCysLysGluCysHisLysCys 256

Search completed: September 30, 2004, 08:54:03  
Job time : 192.047 secs

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DB 257 ProAlaProAsnLeuGluGlyGlyProSerValPheIlePheProAsnIleLysAsp 276  
QY 739 ACCCTCATGATCTCCCGGACCCCTGAGTGCATGCTGGTGGTGGTGGTGGTGGTGGT 798  
DB 277 ValLeuMetIleSerLeuThrProLysValThrCysValValValAspValSerGluAsp 296  
QY 799 GACCTGAGTCAAGTTCACTGAGTGGGCGGTGGAGTGCATATATGCAAGACA 858  
DB 297 AspProAspValGlnIleSerTrpPheValAsnValGluValHisThrAlaGlnThr 316  
QY 859 AAGCCCGGGAGGAGGAGTACACACAGTACCGGTGGTGGTGGTGGTGGTGGTGGTGGT 918  
DB 317 GlnThrHisArgGluAspTyrAsnSerThrIleArgValValSerAlaLeuProIleGln 336  
QY 919 CACGAGGAGTGGCTGAATGGCAGGAGTACAGTGCAGGTCTCCAAAGCCCTCCCA 978  
DB 337 HisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuPro 356  
QY 979 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGACGCCCGGAGAACACACAGGTGTAC 1038  
DB 357 SerProIleGluArgThrIleSerLysIleLysGlyLeuValArgAlaProGlnValTyr 376  
QY 1039 ACCCTGCCCATCCCGGATGAGCTGACCAAGACACAGTGCAGCTGACCTGACCTGGTCT 1098  
DB 377 IleLeuProProAlaGlnLeuSerArgLysAspValSerLeuThrCysLeuVal 396  
QY 1099 AAAGGCTTCTATCCCGACGACATCGCGTGGAGTGGAGCAATCGGCGCGGAGAAC 1158  
DB 397 ValGlyPheAsnProGlyAspIleSerValGluTrpThrSerAsnGlyHisThrGluGlu 416  
QY 1159 AACTAGAACACACGCTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1218  
DB 417 AsnTyrLysAspThrAlaProValLeuAspSerAspGlySerTyrPheIleTyrSerLys 436  
QY 1219 CTCACGTGGACAAAGACGAGTGGCGAGGGAACGTCTTCTCATGCTCCGCTGATGCAT 1278  
DB 437 LeuAspIleLysThrSerLysTrpGluLysThrAspSerPheSerCysAsnValArgHis 456  
QY 1279 GAGGCTCTGCACAAACCATACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAAA 1332  
DB 457 GluGlyLeuLysAsnTyrTyrLeuLysLysThrIleSerArgSerProGlyLys 474

Blank sheet



OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:19:42 ; Search time 159.041 Seconds  
(without alignments)  
4743.430 Million cell updates/sec

Title: US-09-674-716B-19

Perfect score: 2405

Sequence: 1 gaggtgcagtggtggagtc.....ccctgtctccgggtaaatga 1335

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2.1/USPTO.spool/p/US09674716/runat.30092004.070257.25848/app\_query.fasta.1.3164  
-DB=A\_Geneseq\_29Jan04 -QFWT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFWT=pco -NORV=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09674716@cgn.1.1.475@runat.30092004.070257.25848 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_29Jan04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2367	98.4	444	3 AAY32263	Aay32263 Humanised
2	2199.5	91.5	461	2 AAR42162	Aar42162 Anti-HIV-
3	2191	91.1	447	6 AAE33524	Aae33524 Human AQC
4	2191	91.1	447	6 AAE33522	Aae33522 Human AQC
5	2188.5	91.0	449	6 ABP58273	Abp58273 Humanised
6	2188.5	91.0	468	6 ABP58275	Abp58275 Humanised
7	2187	90.9	444	6 AAE35327	Aae35327 Humanised
8	2187	90.9	444	6 AAE34876	Aae34876 BIWA4/8 a
9	2185	90.9	447	6 AAE33523	Aae33523 Human AQC
10	2183	90.8	442	6 ABR39455	AbR39455 Humanised

11	2183	90.8	442	6 ABU08311	Abu08311 Humanised
12	2183	90.8	442	6 ABB80109	Abb80109 Heavy cha
13	2183	90.8	445	6 AAO31101	Aao31101 Human A2-
14	2183	90.8	461	4 AAU07745	Aau07745 Humanised
15	2183	90.8	461	6 ABR39844	AbR39844 Hu266 N56
16	2183	90.8	461	6 ABR39847	AbR39847 Hu266 N56
17	2183	90.8	461	6 ABR39843	AbR39843 Hu266 N56
18	2183	90.8	461	6 ABR39848	AbR39848 Hu266 N56
19	2178	90.6	442	6 ABR39474	AbR39474 Humanised
20	2178	90.6	442	6 ABU08320	Abu08320 Humanised
21	2178	90.6	442	6 ABR39793	AbR39793 Humanised
22	2178	90.6	442	6 ABB80113	Abb80113 Deglycosy
23	2173.5	90.4	449	3 AAY68810	Aay68810 A rat hea
24	2172.5	90.3	451	4 AAE12715	Aae12715 Human rsc
25	2172.5	90.3	451	4 ABUS8807	Abus8807 Nucin 1 (
26	2172.5	90.3	474	5 AAO14065	Aao14065 Heavy cha
27	2172.5	90.3	474	6 ABU08017	Abu08017 Human mon
28	2170	90.2	474	6 AAO18400	Aao18400 Mature hu
29	2166.5	90.1	582	4 AAB81987	Aab81987 Ganglios
30	2161.5	89.9	478	2 AAW63763	Aaw63763 Macaque p
31	2161.5	89.9	478	5 AAU11644	Aau11644 Protein s
32	2161	89.9	477	4 AAU14288	Aau14288 Human nov
33	2160	89.8	475	2 AAR20057	Aar20057 Heavy cha
34	2155.5	89.6	478	2 AAW01820	Aaw01820 Primatise
35	2151.5	89.5	453	3 AAR33311	Aar33311 Humanised
36	2151.5	89.5	453	3 AAY85199	Aay85199 Heavy cha
37	2151.5	89.5	464	5 ABG78151	Abg78151 Human Fv
38	2151.5	89.5	464	5 ABR91842	AbR91842 Human ant
39	2150.5	89.4	451	2 AAW95663	Aaw95663 Mus muscu
40	2150.5	89.4	451	2 AAY50031	Aay50031 Human E27
41	2150.5	89.4	451	3 AAB07473	Aab07473 Amino aci
42	2150.5	89.4	451	4 AAB76952	Aab76952 Full leng
43	2150.5	89.4	451	4 AAB74212	AbA74212 E27 anti-
44	2150.5	89.4	451	6 ABU62798	Abu62798 E27 anti-
45	2150.5	89.4	478	6 AAE37362	Aae37362 Monkey 7B

#### ALIGNMENTS

RESULT 1

AAY32263

ID AAY32263 standard; protein; 444 AA.

XX AC AAY32263;

XX AC AAY32263;

DT 15-FEB-2000 (first entry)

XX DE Humanised anti-CD23 Mab C11 heavy chain.

XX DE Humanised anti-CD23 Mab C11 heavy chain.

XX KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;

XX KW monoclonal antibody; chimeric antibody; humanised antibody;

XX KW complementarity determining region; CDR; autoimmune disease;

XX KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

XX KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

XX KW urticaria; nephrotic syndrome; glomerulonephritis;

XX KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

XX KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulin;

XX KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX KW therapy.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key

XX FT Region

XX FT Region

XX FT Region

XX FT Region

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XX FT Region

Location/Qualifiers

1. .30

/note= "framework region 1"

31. .35

/note= "CDR 1"

36. .49

/note= "framework region 2"

50. .68

/note= "CDR 2"

69. .100

FT Region /note= "framework region 3"  
 FT 101..103  
 FT /note= "CDR 3"  
 FT Region 104..111  
 FT /note= "framework region 4"  
 FT Region 112..444  
 FT /note= "constant region"

XX WO958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX ) GLAXO GROUP LTD.

XX Bonney JNP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX N-PSDB; AA234748.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.

XX Claim 9; Fig 4; 81pp; English.

XX This amino acid sequence represents the heavy chain of humanised anti-  
 CC CD23 (FCRII) monoclonal antibody C11, composed of a human framework  
 CC (HS10K17) and the heavy chain complementarity determining regions (see  
 CC AAY32257-59) of murine antibody C11. The DNA was constructed by splice  
 CC overlap PCR. The invention provides altered antibodies, such as chimeric  
 CC or humanised antibodies, which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions to render them capable of binding to the CD23 type II molecule  
 CC expressed on haematopoietic cells. The antibodies are used to block  
 CC soluble CD23 formation in human therapy, for the treatment of arthritis,  
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,  
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,  
 CC glomerulonephritis, inflammatory bowel disease, ulcerative colitis,  
 CC Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents

XX Sequence 444 AA;

XX Alignment Scores:

Pred. No.: 3,43e-141 Length: 444  
 Score: 2367.00 Matches: 444  
 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.42% Indels: 0  
 DB: 3 Gaps: 0

US-09-674-716B-18 (1-1335) x AAY32263 (1-444)

QY 1 GAGGTGCGAGCTGGTGGGAGCTGGTAAAGCCGGGGGTCCCTTAGACTC 60  
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
 QY 61 TCCTGTGAGCTAGCGGATTCATCTTTCAGTGGCTACTGGATGCTCGGTCCGCGAGCT 120  
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerGlyTyTrpMetSerTrpValArgGlnAla 40  
 QY 121 CCAGGGAAGGGGCTCGAGTGGGTTCCTGAAATTAGATTGAATCTGTAATATTGCAACA 180  
 Db 41 ProGlyLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAspAsnTyAlaThr 60  
 QY 181 CATTATGCGGAGTCTGTGTAAGGGGAAATTCACCAATCTCAAGAGATGATTCAAATCTAGA 240

Db 61 HisTyrAlaGluSerValLysGlyLysPheThrIleSerArgAspSerLysSerArg 80  
 QY 241 CTGTATCTGCAAAATGAACAGCTTGAACACCCAGAGACACAGCCGTGATTACTGTACAGAT 300  
 Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrAsp 100  
 QY 301 TTCATAGACTGGGGCCAGGAAACACATAGTCCACCGTCTCTCTCAGCTCCACCAAGGGCCCA 360  
 Db 101 PheIleAspTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 120  
 QY 361 TCGGTCTTCCCTCGCACCTCTCCAAAGAGCACCTCTGGGGGACAGCGGCGCTGGGC 420  
 Db 121 SerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGly 140  
 QY 421 TGCTGTGTCAGGACTACTTCCCGAACCGGTGACCGTGTCTGTGGAACCTCAGCGCCCTG 480  
 Db 141 CysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu 160  
 QY 481 ACCAGCGGCTGCACACCTTCCCGGCTGCTCTACAGTCTCTCAGGACTCTACTCCCTCAG 540  
 Db 161 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSer 180  
 QY 541 AGCGTGTGAGCTGCTCCCTCCAGCAGCTTGGGACCCAGACCTTACATCTGCAACGTGAAT 600  
 Db 181 SerValValThrValProSerSerLeuGlyThrGlnThrTyrIleCysAsnValAsn 200  
 QY 601 CACAAGCCCGACACACCAAGGTGGACAAAGTGGAGCCCAATCTTGTGACAAACT 560  
 Db 201 HisLysProSerAsnThrLysValAspLysLysValGluProLysSerCysAspLysThr 220  
 QY 661 CACACATGCCACCGTCCCGACGACCTGAACCTCGCGGGGACCCGCTCAGTCTTCTCTCTC 720  
 Db 221 HisThrCysProCysProAlaProGluLeuAlaGlyAlaProSerValPheLeuPhe 240  
 QY 721 CCCCCAAACCCAAAGACACCCCTCATGATCTCCCGACCCCTGAGTGCATCGCTGGTG 780  
 Db 241 ProProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCysValVal 260  
 QY 781 GTGAGCTGAGCCACCAAGACCTGAGTCAAGTTCAGTGTAGTGGACGCGCTGGAG 840  
 Db 261 ValAspValSerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGlu 280  
 QY 841 GTCATATAATGCCAAGACAAAGCCGGGAGGAGCAGTACACAGCAGCAGTACCGTGTGGTC 900  
 Db 281 ValHisAsnAlaLysThrLysProArgGluGlnTyrAsnSerThrTyrArgValVal 300  
 QY 901 AGCGTCTCTCAGCTGCTCGCACGAGTGGCTCAATGGCAAGGAGTACAAAGTGCAGGTC 960  
 Db 301 SerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysVal 320  
 QY 961 TCCAAACAAAGCCCTCCCGACCCCGCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCC 1020  
 Db 321 SerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnPro 340  
 QY 1021 CGAAGACCAAGGTGTACACCTGCCCCCTGCCCCGATGAGTACACCAAGACCAAGGTC 1080  
 Db 341 ArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnVal 360  
 QY 1081 AGCTGACCTGCTGTGTCAAAGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGAGC 1140  
 Db 361 SerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSer 380  
 QY 1141 AATGGCACCGGAGAACAACTACAAAGACCAAGCCCTCCCGTCTGGACTCCGACCGCTCC 1200  
 Db 381 AsnGlyGlnProGluAsnAsnTyrLysThrThrProValLeuAspSerAspGlySer 400  
 QY 1201 TCTCTCTCTCAGCAAGCTCAGCTGGGACAAAGACAGGAGTGGGACAGGGGAACTCTTTC 1260  
 Db 401 PhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPhe 420  
 QY 1261 TCATGCTCGGTGATGATGAGGCTCTGCACAAACCTACACGCAAGAGGCTCTCCCTG 1320

421 SerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu 440  
 Db 1321 TCTCCGGTAAA 1332  
 QY 441 SerProGlyLys 444  
 Db

RESULT 2  
 AAR42162  
 ID AAR42162 standard; protein; 461 AA.  
 XX  
 AC AAR42162;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 27-APR-1994 (first entry)  
 DT  
 XX  
 XX Anti-HIV-1 recombinant antibody 447-52D heavy chain.  
 DE  
 XX  
 XX Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;  
 KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;  
 KW acquired immune deficiency syndrome; chimeric antibody;  
 KW surface glycoprotein gp120; V3 loop.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9319785-A1.  
 FN  
 XX 14-OCT-1993.  
 PD  
 XX 23-MAR-1993; 93WO-US002629.  
 DF  
 XX 01-APR-1992; 92US-00861701.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA  
 XX  
 XX Emini EA, Conley AJ, Mark GE, Johnson LS, Pfarr DS;  
 PI  
 XX WPI; 1993-336600/42.  
 DR N-PSDB; AAQ49834.  
 XX  
 XX New recombinant human antibody - with HIV neutralising activity against  
 PT at least two isolates, useful for preventing or treating infection in  
 PT diagnosis, etc.  
 XX  
 XX Example 9; Fig 2A; 154pp; English.  
 PS  
 XX EBV-transformed cell lines and mouse-human heterohybridomas producing  
 CC human MAbs specific for the gp120 V3 loop of HIV-1 MN isolate were  
 CC obtained. Mab 447-52D was found to recognise the tetrapeptide motif GPGR,  
 CC i.e. the Principal Neutralising Determinant common to the V3 loop of  
 CC different HIV isolates. A recombinant Ab was produced in which the H  
 CC chain V region was derived from 447-52D and to which a signal sequence  
 CC and a H chain intronic sequence are appended, fused to a fragment contg.  
 CC a short intronic segment of the human gamma 1 C region and the human  
 CC gamma 1 encoding domain in its genomic form. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 CC  
 XX SQ Sequence 461 AA;  
 SQ

Alignment Scores:  
 Pred. No.: 1,266-130 Length: 461  
 Score: 2199.50 Matches: 416  
 Percent Similarity: 92.62% Conservative: 11  
 Best Local Similarity: 90.24% Mismatches: 17  
 Query Match: 91.46% Indels: 17  
 DB: 2 Gaps: 2

US-09-674-716B-18 (1-1335) x AAR42162 (1-461)

QY 1 GAGGTGCACCTGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 60  
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
 QY 61 TCGTGTGACCTAGCGGATTCATTCTAGTGGCTACTGGATGCTCTGGGTCCGCCAGGCT 120

21 ThrCysValAlaSerGlyPheThrPheSerAspValTrpLeuAsnTrpValArgGlnAla 40  
 QY 121 CCAGGGAAGGGCTCGAGTGGTCTCTGAAATAGATTGAATCTGATAATTATCAACA 180  
 Db 41 ProGlyLysGlyLeuGluTrpValGlyArgLeuLysSerArgSerArgPheThrThr 60  
 QY 181 CATTATGGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGA 240  
 Db 61 AspTyrAlaAlaSerValLysGlyArgPheThrThrLeuSerArgAspSerLysAsnThr 80  
 QY 241 CTGTATCTGCAAAATGAACAGCCTGAAACCCAGGAGCACAGCCGTGTATTACTGTACAGAT 300  
 Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrSerCysThrThr 100  
 QY 301 -----TTCATAGAC--- 309  
 Db 101 AspGlyPheIleMetIleArgGlyValSerGluAspTyrTyrTyrMetAspVal 120  
 QY 310 TGGGCCCAGGGAACACTAGTCAACGTCTCTCAGCTCTCAGCTCTCAGAGGGCCATCGGTCTTC 369  
 Db 121 TrpGlyLysGlyThrThrValThrValSerSerAlaSerThrLysGlyProSerValPhe 140  
 QY 370 CCCCTGGCACCTCTCTCCAAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGGCTGCTC 429  
 Db 141 ProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuVal 160  
 QY 430 AAGGACTACTTCCCGAACCCGGTGCAGTGTCTGTGAACCTCAGGCGCCCTGACCGAGCGC 489  
 Db 161 LysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGly 180  
 QY 490 GTGCACACTTCCCGCTGTCTCTACAGTCTCTCAGGACTCTCTCCTCAGCAGCGGTGG 549  
 Db 181 ValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSerValVal 200  
 QY 550 ACCGTGCTCCAGCAGCTTGGGCACCCAGACTCATCTGCAACGTGTAATCACAGCCC 609  
 Db 201 ThrValProSerSerSerLeuGlyThrGlnThrTyrTyrLeuCysAsnValAsnHisLysPro 220  
 QY 610 AGCAACACAGGTGACAAAGTGGAGCCCAATCTTGTGACAAAACACTCACATGC 669  
 Db 221 SerAsnThrLysValAspLysValGluProLysSerCysAspLysThrHisThrCys 240  
 QY 670 CCACGTGCGCCAGCACCTGAACTCGCGGGGCGACCCCTCAGTCTCTCTTCCCGCCAAA 729  
 Db 241 ProProCysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProLys 260  
 QY 730 CCCAAGGACACCTCATGATCTCCCGACCCCTGAGGTGACATGCTGTGTGGTGGACGTG 789  
 Db 261 ProLysAspThrLeuMetIleSerArgThrProGluValThrCysValValValAspVal 280  
 QY 790 AGCCACGAGACCTCAGGTCAAGTTCAACTGTAGTGTGAGCGCGCTGGAGGTGCATAAT 849  
 Db 281 SerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGluValHisAsn 300  
 QY 850 GCCAAGACAAAGCCGCGGGAGGACAGTACAAACAGCACCTTACCGTGTGTGTCAGCTCCTC 909  
 Db 301 AlalaThrLysProArgGluGlnTyrAsnSerThrTyrArgValValSerValLeu 320  
 QY 910 ACCGTCTGCACAGGACTGGCTGAATGGCAAGAGTACAAAGTCAAGGTCTCCACAAA 969  
 Db 321 ThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLys 340  
 QY 970 GCGCTCCAGCCCGCCATCCGAGAAAACCATCTCCAAAAGCCAAAGGCGAGCCCGGAGAACCA 1029  
 Db 341 AlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnProArgGluPro 360  
 QY 1030 CAGGTGTACACCTGCCCGCCATCCCGGATGACTGACCAAGAACCAAGGTGACCTGACC 1089  
 Db 361 GlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnValSerLeuThr 380  
 QY 1090 TGCCTGTCAAAGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGAGCAATGGGCAG 1149

Db 381 CysLeuValIysGlyPheTyrProSerAspIleAlaValGluTrpGluSerAsnGlyGln 400  
 QY 1150 CCGAGAACAACTACAGACCCAGCGCTCCGCTGGACTCCGAGCGGCTCCTTCTTCCTC 1209  
 Db 401 ProGluAsnIlyIysThrProProValLeuAspSerAspGlySerPhePheLeu 420  
 QY 1210 TACAGCAAGTCAACGCTGGCAAGACAGTGGCAGCGGGAACGCTTCTTCATGCTCC 1269  
 Db 421 TyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSer 440  
 QY 1270 GTGATCATGAGCTGTGCACACCACTACAGCAGAGAGCTTCCCTGTCTCCGGGT 1329  
 Db 441 ValMetHisGluAlaLeuHisAsnHisIlyThrGlnLysSerLeuSerLeuSerProGly 460  
 QY 1330 AAA 1332  
 Db 461 Lys 461  
 RESULT 3  
 AAE33524  
 ID AAE33524 standard; protein; 447 AA.  
 XX  
 AC AAE33524;  
 XX  
 DT 02-APR-2003 (first entry)  
 XX  
 DE Human AOC2 heavy chain mutant protein, hsaAOC2.

XX Human; very late activation antigen; VLA-1; beta1 containing integrin;  
 KW immunological disorder; inflammatory disorder; skin related condition;  
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;  
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;  
 KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;  
 KW irritable bowel syndrome; colitis; colorectal cancer; perianthitis nodosa;  
 KW atherosclerosis; thyroiditis; aplastic anaemia; rheumatoid arthritis;  
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;  
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;  
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;  
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;  
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;  
 KW graft versus host disease; myocardial ischaemia; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200283854-A2.  
 XX  
 PD 24-OCT-2002.

PF 12-APR-2002; 2002WO-US011521.  
 XX  
 PF 13-APR-2001; 2001US-0283794P.  
 PR 06-JUL-2001; 2001US-0303689P.  
 XX  
 PA (BIOJ) BIOGEN INC.  
 XX  
 PI Lyne PD, Garber EA, Saldanha JW, Karpusas M;  
 XX  
 DR WPI; 2003-093009/08.  
 XX  
 PT New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
 PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,  
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or  
 PT fibrosis.  
 XX  
 PS Example 23; Page 92; 248pp; English.  
 XX  
 PS The present invention relates to novel antibodies that specifically bind  
 CC to very late activation (VLA-1; beta1 containing integrins) antigens and  
 CC methods of using these antibodies to treat immunological disorders. The  
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
 CC mediated immunological or inflammatory disorders such as skin related  
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal  
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung

CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,  
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-  
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,  
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),  
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,  
 CC perianthitis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,  
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid  
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal  
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,  
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or  
 CC immediate hypersensitivity), graft and transplant rejections, graft  
 CC versus host disease, conjunctivitis, swelling occurring after injury,  
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is  
 CC human AOC2 heavy chain mutant protein, hsaAOC2  
 XX  
 SQ Sequence 447 AA;

Alignment Scores:  
 Pred. No.: 4,33e-130 Length: 447  
 Score: 2191.00 Matches: 418  
 Percent Similarity: 94.44% Conservative: 7  
 Best Local Similarity: 92.89% Mismatches: 15  
 Query Match: 91.10% Indels: 10  
 DB: 6 Gaps: 2  
 US-09-674-716b-18 (1-1335) x AAE33524 (1-447)  
 QY 1 GAGTGCAGCTGTGGAGTCTGGGGAGGCTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuValGln 20  
 QY 61 TCTGTGACGTAGCGGATTCATTTCAGTGGCTACTGATGTCTGGTGGCGCAGGCT 120  
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrThrMetSerTrpValArgGlnAla 40  
 QY 121 CCAGGGAAGGGGCTCGAGTGGTGGTGAATAGATTGAATCTGATAATATGCAACA 180  
 Db 41 ProGlyValGlyLeuGluTrpValAlaThrIle-----SerGlyGlyGlyHisThr 57  
 QY 181 CATATGCGGAGTCTGTGAAGGGAATTCACATCTCAAGAGATGATTCAAAATCTAGA 240  
 Db 58 TyrTyrLeuAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 77  
 QY 241 CTGTATCTGCAATGAACAGCTGAAACCGAGGACACAGCGGTGTATTACTGTACAGAT 300  
 Db 78 LeuTyrLeuGlnValMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysThrArg 97  
 QY 301 -----TTCATAGACTGGGCGGAGGAACTAGTACCGCTCTCC 339  
 Db 98 GlyPheGlyAspGlyGlyTyrPheAspValTyrGlyGlnGlyThrLeuValThrValSer 117  
 QY 340 TCAGCTCCACCAAGCGGCTGCTTCCCGCTGGGACCGCTCCAGAGGACCTCT 399  
 Db 118 SerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSer 137  
 QY 400 GGGGGCACAGCGGCTCGGCTGGCTGGTCAAGGACTACTTCCCGGAAACCGGTGACGGTG 459  
 Db 138 GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrVal 157  
 QY 460 TCGTGAACCTCAGGCGGCTGACACAGCGGCTGACACCTTCCCGGCTGTCTCAGTCC 519  
 Db 158 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 177  
 QY 520 TCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGGCTCCAGCAGCTTGGGACCCAG 579  
 Db 178 SerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGln 197  
 QY 580 ACTTACATCTGCAAGTGAATCACAAGCCAGCAACACAGGTTGGACAGAACTGGAG 639  
 Db 198 ThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGlu 217  
 QY 640 CCAATATCTGTGACAAACTCACAATGCTCCCGCTGCCAGCAGCTGAACTCCGCGGG 699

Db 218 ProLysSerCysAspLysThrHisThrCysProCysProAlaProGluAlaAlaGly 237  
 Qy 700 GCACGCTCAGTCTTCTTCCCCCAAAACCCAAAGGACACCCCTCATGATCTCCCGACC 759  
 Db 238 GlyProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThr 257  
 Qy 760 CCTGAGGTCACATCGGTGGTGGCTGAGTGGACCAAGACCCCTGAGGTCAAGTTCAC 819  
 Db 258 ProGluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsn 277  
 Qy 820 TGGTACGTGGACGGCTGGAGGTGCATAATCCCAAGCAAAAGCCGCGGAGGACGATAC 879  
 Db 278 TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyr 297  
 Qy 880 AACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 939  
 Db 298 AsnSerThrTyrArgValValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly 317  
 Qy 940 AAGGAGTCAAGTGCAGGTCTCCAAACAAACCCCTCCAGCCGCCATCGAGAAACCATC 999  
 Db 318 LysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIle 337  
 Qy 1000 TCCAAAGCCAAAGGACCGGACCGGACGACGACGAGTGTACCCCTGCCATCCCGGAT 1059  
 Db 338 SerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAsp 357  
 Qy 1060 GAGCTGACCAAGAACCCAGGTGAGCTGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 1119  
 Db 358 GluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAsp 377  
 Qy 1120 ATGCGCGTGGAGTGGAGAGAGATGGGAGCGGAGGAGAGACACTACAGACACCCCTCCC 1179  
 Db 378 IleAlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProPro 397  
 Qy 1180 GTGCTGGACTCCGACGGTCTCTTCTCTCTACAGACGCTCACCGTGGACGAGCAGG 1239  
 Db 398 ValLeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArg 417  
 Qy 1240 TGGCAGCAGGGAACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1299  
 Db 418 TrpGlnGlnGlnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyr 437  
 Qy 1300 ACGCAGAGAGCGCT 1329  
 Db 438 ThrGlnLysSerLeuSerLeuSerProGly 447

## RESULT 4

AAE33522

ID AAE33522 standard; protein; 447 AA.

XX AC AAE33522;

XX DT

XX DT

XX 02-APR-2003 (first entry)

XX Human AQC2 heavy chain protein.

DE Human; very late activation antigen; VLA-1; beta1 containing integrin;  
 KW immunological disorder; inflammatory disorder; skin related condition;  
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;  
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;  
 KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;  
 KW irritable bowel syndrome; colitis; colorectal cancer; vascular disease;  
 KW atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;  
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;  
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;  
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;  
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;  
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;  
 KW graft versus host disease; myocardial ischaemia.

OS Homo sapiens.

XX PN W0200283854-A2.

XX 24-OCT-2002.  
 XX 12-APR-2002; 2002WO-US011521.  
 XX 13-APR-2001; 2001US-0283794P.  
 PR 06-JUL-2001; 2001US-0303689P.  
 XX (BIOJ ) BIOGEN INC.  
 XX Lyne PD, Garber EA, Saldanha JW, Karpusas M;  
 DR WPI; 2003-093009/08.  
 XX New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
 PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,  
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or  
 PT fibrosis.

Claim 6; Page 75; 248pp; English.

XX The present invention relates to novel antibodies that specifically bind  
 CC to very late activation (VLA-1; beta1 containing integrins) antigens and  
 CC methods of using these antibodies to treat immunological disorders. The  
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
 CC mediated immunological or inflammatory disorders such as skin related  
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal  
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung  
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,  
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-  
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,  
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),  
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,  
 CC periarthritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,  
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid  
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal  
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,  
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or  
 CC immediate hypersensitivity), graft and transplant rejections, graft  
 CC versus host disease, conjunctivitis, swelling occurring after injury,  
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is  
 CC human AQC2 heavy chain protein

Sequence 447 AA;

## Alignment Scores:

Pred. No.: 4,33e-130 Length: 447  
 Score: 2191.00 Matches: 418  
 Percent Similarity: 94.44% Conservative: 7  
 Best Local Similarity: 92.89% Mismatches: 15  
 Query Match: 91.10% Indels: 10  
 DB: 6 Gaps: 2

US-09-674-716B-18 (1-1335) x AAE33522 (1-447)

Qy 1 GAGGTGAGTGGTGGAGTCTGGGGGAGGCTGGTAAAGCCCGGGGGTCCCTTAGCATC 60  
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
 Qy 61 TCTGTGCACCTAGCGAATTCACCTTCAGTGGTACTGAGTGTCTCGGTCCGCGCGCT 120  
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrThrMetSerTrpValArgGlnAla 40  
 Qy 121 CCAGGGAAGGGCTCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180  
 Db 41 ProGlyLysGlyLeuGluTrpValAlaThrIle-----SerGlyGlyGlyHisThr 57  
 Qy 181 CATPATCCGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240  
 Db 58 TyrTyrLeuAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 77  
 Qy 241 CTGTATCTGCAATGACAGCCTGMAAACCGAGACACACCGCTGTATTACTGTACAGAT 300



Percent Similarity: 94.48%      Conservative: 13  
 Best Local Similarity: 91.61%      Mismatches: 12  
 Query Match: 91.00%      Indels: 13  
 DB: 6      Gaps: 3

US-09-674-716B-18 (1-1335) x ABP58273 (1-449)

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QY 1 GAGTGCAGCTGGTGGAGTCTGGGGAGGCTGGTAAGCCCGGGGGTCCCTAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCCTGTGACGTAGCGGATTCACATTTTCAGTGGCTACTGGATGTCTCTGGGTCCCGCAGGCT 120
DB 21 SerCysAlaGlySerGlyPheThrPheSerAsnTyrGlyMetSerTrpValArgGlnAla 40
QY 121 CCAGGAAGGGCTCGAGTGGTTCGTAATAGATTGAATCTGATATTAATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValAlaSerIleArg-----SerGlyGlyArgThr 58
QY 181 CATTATGGGAGTCTGCAAGGGNAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240
DB 59 TyrTyrSerAspAsnValGlyArgPheThrIleSerArgGluAsnAlaLysAsnSer 78
QY 241 CTGTATCTGCAAAATGAACAGCTGAAACCCGAGACACAGCCGTGTATTACTGT- 294
DB 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysValArg 98
QY 295 -----ACAGATTTCATAGACTGGGCGCAGGGAACACTAGTACCC 333
DB 99 TyrAspHisTyrSerGlySerSerAspTyr-----TrpGlyGlnGlyThrLeuValThr 116
QY 334 GTCTCTCAGCTCCACCAAGGGGCCATCGGTCTTCCCGCTGGCAGCCCTCTCCCAAGAGC 393
DB 117 ValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSer 136
QY 394 ACCCTGGGGCACAGCGCCCTGGGCTGCTGTCTCAAGGACTACTTCCCGAACCGGTG 453
DB 137 ThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProVal 156
QY 454 ACGGTGTCTGGAATCTCAGCGGCTGACACAGCGGTGACACCTTCCCGGCTGTCTTA 513
DB 157 ThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeu 176
QY 514 CAGTCTCAGGACTACTCTCCTCAGCAGCTGTGTGACCGTGCCTCCAGCAGCTTGGCG 573
DB 177 GlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGly 196
QY 574 ACCCAGACTACTCTGCAAGTGAATCACAAGCCCGACACACCAAGGTGGACAGAA 633
DB 197 ThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLys 216
QY 634 GTGGAGCCCCAAATCTGTGACAAACTCACATGCCCCCGCTGCCAGCAGCCTGAATC 693
DB 217 ValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeu 236
QY 694 GCGGGGACCGCTCAGTCTTCTCTTCTTCCCGGCAAAACCCAGGACACCTCATGATC 753
DB 237 LeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSer 256
QY 754 CGGACCCCTGAGGTGCATGCTGGTGTGGAGCTGAGCCACGACCCCTGAGGTCAAG 813
DB 257 ArgThrProGluValThrCysValValValAspValSerHisGluAspProGluValLys 276
QY 814 TTCAACTGGTACGTGGACGGGTGGAGGTGATATGCAAGACAAAGCCCGGGAGGAG 873
DB 277 PheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu 296
QY 874 CAGTACACAGCAGTACCGTGTGTGCTCAGCTCTCCTCAGGCTCCGACCCAGGACTGGCTG 933
DB 297 GlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeu 316
QY 934 AATGCAAGGAGTACAAGTCAAGTCTCCAAAGAGCCCTCCAGAGCCCGCCCATCGAGAA 993

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DB 317 AsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLys 336
QY 994 ACCATCTCCAAAGCCAAAGCGGAGCCCGAGAACACCAAGAGTGTACACCTTGCCCCATCC 1053
DB 337 ThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSer 356
QY 1054 CCGGATGAGCTACCAAGAACAGGTCAGCTGACCTGCTGGTCAAGGCTTCTATCCC 1113
DB 357 ArgAspGluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrPro 376
QY 1114 AGCGACATCGCCGTGAGTGGAGAGCAATGGCGAGCCGAGAACAACTACAGAACACG 1173
DB 377 SerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThr 396
QY 1174 CTTCCCGTGTGACTCCGACCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG 1233
DB 397 ProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLys 416
QY 1234 AGCAGTGGCGAGCGGGAACGCTTCTCATGCTCGTGCATGATGATGAGCTCTGCACAA 1293
DB 417 SerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsn 436
QY 1294 CACTACAGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA 1332
DB 437 HistTyrThrGlnLysSerLeuSerLeuSerProGlyLys 449

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RESULT 6  
 ABP58275  
 ID ABP58275 standard; protein; 468 AA.  
 XX  
 AC ABP58275;  
 XX  
 XX 23-OCT-2003 (revised)  
 DT 31-MAR-2003 (first entry)  
 XX  
 DE Humanised 3D6 antibody heavy chain.  
 XX  
 KW Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;  
 KW human; humanised antibody; antibody; Alzheimer's disease;  
 KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.  
 XX  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= Signal\_peptide  
 FT Protein 20..468  
 FT /label= Mature\_peptide  
 FT /note= "the mature heavy chain is claimed in Claim 5"  
 FT Region 20..138  
 FT /note= "heavy chain variable region, claimed in Claim 4"  
 FT Region 50..54  
 FT /note= "CDR1"  
 FT Region 69..85  
 FT /note= "CDR2"  
 FT Region 118..127  
 FT /note= "CDR3"  
 XX  
 PN WO200288306-A2.  
 XX  
 PD 07-NOV-2002.  
 XX  
 XX 26-APR-2002; 2002WO-US011853.  
 XX  
 XX 30-APR-2001; 2001US-0287539P.  
 XX  
 XX (ELIL ) LILLY & CO ELI.  
 XX  
 XX Taurushita N, Vasquez M;  
 XX WPI; 2003-183835/18.  
 DR

DR N-PSDB; AB224633, AB224635.  
 XX New humanized forms of mouse 3D6 antibodies, useful for treating Down's  
 PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral  
 PT amyloid angiopathy, or for inhibiting formation of or reducing Abeta  
 PT plaque in the brain.  
 XX Disclosure; Page 13-14; 54pp; English.  
 XX  
 XX The present sequence is that of a preferred heavy chain of a humanised  
 CC antibody of the present invention. In the variable region of this  
 CC sequence, the complementarity determining regions (CDRs) originate from  
 CC murine monoclonal antibody 3D6 and the framework region from human  
 CC germline VH segment DP-45 and J segment JH4. Novel humanised antibodies  
 CC of the invention have CDRs from 3D6 and human framework sequences. These  
 CC humanised antibodies have binding affinities (affinity and epitope  
 CC location) approximately the same as those of the mouse 3D6 antibody. The  
 CC invention includes antibodies, single chain antibodies, and their  
 CC fragments, as well as nucleotide sequences, vectors, transformed host  
 CC cells, and methods of using the humanised antibody to treat, prevent,  
 CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology  
 CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or  
 CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation of  
 CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise  
 CC OS field)  
 XX  
 XX Sequence 468 AA;  
 SQ

Alignment Scores:  
 Pred. No.: 6,266-130 Length: 468  
 Score: 2188.50 Matches: 415  
 Percent Similarity: 94.48% Conservative: 13  
 Best Local Similarity: 91.61% Mismatches: 12  
 Query Match: 91.00% Indels: 13  
 DB: Gaps: 3

US-09-674-716B-18 (1-1335) x ABP58275 (1-468)

QY 1 GAGGTGACGCTGCTGGAGTCTGGGGAGGCTTGTAAAGCCGGGGTCTCTAGACTC 60  
 DB 20 GluValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39  
 QY 61 TCTGTGACGCTAGCGATTCCTTTCAGTGGCTACTGGATGCTCTGGTCCGCGAGCT 120  
 DB 40 SerCysAlaGlySerGlyPheThrPheSerAsnTyrGlyMetSerTrpValArgGlnAla 59  
 QY 121 CCAGGAGGGGCTGAGTGGCTGCTGAATAGATTGAATCTGAATATTCACACA 180  
 DB 60 ProGlyLysGlyLeuGlnTrpValAlaSerIleArg-----SerGlyGlyArgThr 77  
 QY 181 CATTATCGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240  
 DB 78 TyrTyrSerAspAsnValLysGlyArgPheThrIleSerArgGluAsnAlaLysAsnSer 97  
 QY 241 CTGTATCTCAATGAACAGCTGTAACACCGAGGACACAGCGCTTATTACTGT----- 294  
 DB 98 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysValArg 117  
 QY 295 -----ACAGATTTCATAGACTGGGGCCAGGGAACTAGTACCTAGTCACC 333  
 DB 118 TyrAspHisTyrSerGlySerSerAspTyr-----TrpGlyGlnGlyThrLeuValThr 135  
 QY 334 GTCTCTCAGCTCCACCAAGGGCCATCGGTCTTCCCGCTGGGACCTCTCTCAAGAGC 393  
 DB 136 ValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSer 155  
 QY 394 ACCTCTGGGGGACACAGCGCTGGCTGCTGGTCAAGGACTACTTCCCGAACCGGTG 453  
 DB 156 ThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProVal 175  
 QY 454 ACGGTGTCTGGAATCTAGCGCCCTGACACAGCGGCTGCACACCTTCCCGGTGTCTTA 513  
 DB 176 ThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeu 195

QY 514 CAGTCTCAGGACTCTTACTCTCCCTCAGCAGCGTGGTGACCGTCCCTCAGCAGCTTGGGC 573  
 DB 196 GlnSerSerGlyLeuTyrSerLeuSerValValThrValProSerSerSerLeuGly 215  
 QY 574 ACCCAGACCTCATCTGCAACGCTGAATCAACAGCCAGCAACACCAAGGTGACAAAGAA 633  
 DB 216 ThrGlnThrTrpIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 235  
 QY 634 GTGAGCCCAAAATCTTGTGCACAAAACACTCACATGCCCAACCGTCCAGCAGCTGAATC 693  
 DB 236 ValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeu 255  
 QY 694 GCGGGGGACCGCTGACTCTTCTCTCCCTCCCAAAACCAAGGACACCTCATGATCTCC 753  
 DB 256 LeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIleSer 275  
 QY 754 CGGACCCCTGAGGTCACTGCTGCTGGTGGTGGACGCGAGCCAGCAAGACCTGAGGTCAAG 813  
 DB 276 ArgThrProGluValThrCysValValValAspValSerHisGluAspProGluValLys 295  
 QY 814 TTCACTGTGATGTCGACCGCTGGAGTGCATATGCCAAGCAACAGCCGCGGAGGAG 873  
 DB 296 PheAsnTrpTrpValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu 315  
 QY 874 CAGTACCAACAGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 933  
 DB 316 GlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeu 335  
 QY 934 ATGGCAAGGAGTACAAAGTGCAGGTCTCCAAACAAGCCCTCCAGCCCTCCAGAAA 993  
 DB 336 AsnGlyLysGlnTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLys 355  
 QY 994 ACCATCTCAAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCCCATCC 1053  
 DB 356 ThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSer 375  
 QY 1054 CGGGATGAGTGCACCAAGAACAGGTGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113  
 DB 376 ArgAspGluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrPro 395  
 QY 1114 AGCGACATGCGCTGGAGTGGGAGACATGGCGAGGAGCACTACAGCAAGCTACAGACCCAG 1173  
 DB 396 SerAspIleAlaValGlnTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThr 415  
 QY 1174 CTTCCCGTGTGACTCCGACCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1233  
 DB 416 ProProValLeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLys 435  
 QY 1234 AGCAGTGGCAGCAGGGGAAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1293  
 DB 436 SerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsn 455  
 QY 1294 CACTACACGAGCAAGAGCTCTCCCTGCTCTCCGGGTAAA 1332  
 DB 456 HisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 468

RESULT 7  
 AAE35327  
 ID AAE35327 standard; protein; 444 AA.  
 XX AC AAE35327;  
 XX 17-JUN-2003 (first entry)  
 XX Humanised murine antibody BIWA4 heavy chain protein.  
 DE CD44; cytotoxic drug; therapy; cancer; tumour; minimal residual disease;  
 KW antigen; cytostatic; BIWA4 antibody; murine.  
 XX Homo sapiens.  
 OS  
 PN EP1258255-A1.



XX 20-NOV-2002.  
 XX 18-MAY-2001; 2001EP-00112227.  
 XX 18-MAY-2001; 2001EP-00112227.  
 XX (BOEH ) BOEHRINGER INGENELHEIM INT GMBH.  
 XX Adolf G, Heider K, Patzelt E, Sproll M;  
 XX WPI; 2003-177273/18.  
 XX N-PSDB; AAD53977.  
 XX New compound useful for treatment of cancer comprises CD44 specific  
 PT antibody molecule conjugated to a highly cytotoxic drug, which cleaves  
 PT under intracellular conditions.  
 XX Claim 7; Page 15-16; 31pp; English.  
 XX The invention relates to a compound comprising CD44 specific antibody  
 CC molecule conjugated to a highly cytotoxic drug, which cleaves under  
 CC intracellular conditions. The compound is used in pharmaceutical  
 CC composition for the treatment of cancer, solid tumours, and as an  
 CC adjuvant to surgical intervention to treat minimal residual disease. The  
 CC present sequence is humanised murine antibody BIWA4 heavy chain protein  
 CC used in the invention  
 XX SQ Sequence 444 AA;  
 Alignment Scores:  
 Pred. No.: 7,74e-130 Length: 444  
 Score: 2187.00 Matches: 415  
 Percent Similarity: 95.09% Conservative: 11  
 Best Local Similarity: 92.63% Mismatches: 14  
 Query Match: 90.94% Indels: 8  
 DB: 6 Gaps: 3  
 US-09-674-716B-18 (1-1335) x AAE35327 (1-444)  
 QY 1 GAGGTGACGTGGTGGAGTCTGGGGAGGCTGGTAAGCCGGGGTCCCTTAGACTC 60  
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 20  
 QY 61 TCCTGTGACGTAGCGGATTCACATTTTCAGTGGCTACTGGATGCTCTGGTCCGCCAGGCT 120  
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAspMetSerTrpValArgGlnAla 40  
 QY 121 CCAGGAGGGCTCGAGTGGTTCCTGAATAGATTGAATCTGATAATTATGCAACA 180  
 Db 41 ProGlyLysGlyLeuGluTrpValSerThrIle-----SerSerGlyGlySerTyrThr 58  
 QY 181 CATTATGGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240  
 Db 59 TyrTyrLeuAspSerIleGlyValGlyArgPheThrIleSerArgAspAsnAlaLysAsnSer 78  
 QY 241 CTGATCTGCAATGAACAGCTGTGAACACCGAGGACACAGCGGTGTATTACTGTACA--- 297  
 Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98  
 QY 298 -----GATTTCATAGACTGGGCCAGGAGACACTAGTCACCGTCTCTCAGCTCC 348  
 Db 99 GlnGlyLeuAspTyr-----TrpGlyArgGlyThrLeuValThrValSerSerAlaSer 116  
 QY 349 ACCAAGGGCCCATCGGTCTTCCCTTGGCACCTCTCCCAAGAGACACCTCTGGGGGACCA 408  
 Db 117 ThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThr 136  
 QY 409 GCGGCCCTGGGCTGCTGGTCAAGACTACTTCCCGAACCGGTGACGGTGTCTGTGAAC 469  
 Db 137 AlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSerTrpAsn 156  
 QY 469 TCAGGCGCCCTGACCCAGCGGGGTGCACACCTTCCCGGGTGTCTCTACAGTCTCAGGACTC 528

Db 157 SerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeu 176  
 QY 529 TACTCTCTCAGCAGCGTGGTGCACCGTCCCTCAGCAGCTTGGGCACCCAGACCTACATC 588  
 Db 177 TyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThrTyrIle 196  
 QY 589 TGCACGCTGAATCACAAGCCCAAGCAACACACAGGTGGCAAGAAAGTGGAGCCCAATCT 648  
 Db 197 CysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluProLysSer 216  
 QY 649 TGTGACAAAACCTCACACATGCCACCGTCCCGCAGCACCTGAACCTCGCGGGGACCGTCA 708  
 Db 217 CysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSer 236  
 QY 709 GTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTC 768  
 Db 237 ValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrProGluVal 256  
 QY 769 ACATGCGTGGTGGTGGACGTGACCCAGGAGCCCTGAGTCAAGTCAAGTCAACTGTTACGTC 828  
 Db 257 ThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrpTyrVal 276  
 QY 829 GACGGCGTGGAGGTGCATTAATGCCAAGACAAAGCCCGGGAGGAGCAGTACACACGACG 888  
 Db 277 AspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsnSerThr 296  
 QY 889 TACCGTGTGGTGGTGGTCTCTCAGCTCCCGTCCGACGAGGACTGGCTGAATGCCAAGGAGTAC 948  
 Db 297 TyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyr 316  
 QY 949 AAGTGAAGGTCTCCCAAAAGCCCTCCCGAGCCCATCGAGAAAACCATCTCCAAAGCC 1008  
 Db 317 LysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAla 336  
 QY 1009 AAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACC 1068  
 Db 337 LysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThr 356  
 QY 1069 AACAACACGTCAGCTGACCTGACCTGGCTGCAAGGCTTCTATCCAGCGACATCGCCGCTG 1128  
 Db 357 LysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal 376  
 QY 1129 GAGTGGAGAGCAATGGCGAGCCGGAGAAACAACACTACAAGACCAACGCTCCGCTGGAC 1188  
 Db 377 GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProValLeuAsp 396  
 QY 1189 TCCGACGGCTCTCTCTCTCTCTACACAGCTCACCGTGGACAGAGCAGGTGGCAGCAG 1248  
 Db 397 SerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGln 416  
 QY 1249 GGAACGCTCTTCTCATGCTCCGTCATGAGCTCTGCACAAACCATACACGACGAGAG 1308  
 Db 417 GlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLys 436  
 QY 1309 AGCT 1332  
 Db 437 SerLeuSerLeuSerProGlyLys 444  
 RESULT 8  
 AAE34876  
 ID AAE34876 standard; protein; 444 AA.  
 XX AAE34876;  
 XX 28-MAY-2003 (first entry)  
 XX BIWA4/8 antibody heavy chain mature protein.  
 XX BIWA8 antibody; heavy chain variable region; light chain variable region;  
 KW VH; VL; CD44v6; medicament; cancer; antibody therapy.  
 XX Unidentified.  
 OS

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XX WO200294879-A1.
XX 28-NOV-2002.
XX 17-MAY-2002; 2002WO-BP005467.
XX 18-MAY-2001; 2001EP-00112237.
XX 26-SEP-2001; 2001US-0325147P.
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX Adolf G, Ostermann E, Patzelt E, Sproll M, Heider K;
XX Miglietta JJ, Van Dongen AAMS;
XX N-PSDB; AAD53212, AAD53215.
XX WPI; 2003-129413/12.
XX New antibodies specific for an epitope coded by the variant exon of the
XX CD44 gene, useful for treating cancer, including non-small cell lung,
XX breast, head and neck, ovarian and lung cancer.
XX Claim 24; Col 44; 78pp; English.
XX The present invention relates to novel antibody molecules comprising a
XX variable region of the heavy (VH) and/or light chain (VL) of CD44v6
XX specific humanised antibody called Biw48 and Biw44. Sequences of the
XX invention are useful for manufacturing a medicament and for treating
XX cancer including colorectum, non-small cell lung, breast, head and neck,
XX ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the
XX brain. They are also useful in antibody therapy. The present sequence is
XX Biw44/8 antibody heavy chain mature protein. This sequence is used in the
XX exemplification of the invention.
XX SQ Sequence 444 AA;

Alignment Scores:
Pred. No.: 7-74e-130 Length: 444
Score: 2187.00 Matches: 415
Percent Similarity: 95.09% Conservative: 11
Best Local Similarity: 92.63% Mismatches: 14
Query Match: 90.94% Indels: 8
DB: 6 Gaps: 3

US-09-674-716B-18 (1-1335) x AAE34876 (1-444)
QY 1 GAGTGCACCTGGTGGAGTCTGGGGAGGCTTGCTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCTGTGACGTAGCGGATCTCTTTCAGTGGCTACTGGATCTCTGGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAspMetSerTyrValArgGlnAla 40
QY 121 CAGGGAAGGGCTGAGTGGGTCTGTAATAGATTGAATCTGTAATATTCACACA 180
DB 41 ProGlyLysGlyLeuGluTrpValSerThrIle-----SerSerGlyGlySerTyrThr 58
QY 181 CATTATCGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB 59 TyrTyrLeuAspSerIleLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSer 78
QY 241 CRTATCTCAATGAATGAAGCTGAAACCGAGGACACAGCCGTCTATTACTGTACA--- 297
DB 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98
QY 298 -----GATTTCATACATGGGGCCAGGGAACACTAGTCAACCGTCTCTCAGCCCTCC 348
DB 99 GlnGlyLeuAspTyr-----TrpGlyArgGlyThrLeuValThrValSerSerAlaSer 116
QY 349 ACCAAGGGCCCATCGGTCTTCCCTTGGCACCTCTCCAGAGACCTCTTGGGGGACACA 408

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DB 117 ThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThr 136
QY 409 GCGGCCCTGGGTGCTGTCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTCTGGGAAC 468
DB 137 AlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSerTrpAsn 156
QY 469 TCAGGCGCCTGACACAGCGCGTGCACACTTCCGGGTGTCTACAGTCTCAGTCTCAGACTC 528
DB 157 SerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeu 176
QY 529 TACTCCTCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTCGGGCAACCCAGACCTACATC 588
DB 177 TyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThrTyrIle 196
QY 589 TGAACGTGAATCACAAGCCGACACACAGGTGGAGCAAGAAAGTGGAGCCCAAACTCT 648
DB 197 CysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluProLysSer 216
QY 649 TGTGACAAAACACTCACACATGCCACCGTCCCGACGACCTGAACCTCGCGGGGACCCGCTCA 708
DB 217 CysAspLysThrHisThrCysProCysProAlaProGluLeuGlyGlyProSer 236
QY 709 GTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGNACCCCTGAGGTC 768
DB 237 ValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrProGluVal 256
QY 769 ACATGCGTGTGTGGTGGACGTGAGCCAGCAAGACCTCGAGTCAAGTCAACTGGTACGTCG 828
DB 257 ThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrpTyrVal 276
QY 829 GACGGGTGGAGTGTGATTAATCCAAAGCAAAAGCCCGGAGGAGCAGTACAAACAGCAGC 888
DB 277 AspGlyValGluValHisAlaLysThrLysProArgGluGluGlnTyrAsnSerThr 296
QY 889 TACCGTGTGTGACGCTCTCCCGTCCGACGAGTGGCTGAATCGCAAGGAGTAC 948
DB 297 TyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyr 316
QY 949 AAGTGAAGGTCTTCCAAAGACCTCCCGAGCCCGCCATCGAGAAAACCATCTCCAAAGCC 1008
DB 317 LysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAla 336
QY 1009 AAAGGCGCCCGCCGAGAACACAGGTGTACACCTCCCGCCATCCCGGATGAGTGCACC 1068
DB 337 LysGlyGlnProArgGluProGlnValTyrThrLeuProSerArgAspGluLeuThr 356
QY 1069 AAGAACCGAGTCTGACCTGACCTCCCTGGTCAAGGCTTCTATCCCGACGACATCGCCGTG 1128
DB 357 LysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal 376
QY 1129 GAGTGGAGAGCAATGGGAGCGGAGAGAACTACAGACCCGCTCCCGTCTGGAC 1188
DB 377 GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProValLeuAsp 396
QY 1189 TCCGACGCTCTCTTCTCTCTACAGAGCTCACCGTGGAGCAAGAGCAGGTGGCAGCAG 1248
DB 397 SerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGln 416
QY 1249 GGAAGCTCTCTCATGCTCCGCTGATGATGAGCTCTGCACACCACTACAGCGAGAG 1308
DB 417 GlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLys 436
QY 1309 AGCTCTCCCTGCTCCGGGTAAA 1332
DB 437 SerLeuSerLeuSerProGlyLys 444

RESULT 9
AAE33523
ID AAE33523 standard; protein; 447 AA.
XX
AC AAE33523;
XX
DT 02-APR-2003 (first entry)

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XX DE Human AOC2 heavy chain mutant protein, hAOC2.  
 XX KW Human; very late activation antigen; VLA-1; betal containing integrin;  
 KW immunological disorder; inflammatory disorder; skin related condition;  
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;  
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;  
 KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;  
 KW irritable bowel syndrome; colitis; colorectal cancer; vascular disease;  
 KW atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;  
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;  
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;  
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;  
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;  
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;  
 KW graft versus host disease; myocardial ischaemia; mutant; mutein.  
 XX OS Homo sapiens.  
 XX KW WO200203854-A2.  
 XX PD 24-OCT-2002.  
 XX PF 12-APR-2002; 2002WO-US011521.  
 XX PR 13-APR-2001; 2001US-0283794P.  
 XX PR 06-JUL-2001; 2001US-0303689P.  
 XX PA (BIOJ ) BIOGEN INC.  
 XX PI Lyne PD, Garber EA, Saldanha JW, Karpusas M;  
 XX WPI; 2003-093009/08.  
 XX PT New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
 PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,  
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or  
 PT fibrosis.  
 XX PS Example 23; Page 91-92; 248pp; English.  
 XX CC The present invention relates to novel antibodies that specifically bind  
 CC to very late activation (VLA-1; betal containing integrins) antigens and  
 CC methods of using these antibodies to treat immunological disorders. The  
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
 CC mediated immunological or inflammatory disorders such as skin related  
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal  
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung  
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,  
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-  
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,  
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),  
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,  
 CC periarthritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,  
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid  
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal  
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,  
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or  
 CC immediate hypersensitivity), graft and transplant rejections, graft  
 CC versus host disease, conjunctivitis, swelling occurring after injury,  
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is  
 XX human AOC2 heavy chain mutant protein, hAOC2

Alignment Scores:  
 Pred. No.: 1,048-129 Length: 447  
 Score: 2185.00 Matches: 417  
 Percent Similarity: 94.22% Conservative: 7  
 Best Local Similarity: 92.67% Mismatches: 16  
 Query Match: 90.85% Indels: 10  
 DB: 6 Gaps: 2

US-09-674-716B-18 (1-1335) x AAE33523 (1-447)  
 QY 1 GAGGTGAGCTGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60  
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
 QY 61 TCTGTGACACTAGCGGATTCATTTTCAGTGGCTACTGGATGTCCTGGGTCCCGCAGGCT 120  
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrThrMetSerTrpValArgGlnAla 40  
 QY 121 CCAGGGAAGGGGCTCCAGTGGTGTGTAATAGATTGAAATCTGATAATTATTAATCAACA 180  
 Db 41 ProGlyLysGlyLeuGluTrpValAlaThrIle-----SerGlyGlyGlyHisThr 57  
 QY 181 CATTATCGCGAGTCTGTGAAGGGGAAATTCACATCTCAAGAGATGATTCAAATCTAGA 240  
 Db 58 TyrTyrLeuAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 77  
 QY 241 CTGTATCTGCATAATGAACAGCTGAAACCGAGGACACACGCGTGTATTACTGTACAGAT 300  
 Db 78 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysThrArg 97  
 QY 301 -----TTCATAGACTGGGGGCGAGGGAACACTAGTCAACCGTCTCC 339  
 Db 98 GlyPheGlyAspGlyGlyTyrPheAspValTrpGlyGlnGlyThrLeuValThrValSer 117  
 QY 340 TCAGCCTCCACCAAGGGCCCATCGTCTTCCCTCGCACCTCTCTCCAGAGACACTCT 399  
 Db 118 SerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSer 137  
 QY 400 GGGGGACACAGCGGCTCGTGGCTCGTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTG 459  
 Db 138 GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrVal 157  
 QY 460 TCGTGGAACTCAGGCGCCCTGACAGCGGCTGCACACCTTCCCGGCTGCTTACAGTCC 519  
 Db 158 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 177  
 QY 520 TCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTCCACAGAGCTGGGCACCCAG 579  
 Db 178 SerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGln 197  
 QY 580 ACCTACATCTGCAACGTGAATCAAGCCCGACCAACCAAGGTGGACAGAAGTGGAG 639  
 Db 198 ThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGlu 217  
 QY 640 CCCAAATCTTGTACAAAACCTACACATGCCCCCGTCCCGACACCTGACCTGCGGGGG 699  
 Db 218 ProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuGly 237  
 QY 700 GCACCGTCACTCTCTCTCTTCCCCCAAAACCAAGACACCCCTCATGTCTCCCGAAC 759  
 Db 238 GlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThr 257  
 QY 760 CTGAGGTACATGCTGGTGGTGGAGCGTGGAGCCAGAGACCCCTGAGTCAAGTTCAC 819  
 Db 258 ProGluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsn 277  
 QY 820 TGTGTACGTGACGCGTGGAGGTGCATATGCCAACACAAAGCCGCGGAGGAGCAGTAC 879  
 Db 278 TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyr 297  
 QY 880 AACAGACGTACCGTGTGGTCAACCGTCTCCACCGTCTCCACCGAGTGGCTGAATGCC 939  
 Db 298 GlnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly 317  
 QY 940 AAGAGGTACAGTGAAGGTCTCCCAAGAGCCCTCCCGACCCCTCCAGAGAACCATC 999  
 Db 318 LysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIle 337  
 QY 1000 TCCAAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTACACCTGCCCCCATCCCCGGAT 1059  
 Db 338 SerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAsp 357



Db 299 SerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysVal 318  
QY 961 TCCAAAGAGCCCTCCAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCC 1020  
Db 319 SerAsnLysAlaLeuProAlaProIleGluLysThrLysLysAlaLysGlyLysPro 338  
QY 1021 CGAGAACACAGGTGTACACCTGCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 1080  
Db 339 ArgGluProGlnValTyrThrLeuProSerArgAspGluLeuThrLysAsnGlnVal 358  
QY 1081 AGCTGACCTCGCTGTCAGAGGCTCTATCCAGCAGCATCGCGTGGAGGAGC 1140  
Db 359 SerLeuThrCysLeuValGlyGlyPheTyrProSerAspIleAlaValGluTrpGluSer 378  
QY 1141 AATGGGACCGGAGAACCAACTACAAGACCGCTCCCTCCCTCCCTCCCTCCCTCC 1200  
Db 379 AsnGlyGlnProGluAsnAsnTyrLysThrProValLeuAspSerAspGlySer 398  
QY 1201 TTCCTCTCTACAGCAAGCTCACCGTGCACAGAGCAGGTGGCAGGAGGAGCTTTC 1260  
Db 399 PhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPhe 418  
QY 1261 TCATGCTCCGTGATGATGAGGCTCTGCACCAACCACTACAGCAGAGAGCTCTCCCTG 1320  
Db 419 SerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu 438  
QY 1321 TCTCCGGGTAAA 1332  
Db 439 SerProGlyLys 442  
RESULT 11  
ID ABU08311 standard; protein; 442 AA.  
AC ABU08311;  
DT 22-MAY-2003 (first entry)  
XX Humanised 266 antibody heavy chain.  
DE Mouse; cognition; Abeta peptide associated disorder; anti-Abeta antibody;  
KW cognitive impairment; Alzheimer's disease; Down's syndrome;  
KW cerebral amyloid angiopathy; vascular dementia; neurotropic;  
KW mild cognitive impairment; antibody 266; heavy chain; humanised; mutant;  
KW mutin.  
XX Mus sp.  
OS Synthetic.  
XX WO2003015691-A2.  
XX 27-FEB-2003.  
PF 14-AUG-2002; 2002WO-US021323.  
PR 17-AUG-2001; 2001US-0313222P.  
PR 28-MAY-2002; 2002US-0383846P.  
XX (ELIL ) LILLY & CO ELI.  
XX PA Bales KR, Dodart JF, Paul SM;  
PI WPI; 2003-268234/26.  
DR Effecting rapid improvement of cognition in a subject having Alzheimer's  
XX disease, Down's syndrome, cerebral amyloid angiopathy, or mild cognitive  
PT impairment, comprises administering anti-A beta antibody.  
XX  
PS Disclosure; Page 21-23; 85pp; English.  
XX The present invention relates to a method for effecting rapid improvement  
CC of cognition in a subject having a condition or disease related to the  
CC Abeta peptide. The method comprises administering an anti-Abeta antibody.

CC The method is useful for treating cognitive impairments associated with  
CC Abeta peptide including those involved in Alzheimer's disease, Down's  
CC syndrome, cerebral amyloid angiopathy, certain vascular dementia, and  
CC certain forms of mild cognitive impairment. The anti-Abeta antibody is  
CC useful for preparing a medicament for effecting rapid improvement in  
CC cognition in a subject having Alzheimer's disease, Down's syndrome,  
CC cerebral amyloid angiopathy, or mild cognitive impairment. The present  
CC sequence represents a preferred heavy chain for a humanised 266 antibody  
XX  
SQ Sequence 442 AA;  
Alignment Scores: 1.38e-129 Length: 442  
Pred. No.: 2183.00 Matches: 414  
Score: 95.72% Conservative: 11  
Percent Similarity: 93.24% Mismatches: 17  
Best Local Similarity: 90.77% Indels: 2  
Query Match: 6 Gaps: 1  
DB: 1  
US-09-674-716b-18 (1-1335) x ABU08311 (1-442)  
QY 1 GAGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
QY 61 TCCTGTGCGAGTAGCGGATTCTCTTCTGCTGGTACTGCTGGTCTGGTCTGGTCTGGT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrSerMetSerTrpValArgGlnAla 40  
QY 121 CCAGGAAGGGGCTCGAGTGGGTGCTGAAATAGATTTGAAATCTGATATTAATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluLeuValAlaGlnIle-----AsnSerValGlyAsnSerThr 58  
QY 181 CATATGCGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCATCAATCTAGA 240  
Db 59 TyrTyrProAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThr 78  
QY 241 CTGTATCTGCAAAATGAACAGCCTGAAACCGAGGACACAGCCGCTGTATTACTGTACAGAT 300  
Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAlaSer 98  
QY 301 TTCATGAGTGGGGCGAGGAAACACTAGTACACCGTCTCTCTGAGCTTCCACCAAGGCCCA 360  
Db 99 GlyAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 118  
QY 361 TCGGTCTTCCCTCCCTGCGACCTCTCCAGAGCACCTCTGGGGGACAGCGGCGCTGGGC 420  
Db 119 SerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGly 138  
QY 421 TGCCTGCTCAAGGACTACTTCCCGAACCGGTGACCGTGTCTGGAACCTCAGCGCCCTG 480  
Db 139 CysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu 158  
QY 481 ACCAGCGGCTGCACACCTTCCCGGCTGCTCCTACAGTCTCCTCAGACTCTACTCCCTCAGC 540  
Db 159 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLysLeuSerLeuSer 178  
QY 541 AGCGTGTGACCGTGGCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGCTGAAT 600  
Db 179 SerValValThrValProSerSerSerLeuGlyThrGlnThrThrIleCysAsnValAsn 198  
QY 601 CACAGCCCGAGAACACCAAGGTGGACAGAAAGTGGAGCCCAAACTCTGTGACAAACT 660  
Db 199 HisLysProSerAsnThrLysValAspLysLysValGluProLysSerCysAspLysThr 218  
QY 661 CACATATGCCACCGTGGCCAGCACTGAACTCCGCGGGGACCGCTCAGTCTTCTCTTCTTC 720  
Db 219 HisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPhe 238  
QY 721 CCCCCAAAACCAAGGACCCCTCATGATCTCCCGACCCCTCAGGTTCATCGGTGGT 780  
Db 239 ProProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCysValVal 258

QY 781 GTGAGCTGAGCAGCAGACCTGAGGTCAAGTTCAACTGCTGAGCGGTGAG 840  
 Db |||||  
 QY 259 ValAspValSerHisGluAspProGluValLysPheAsnTrpValAspGlyValGlu 278  
 Db |||||  
 QY 841 GTGCATAATGCCAAGCAGCAGCGGAGAGCAGTACAAACAGCAGCAGTACGTTGCTC 900  
 Db |||||  
 QY 279 ValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValVal 298  
 Db |||||  
 QY 901 AGCGTCTCACGCTGCTGACAGCAGTGGCTGAATGCCAAGGAGTACAGTGCAGTGC 960  
 Db |||||  
 QY 299 SerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysVal 318  
 Db |||||  
 QY 961 TCAACAAAGCCCTCCAGCCCATCGAAGAAACCATCTCCAAAGCCAAAGGCGAGCCC 1020  
 Db |||||  
 QY 319 SerAsnLysAlaLeuProAlaProLleGluLysThrLysLysAlaLysGlyGlnPro 338  
 Db |||||  
 QY 1021 CGAGAACCAACAGGTGTACACCTGCTGCCCATCCCGGATGAGCTGACCAAGAACCCAGTGC 1080  
 Db |||||  
 QY 339 ArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnVal 358  
 Db |||||  
 QY 1081 AGCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGC 1140  
 Db |||||  
 QY 359 SerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSer 378  
 Db |||||  
 QY 1141 AATGGCAGCCGAGAACCACTACAGACACCGCTCCCGTCTGGACTCCGAGCGTCC 1200  
 Db |||||  
 QY 379 AsnGlyGlnProGluAsnAsnTyrLysThrThrProProValLeuAspSerAspGlySer 398  
 Db |||||  
 QY 1201 TTCTTCTCTACAGCAAGCTCACCTGGACAGAGCAGTGGCAGCGGAGAGCTCTTC 1260  
 Db |||||  
 QY 399 PhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPhe 418  
 Db |||||  
 QY 1261 TCATGCTCCGTCATGATGAGGCTCTGCACACCACTACAGCAGAGAGGCTCTCCCTG 1320  
 Db |||||  
 QY 419 SerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu 438  
 Db |||||  
 QY 1321 TCTCCGGTAAA 1332  
 Db |||||  
 QY 439 SerProGlyLys 442  
 Db |||||

## RESULT 12

ABB80109  
 ID ABB80109 standard; protein; 442 AA.  
 XX  
 AC ABB80109;  
 XX  
 DT 13-JUN-2003 (first entry)  
 XX  
 DE Heavy chain.  
 XX  
 KW Complementarity determining region; CDR; humanised; mouse; 266; light;  
 KW heavy; variable; domain; antibody; preclinical; clinical;  
 KW Alzheimer's disease; epitope; amyloid beta peptide; Abeta;  
 KW central nervous system; plasma.  
 XX  
 OS Homo sapiens.  
 OS Mus musculus.  
 XX  
 PN WO2003015617-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 16-AUG-2002; 2002WO-US026321.  
 XX  
 PR 17-AUG-2001; 2001US-0313221P.  
 PR 17-AUG-2001; 2001US-0313224P.  
 PR 23-OCT-2001; 2001US-0334987P.  
 XX  
 XX (UNIW ) UNIV WASHINGTON.  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Holtzman DM, Demattos R, Bales KR, Cummins DJ, Paul SM;  
 XX

DR WPI; 2003-278505/27.  
 XX Diagnosing preclinical or clinical Alzheimer's disease in a subject by  
 PT administering an antibody which specifically binds an epitope.  
 XX  
 XX Disclosure; Page 15-16; 64pp; English.  
 XX  
 CC The sequences given in AAG80104-09 represent preferred antibodies of the  
 CC invention. This sequence represents the preferred heavy chain. The  
 CC humanised antibody of the invention may be used for diagnosing  
 CC preclinical or clinical Alzheimer's disease. The antibody specifically  
 CC binds an epitope, preferably the amyloid beta peptide (Abeta). The  
 CC antibodies sequester Abeta from its bound, circulating form in blood and  
 CC alter clearance of soluble and bound forms of Abeta in central nervous  
 CC system and plasma. The antibodies specifically bind an epitope  
 CC representing amino acids 13-28 of the Abeta molecule  
 XX  
 SQ Sequence 442 AA;

## Alignment Scores:

Pred. No.: 1-38e-129 Length: 442  
 Score: 2183.00 Matches: 414  
 Percent Similarity: 95.72% Conservative: 11  
 Best Local Similarity: 93.24% Mismatches: 17  
 Query Match: 90.77% Indels: 2  
 DB: 6 Gaps: 1

US-09-674-716B-18 (1-1335) x ABB80109 (1-442)

QY 1 GAGTGCAGCTGTGTGAGTCTGGGAGAGCTGTGTAACCCGGGGTCCCTTAGACTC 60  
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
 QY 61 TCCTGTGACGTAGCCGATTCACCTTCAGTGGCTACTGGATGCTCTGGTCCGCCAGGCT 120  
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrSerMetSerTrpValArgGlnAla 40  
 QY 121 CAGGGAAGGGCTCGAGTGGTGTGTAAGGGAATTCACCATCTCAAGAGATGATCAAAATCTG 180  
 Db 41 ProGlyGlyGlyLeuGluLeuValAlaGlnIle-----AsnSerValGlyAsnSerThr 58  
 QY 181 CATTATGCGGAGTCTGTGAAGGGAATTCACCATCTCAAGAGATGATCAAAATCTG 240  
 Db 59 TyrTyrProAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysThr 78  
 QY 241 CTGTATCTGCAATGAACAGCTGAAACCCGAGGACACAGCGGTGTATTACTGTACAGAT 300  
 Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaSer 98  
 QY 301 TTCATAGACTGGGCCAGGGAACACTAGTCACCGCTCTCCTCAGCTCCACCAAGGCCCA 360  
 Db 99 GlyAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 118  
 QY 361 TCGGTCTTCCCTCCGACCCCTCTCCAAAGAGCACCTCTGGGGGCACAGCGCCCTGGGC 420  
 Db 119 SerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGly 138  
 QY 421 TGCTGTGTCAGGACTACTTCCCGNACCGGTGAGGTGCTCGTGGAACTCAGCGCCCTG 480  
 Db 139 CysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu 158  
 QY 481 ACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGC 540  
 Db 159 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSer 178  
 QY 541 AGCGTGTGACGTGCTCCCTCGAGCTTGGGACCCAGACCTACATCTGCAACGTGAAT 600  
 Db 179 SerValValThrValProSerSerLeuGlyThrGlnThrTyrIleCysAsnValAsn 198  
 QY 601 CACAAGCCAGCAACACCAAGGTGGACAGAAGTGGAGGCCCAAAATCTGTGACAAAAC 660  
 Db 199 HisLysProSerAsnThrLysValAspLysLysValGluProLysSerCysAspLysThr 218



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Db      219  AspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGlyProSerVal 238
QY      712  TTCCTCTTCCCAAAACCCAGGACACCTCATGATCTCCGGACCCCTGAGTCA 771
Db      239  PheLeuPheProLysProLysAspThrLeuMetIleSerArgThrProGluValThr 258
QY      772  TGGCTGGTGTGACGTGACGACCAAGACCCCTGAGCTCAAGTTCACCTGGTACGTGAC 831
Db      259  CysValValValAspValSerHisGluAspProGluValLysPheAsnTrpTyrValAsp 278
QY      832  GGGCTGGAGTGCATATATGCGAAGACAAAGCCCGGGAGGAGACGATACACGACGGRAC 891
Db      279  GlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyr 298
QY      892  CGTGTGGTGTGACGTCTCACCGTCCCTGACACAGGACTGCTGAATGGCAAGGAGTACAG 951
Db      299  ArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLys 318
QY      952  TGCAGGTCTCCAAAGACCCCTCCAGCCCTCGAGCCCAACCAACCATCTCCAAAGCCAAA 1011
Db      319  CysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaLys 338
QY      1012  GGGCAGCCCGAGAACACAGGTGTACACCTGCCCTCCATCCCGGATGAGTGCACGAG 1071
Db      339  GlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLys 358
QY      1072  AACCAAGTGTGACGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1131
Db      359  AsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGlu 378
QY      1132  TGGAGAGCAATGGGAGCGGAGGAGACAACTACAGACACACCTCCCGTGTGACTGCC 1191
Db      379  TrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProValLeuAspSer 398
QY      1192  GACGGTCTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGG 1251
Db      399  AspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGly 418
QY      1252  AACGTTCTTCATGCTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1311
Db      419  AsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSer 438
QY      1312  CTCTCCCTGCTCCGGGTAAA 1332
Db      439  LeuSerLeuSerProGlyLys 445

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## RESULT 14

AAU07745

ID AAU07745 standard; protein; 461 AA.

XX AC

XX AC

XX AC

DT 04-DEC-2001 (first entry)

XX XX

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XX XX

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PN      WO200162801-A2.
XX      30-AUG-2001.
XX      26-FEB-2001; 2001WO-US006191.
XX      24-FEB-2000; 2000US-0184601P.
PR      08-DEC-2000; 2000US-0254465P.
PR      08-DEC-2000; 2000US-0254498P.
XX      (UNIV ) UNIV WASHINGTON.
PA      (ELIL ) LILLY & CO ELI.
XX      Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;
PI      Vasquez M;
XX      WPI; 2001-550087/61.
XX      New humanized antibody for the treatment of Alzheimer's comprises the
PT      inhibition and reduction of the formation of amyloid plaques.
PT      Example 13; Fig 5; 63pp; English.
XX      The invention relates a humanised antibody that specifically binds an
CC      epitope contained within positions 13-28 of amyloid beta peptide, Abeta.
CC      The antibody is useful to inhibit and reduce the formation of amyloid
CC      plaques or the effects of toxic soluble Abeta species in humans their
CC      fragments are used for the manufacture of a medicament. This includes the
CC      prolonged expression of recombinant sequences of them in human tissues
CC      for the treatment of clinical/pre-clinical Alzheimer's disease, Down's
CC      syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the
CC      antibody is used to sequester Abeta into plasma, brain or cerebrospinal
CC      fluid to prevent/reverse accumulation of the Abeta peptide within the
CC      brain thereby improving cognition. The present sequence is the heavy
CC      chain of a humanised monoclonal antibody, Hu266, based on the mouse
CC      antibody 266
XX      SQ Sequence 461 AA;

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## Alignment Scores:

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Pred. No.: 1.39e-129 Length: 461
Score: 2183.00 Matches: 414
Percent Similarity: 95.72% Conservative: 11
Best Local Similarity: 93.24% Mismatches: 17
Query Match: 90.77% Indels: 2
DB: 4 Gaps: 1

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US-09-674-716B-18 (1-1335) x AAU07745 (1-461)

```

QY      1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGTAAGCCCGGGGGTCCCTTAGACTC 60
Db      20 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
QY      61 TCCTGTGCAGCTAGCGGATTCACCTTTCAGTGGCTACTGGATGCTCTGGGTCCGCCAGGCT 120
Db      40 SerCysAlaAlaSerGlyPheThrPheSerArgTyrSerMetSerTrpValArgGlnAla 59
QY      121 CCAGGGAAGGGCTCGAGTGGTCTGTAAGGAAATTCACCATCTCAAGAGATGATTCAAAATCTCA 180
Db      60 ProGlyLysGlyLeuGluLeuValAlaGlnIle-----AsnSerValGlyAsnSerThr 77
QY      181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTCA 240
Db      78 TyrTyrProAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThr 97
QY      241 CTGTATCTCAATGAACAGCTGAAACCCAGGAGACACAGCCGTGTATCTGTACAGAT 300
Db      98 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaSer 117
QY      301 TTCATAGACTGGGGCCAGGGAACACTAGTCAACCGTCTCTCAGCCCTCCACCAAGGGCCCA 360
Db      118 GlyAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 137

```

Humanised monoclonal antibody Hu266, heavy chain.

Monoclonal antibody; Hu266; neotropic; neuroprotective; Abeta peptide;  
 Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;  
 gene therapy.

Mus sp.

Homo sapiens.

Synthetic.

Key

Location/Qualifiers

1..19

/label= Signal peptide

20..461

/label= Mature Hu266 heavy chain

/note= "This sequence is specifically claimed in claim

17"

FT

FT



QY 361 TCAGTCTTCCCTGGACACCTCTCCAAAGAGACCTCTCTGGGGGACAGCGGCCCTGGGC 420  
Db 138 SerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGly 157  
QY 421 TGCGTGTCAAGGACTACTCCCGAACCGGTGACGGTGTCTGGGAACCTCAGCGCCCTG 480  
Db 158 CysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu 177  
QY 481 ACCAGCGCGTGCACACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGC 540  
Db 178 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSer 197  
QY 541 AGCGTGTGACGTCCTCCCTCAGCAGCTTGGGACCCAGACCTACATCTCCACGTCGAAT 600  
Db 198 SerValValThrValProSerSerSerLeuGlyThrGlnThrTyrIleCysAsnValAsn 217  
QY 601 CACAAGCCACCAACACCAAGGTGGACAAAGAGTGGAGGCCAATACTTGTGACAAAAC 660  
Db 218 HisLysProSerAsnThrLysValAspLysLysValGluProLysSerCysAspLysThr 237  
QY 661 CACACATCCACCGTGCACAGCCTGAACTCCGGGGGACCGTCAGTCTTCTCTTC 720  
Db 238 HisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPhe 257  
QY 721 CCCCACAAACCAAGCACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGTG 780  
Db 258 ProProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCysValVal 277  
QY 781 GTGACGTGAGCCACGACAGACCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 840  
Db 278 ValAspValSerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGlu 297  
QY 841 GTGCAATATGCCAAGACCAAGCCGGGAGGAGGAGTACACAGCACTACCGTGTGTC 900  
Db 298 ValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValVal 317  
QY 901 AGCGTCTCTCACCGTCTCTGCACAGACCTGGTGAATGGCAAGGAGTACAAGTCAAGT 960  
Db 318 SerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysVal 337  
QY 961 TCACACAAAGCCCTCCGACCCCTCCAGAACCACTCCAAAGCCAAAGGCGAGCC 1020  
Db 338 SerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnPro 357  
QY 1021 CCAGAACCAACAGGTGTACACCTCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCC 1080  
Db 358 ArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnVal 377  
QY 1081 AGCCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGC 1140  
Db 378 SerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSer 397  
QY 1141 AATGGCGACCGGAGAACACTACAGACCCGCTCCGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
Db 398 AsnGlyGlnProGluAsnAsnTyrLysThrThrProProValLeuAspSerAspLysSer 417  
QY 1201 TTCTTCTCTCTACAGCAAGCTCAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGC 1260  
Db 418 PhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPhe 437  
QY 1261 TCATGCTCGTGTGATGATGAGCTCTGCAACACCACTACACGACAGAGGCTCTCCCTG 1320  
Db 438 SerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu 457  
QY 1321 TCTCCGGGTAAA 1332  
Db 458 SerProGlyLys 461

RESULT 15  
ID ABR39844  
XX ABR39844 standard; protein; 461 AA.  
AC ABR39844;

XX 18-AUG-2003 (first entry)  
DT Hu266 N56T heavy chain.  
XX Amyloid-beta; Abeta; antibody 266; neurotropic; neuroprotective; CDR;  
KW immunostimulant.  
XX Homo sapiens.  
XX MO2003016466-A2.  
XX 27-FEB-2003.  
XX 14-AUG-2002; 2002WO-US021322.  
XX 17-AUG-2001; 2001US-0313224P.  
XX (ELIL ) LILLY & CO ELI.  
XX Jia AY, Tsurushita N, Vasquez MJ;  
XX WPI; 2003-278557/27.  
XX N-PSDB; ACC47228.  
XX New antibodies comprising a heavy chain and a light chain complementarity  
PT determining regions from antibody 266, for treating and preventing  
PT conditions associated with the A beta peptide, e.g. Alzheimer's disease  
PT or Down syndrome.  
XX Disclosure; Fig 3; 82pp; English.  
XX The invention relates to an anti-Abeta (amyloid-beta peptide) antibody  
CC 266. The antibodies are useful for treating and preventing conditions  
CC associated with the Abeta peptide, such as Alzheimer's disease, Down  
CC syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in  
CC humans; for determining whether a human subject will respond to treatment  
CC using humanized antibodies against Abeta; for treating, preventing and  
CC reversing cognitive decline in clinical or pre-clinical Alzheimer's  
CC disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting  
CC formation of amyloid plaques of the effects of toxic soluble Abeta  
CC species in humans. Treatment of the patients with antibody will inhibit  
CC or prevent cognitive decline typically associated with disease  
CC progression and reverses it. The present sequence represents a humanised  
CC anti-Abeta antibody 266 N56T heavy chain  
XX SQ Sequence 461 AA;  
Alignment Scores:  
Pred. No.: 1.39e-129 Length: 461  
Score: 2183.00 Matches: 414  
Percent Similarity: 95.72% Conservative: 11  
Best Local Similarity: 93.24% Mismatches: 17  
Query Match: 90.77% Indels: 2  
DB: Gaps: 1  
US-09-674-716B-18 (1-1335) x ABR39844 (1-461)  
QY 1 GAGTGCAGTGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGCTCCTTAGACTC 60  
Db 20 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39  
QY 61 TCCTGTGCGAGTACGGGATTCACATTCAGTGGCTGCTGGATGTCTGGTCCGCGCAGGCT 120  
Db 40 SerCysAlaAlaSerGlyPheThrPheSerArgTyrSerMetSerTrpValArgGlnAla 59  
QY 121 CCAGGGAAGGGGCTCGAGTGGTTCGTAATAGATTGAAATCTGTAATATTATGTAACA 180  
Db 60 ProGlyLysGlyLeuGluLeuValAlaGlnIle-----AsnSerValGlyThrSerThr 77  
QY 181 CATATGCGGAGTCTGCGAGCGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240  
Db 78 TyrTrpProAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThr 97



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:54:09 ; Search time 175.104 Seconds  
(without alignments)  
4906.833 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 2405

Sequence: 1 gaggtgcagctgtggagtc.....ccctgtctccggtaaatga 1335

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 2702124

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

1	2191	91.1	447	16	US-10-474-832-4	Sequence 4, Appli
2	2191	91.1	447	16	US-10-474-832-6	Sequence 6, Appli
3	2187	90.9	444	14	US-10-150-475A-6	Sequence 6, Appli
4	2187	90.9	444	16	US-10-704-522-6	Sequence 6, Appli
5	2187	90.9	444	16	US-10-645-215-6	Sequence 6, Appli
6	2185	90.9	447	16	US-10-474-832-5	Sequence 5, Appli
7	2183	90.8	442	12	US-10-226-435A-12	Sequence 12, Appli
8	2183	90.8	445	14	US-10-320-231A-79	Sequence 79, Appli
9	2173.5	90.4	449	9	US-09-736-371B-21	Sequence 21, Appli
10	2173.5	90.4	449	15	US-10-463-442-21	Sequence 21, Appli
11	2172.5	90.3	451	9	US-09-822-698A-26	Sequence 26, Appli
12	2172.5	90.3	474	14	US-09-848-832-3	Sequence 3, Appli
13	2172.5	90.3	474	14	US-10-225-108A-3	Sequence 1, Appli
14	2172.5	90.3	474	15	US-10-461-148-1	Sequence 32, Appli
15	2170	90.2	663	12	US-10-412-406-33	Sequence 33, Appli
16	2170	90.2	4852	12	US-10-412-406-33	Sequence 46, Appli
17	2169	90.2	446	16	US-10-408-901-46	Sequence 38, Appli
18	2167	90.1	446	16	US-10-408-901-38	Sequence 26, Appli
19	2166	90.1	469	16	US-10-656-769-26	Sequence 8, Appli
20	2161.5	89.9	478	9	US-09-948-429B-8	Sequence 8, Appli
21	2161.5	89.9	478	12	US-09-758-173-8	Sequence 8, Appli
22	2161.5	89.9	478	13	US-10-124-905-8	Sequence 8, Appli
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25	2161	89.9	477	15	US-10-291-265-395	Sequence 4, Appli
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27	2158	89.7	469	16	US-10-656-769-20	Sequence 42, Appli
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29	2151.5	89.5	453	9	US-09-802-077-8	Sequence 8, Appli
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31	2151.5	89.5	453	10	US-09-925-179-8	Sequence 26, Appli
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34	2151.5	89.5	464	15	US-10-029-988B-26	Sequence 26, Appli
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36	2150.5	89.4	451	9	US-09-920-171-18	Sequence 2, Appli
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39	2150.5	89.4	451	14	US-10-292-869-2	Sequence 71, Appli
40	2148	89.3	452	10	US-09-726-258-71	Sequence 14, Appli
41	2147.5	89.3	451	9	US-09-920-171-14	Sequence 16, Appli
42	2147.5	89.3	451	9	US-09-920-171-16	Sequence 65, Appli
43	2147.5	89.3	451	10	US-09-925-179-65	Sequence 14, Appli
44	2147.5	89.3	451	14	US-10-113-996-14	Sequence 16, Appli
45	2147.5	89.3	451	14	US-10-113-996-16	

ALIGNMENTS

RESULT 1  
US-10-474-832-4  
; Sequence 4, Application US/10474832  
; Publication No. US20040081651A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; TITLE OF INVENTION: ANTIBODIES TO VLA-1  
; FILE REFERENCE: A101 PCT  
; CURRENT APPLICATION NUMBER: US/10/474,832  
; CURRENT FILING DATE: 2003-10-14  
; PRIOR APPLICATION NUMBER: 60/283,794  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/303,689  
; PRIOR FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: polypeptide  
US-10-474-832-4

Alignment Scores:  
 Pred. No.: 6,93e-134 Length: 447  
 Score: 2191.00 Matches: 418  
 Percent Similarity: 94.44% Conservative: 7  
 Best Local Similarity: 92.89% Mismatches: 15  
 Query Match: 91.10% Indels: 10  
 DB: 16 Gaps: 2

US-09-674-716B-18 (1-1335) x US-10-474-832-4 (1-447)

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QY 1 GAGGTGACGTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
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QY 61 TCCTGTGACAGTACCGGATTCACCTTCAGTGGCTACTGATGCTCTGGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrThrMetSerTrpValArgGlnAla 40
QY 121 CCAGGGAAGGGGCTCGAGTGGGTGCTGAAATAGATTGAAATCTGATAATTATGCAACA 180
Db 41 ProGlyValGlyLeuGluTrpValAlaThrIle-----SerGlyGlyGlyHisThr 57
QY 181 CATTATCGGAGTCTGTGAAGGGAAATTCACATCTCAAGAGATGATTCAAAATCTAGA 240
Db 58 TyrTyrLeuAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 77
QY 241 CTGTATCTGCAATGAACAGCTGAAACCGAGGACACAGCCGCTGTATTACTGTACAGAT 300
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QY 301 -----TTCATAGACTGGGCGCAGGGAACACTAGTACACCTCTCC 339
Db 98 GlyPheGlyAspGlyGlyTyrPheAspValTyrGlyGlnGlyThrLeuValThrValSer 117
QY 340 TCAGCTCCACCAAGGGCCATCGCTCTCCCGCTGGCACCCTCTCCCAAGAGCACTCT 399
Db 118 SerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSer 137
QY 400 GGGGGCACAGCGCCCTCGGCTGCTGTCAAGGACTACTTCCCGGAACCGGTGACGGTG 459
Db 138 GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrVal 157
QY 460 TCGTGAATCAGGCGCCCTGACAGCGCGTGCACACCTTCCCGCTGCTCTACAGTCC 519
Db 158 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 177
QY 520 TCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGCCACCCAG 579
Db 178 SerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGln 197
QY 580 ACTTACATCTGAACGTGAATCACAAGCCCAACACCAAGTGGACAAAGAACTGGAG 639
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QY 640 CCAAAATCTGTGACAAACTCACATGCCCCACCGTCCAGCAGCACTGAACTCGCGGG 699
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QY 700 GCACCGTCACTCTTCTTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCGGACC 759
Db 238 GlyProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThr 257
QY 760 CTTGAGTTCACATGCTGTGTGGTGGAGCTGACCGACGAGACCTTGAGTCAAGTTCAC 819
Db 258 ProGluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsn 277
QY 820 TGGTACGTGGAGCGGTGGAGTGCATATATGCAAGACAAAGCCCGGGAGGAGCAGTAC 879
Db 278 TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyr 297
QY 880 AACAGCACCTACCGTGTGTGCTGACGCTCTCACCGTCTCCAGCAGGACTGCTGATGCG 939

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QY 940 AAGGATACAAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCAATC 999
Db 318 LysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIle 337
QY 1000 TCCAAAGCCAAAGGAGGAGCCCGGAGAACACACAGTGTACACCTGCTCCCGCATCCCGGAT 1059
Db 338 SerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAsp 357
QY 1060 GAGTGTACCAAGAACACAGGTCAACCTGACCTGCTGCTCAAGGCTTCTATCCACGAC 1119
Db 358 GluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAsp 377
QY 1120 ATCGCGTGGAGTGGGAGACAAATGGGAGCCGAGAGAACAACTACAGACCAAGCCCTCC 1179
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QY 1180 GTGTGTGACTCCGACCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAG 1239
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QY 1240 TGGCAGCAGGAGGACGCTCTTCTCATGCTCCGCTGATGCATGAGCTCTGCACACCACTAC 1299
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QY 1300 ACGCAGAAAGACCTCTCCCTGTCTCCGGGT 1329
Db 438 ThrGlnLysSerLeuSerLeuSerProGly 447

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RESULT 2  
 US-10-474-832-6  
 ; Sequence 6, Application US/10474832  
 ; Publication No. US20040081651A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BIOGEN, INC.  
 ; TITLE OF INVENTION: ANTIBODIES TO VLA-1  
 ; FILE REFERENCES: A101 PCT  
 ; CURRENT APPLICATION NUMBER: US/10/474,832  
 ; PRIOR FILING DATE: 2003-10-14  
 ; PRIOR APPLICATION NUMBER: 60/283,794  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/303,689  
 ; PRIOR FILING DATE: 2001-07-06  
 ; NUMBER OF SEQ ID NOS: 70  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 447  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: polypeptide  
 US-10-474-832-6

Alignment Scores:  
 Pred. No.: 6,93e-134 Length: 447  
 Score: 2191.00 Matches: 418  
 Percent Similarity: 94.44% Conservative: 7  
 Best Local Similarity: 92.89% Mismatches: 15  
 Query Match: 91.10% Indels: 10  
 DB: 16 Gaps: 2

US-09-674-716B-18 (1-1335) x US-10-474-832-6 (1-447)

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QY 1 GAGGTGACGTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
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QY 61 TCCTGTGACAGTACCGGATTCACCTTCAGTGGCTACTGATGCTCTGGGTCCGCCAGGCT 120
Db 61 TCGTGTGACAGTACCGGATTCACCTTCAGTGGCTACTGATGCTCTGGGTCCGCCAGGCT 120
QY 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrThrMetSerTrpValArgGlnAla 40
Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrThrMetSerTrpValArgGlnAla 40

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QY 121 CCAGGAGGGCTCGAGTGGTTCGTAATAGATTGAATCTGATAATTATGCAACA 180  
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QY 181 CATTATGGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGA 240  
Db 58 TyTrpLeuAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 77  
QY 241 CTGTATCTGCAATGAACAGCTGAACACCGAGACACAGCCGTGTATTACTGTACAGAT 300  
Db 78 LeuTyLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyTrpCysThrArg 97  
QY 301 -----TTCATAGACTGGGGCCAGGGAACACTAGTCAACCGTCTCC 339  
Db 98 GlyPheGlyAspGlyGlyTyTrpPheAspValTrpGlyGlnGlyThrLeuValThrValSer 117  
QY 340 TCAGCTCTCCACAGGGCCCATCGGTCTTCCCTCGCACCTCTCTCAAGAGACCTCT 399  
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QY 460 TCGTGGAACTCAGGCGCTCACCAGCGCGTGCACACCTTCCCGGTGCTCTACAGTCC 519  
Db 158 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 177  
QY 520 TCAGGACTCTACTCCCTCAGAGGTGTGTACCGTCCCTCCAGCAGCTGGGACCCAG 579  
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QY 640 CCCAAATCTGTGACAAACTCACATGCCACCGTCCCGCAGCACCTGAACCTCGCGGG 699  
Db 218 ProLysSerCysAspLysThrHisThrCysProCysProAlaProGluAlaAlaGly 237  
QY 700 GCACCGTCACTCTCTCTCCCGCCAAACCAAGGACACCTCATCATCTCCCGGACC 759  
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QY 820 TCGTACGTGGAGCGGTGAGTGCATTAATCCAGACAAAGCCGCGGAGGACACTAC 879  
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QY 940 AAGAGTACAGTCAAGTCTCCAAAGCCCTCCAGCCCGCCATCGAGAAACCCATC 999  
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Db 338 SerLysAlaLysGlyLysProArgGluProGlnValTyTrpLeuProProSerArgAsp 357  
QY 1060 GAGCTGACAAAGAACAGGTCAAGTCCCTGGTCAAGGGTCTTATCCAGCGAAC 1119  
Db 358 GluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAsp 377  
QY 1120 ATCGCGGTGGAGTGGAGCAATGGGAGCGGAGAACACTACAAGACCCAGCTCC 1179  
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Db 398 ValLeuAspSerAspGlySerPhePheLeuTySerLysLeuThrValAspLysSerArg 417  
QY 1240 TGGCAGCAGGGAAACGTCTTCTATGCTCCGTGATGATGAGGCTCTGCACACCACTAC 1299  
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QY 1300 ACGCAGAACAGCGCTCTCCCTGTCTCCGGGT 1329  
Db 438 ThrGlnLysSerLeuSerLeuSerProGly 447  
RESULT 3  
US-10-150-475A-6  
; Sequence 6, Application US/10150475A  
; Publication No. US20030103985A1  
; GENERAL INFORMATION:  
; APPLICANT: AGOLF, G. et al.  
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates  
; FILE REFERENCE: 1/1211  
; CURRENT APPLICATION NUMBER: US/10/150,475A  
; CURRENT FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: US 60/307,451  
; PRIOR FILING DATE: 2001-07-24  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Humanised  
US-10-150-475A-6  
Alignment Scores:  
Pred. No.: 1,26e-133 Length: 444  
Score: 2187.00 Matches: 415  
Percent Similarity: 95.09% Conservative: 11  
Best Local Similarity: 92.63% Mismatches: 14  
Query Match: 90.94% Indels: 8  
DB: 14 Gaps: 3  
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QY 121 CCAGGGAAGGGCTCGAGTGGTGTGTAATTTAGATTGAATCTGATAATTATGCAACA 180  
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QY 409 GCAGCCCTGGGTGCCTGTGTCAGAGACTACTTCCCGGAACCCGGTGACGGTGTCTGTGAAC 468

Db 137 AlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSerTrpAsn 156  
QY 469 TCAGGGCGCCTCAGCAGCGCGTGCACACTTCCCGGCTGCTCCTACAGTCTCCTCAGGACTC 528  
Db 157 SerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeu 176  
QY 529 TACTCCCTCAGCAGCGTGTGTCACCGTCCCTCAGCAGCTTGGGACCCAGCAGCTACATC 588  
Db 177 TyrSerLeuSerSerValValThrValProSerSerLeuGlyThrGlnThrTyrlle 196  
QY 589 TCGACGTGAATCAGACGCCAGCAGCAGCAGGTTGGACAGAGTGGAGCCCAATCT 648  
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Db 277 AspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnLysThrAsnSerThr 296  
QY 889 TACCGTGTGTCAGCGTCTCAGCTCCTGACAGGAGTCTGCTCAAGTGGCAAGGAGTAC 948  
Db 297 TyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyr 316  
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Db 337 LysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThr 356  
QY 1069 AAGAACAGGTGAGCTGACCTGCTGCTCAAGGCTTCTATCCAGCAGCAGTCCCGCTG 1128  
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Db 437 SerLeuSerLeuSerProGlyLys 444

## RESULT 4

US-10-704-522-6

; Sequence 6, Application US/10704522

; Publication No. US20040120949A1

; GENERAL INFORMATION:

; APPLICANT: Adol, Gunther

; APPLICANT: Baumann, Michael

; APPLICANT: Heider, Karl-Heinz

; TITLE OF INVENTION: Compositions and methods for treating cancer using

; TITLE OF INVENTION: cytotoxic CD44 Antibody Immunocjugates

FILE REFERENCE: 1/1414  
CURRENT APPLICATION NUMBER: US/10/704,522  
CURRENT FILING DATE: 2003-11-07  
PRIOR APPLICATION NUMBER: US 60/429,516  
PRIOR FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: EP 02024881  
PRIOR FILING DATE: 2002-11-08  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 444  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain  
US-10-704-522-6

Alignment Scores: 1,26e-133 Length: 444  
Pred. No.: 2187.00 Matches: 415  
Score: 2187.00 Conservative: 11  
Percent Similarity: 95.09% Mismatches: 14  
Best Local Similarity: 92.63% Indels: 8  
Query Match: 90.94% Gaps: 3  
DB: 16  
US-09-674-716B-18 (1-1335) X US-10-704-522-6 (1-444)

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Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAspMetSerTrpValArgGlnAla 40  
QY 121 CCAGGAAGGGCTCGAGTGGTGTGTAATAGTAATCTGTAATCTATATGCAACA 180  
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QY 181 CATTATCGGAGTCTGTGAGGGGAATTCACCATCTCAGAGATGATTCAAAATCTAGA 240  
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QY 241 CTGTATCTGCAAAATGAACAGCTGTGAAACCCAGGACACAGCGCTGTATTACTGTACA --- 297  
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Db 137 AlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSerTrpAsn 156  
QY 469 TCAGGCGCCTGACAGCGGCTGACACCTTCCCGGTGTCTCAGTCCCTCAGCTCAGGACTC 528  
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QY 529 TACTCCCTCAGCAGCGTGTGACCGGTGCGCTCCAGCAGCTTGGGACCCAGACCTACATC 588  
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Db 237 ValPheLeuPheProProLysAspThrLeuMetIleSerArgThrProGluVal 256
QY 769 ACATCGGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 828
Db 257 ThrCysValValValValValValValValValValValValValValValValVal 276
QY 829 GACGGCGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 888
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RESULT 5
US-10-645-215-6
; Sequence 6, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/10/645,215
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-645-215-6
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Alignment Scores:
Pred. No.: 1,26e-133 Length: 444
Score: 2187.00 Matches: 415
Percent Similarity: 95.09% Conservative: 11
Best Local Similarity: 92.63% Mismatches: 14
Query Match: 90.94% Indels: 8
DB: 16 Gaps: 3
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US-09-674-716B-18 (1-1335) x US-10-645-215-6 (1-444)

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QY 1 GAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGATGTCCTGGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAspMetSerTrpValArgGlnAla 40
QY 121 CCAGGGAAGGGGCTCCAGTGGTTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTC 180
Db 41 ProGlyLysGlyLeuGluTrpValSerThrIle-----SerSerGlyGlySerTyrThr 58
QY 181 CATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240
Db 59 TyrTyrLeuAspSerIleLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSer 78
QY 241 CTGTATCTGCAATGAACAGCCTGAAACCGAGAGACACAGCCGCTGTATTACTGTACA 297
Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98
QY 298 -----GATTTCATAGACTGGGCCAGGGAACACTAGTCAACCGTCTCTCTCAGCCTCC 348
Db 99 GlnGlyLeuAspTyr-----TyrGlyArgGlyThrLeuValThrValSerSerAlaSer 116
QY 349 ACCAAGGGCCCATCGCTCTTCCCGTGGACCCCTCTCCAGAGCAGCAGCAGCAGCAGC 408
Db 117 ThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThr 136
QY 409 CGCGCCCTGGCTGCTGGTCAAGGAGTACTTCTCCCGAACCGGTGAGCGGTGCTGGGAAC 468
Db 137 AlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSerTrpAsn 156
QY 469 TCAGGGCCCTGACACGAGCGCGTGCACCTTCCCGGCTGTCTCTACAGTCTCTCAGACTC 528
Db 157 SerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeu 176
QY 529 TACTCCCTCAGCAGCTGGTGCCTCCCTCCAGCAGCTTGGGCCACCCAGACCTCATC 588
Db 177 TyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThrTyrIle 196
QY 589 TGCAACGTGAATCACAAGCCCGACCAACACCAAGTGGCAAGAAAGTGGAGCCCAATCT 648
Db 197 CysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluProLysSer 216
QY 649 TGTGCAAAACTCACATGCTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGT 708
Db 217 CysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSer 236
QY 709 GTCTTCCTCTTCCCGCCAAACCCAAAGACACACCTCATGATCTCCCGGAGCCCTGAGGTC 768
Db 237 ValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrProGluVal 256
QY 769 ACATCGGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 828
Db 257 ThrCysValValValValValValValValValValValValValValValValVal 276
QY 829 GACGGCGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 888
Db 277 AspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsnSerThr 296
QY 889 TACCGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 948
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398 ValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArg 417  
1240 TGGCAGCAGGGGAGCGCTTCTCATGCTCCCTGATGATGAGGCTCTGCACAACCATAC 1299  
418 TrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyr 437  
1300 ACGCAGAGAGCGCTCTCCCTGCTCCGGGT 1329  
438 ThrGlnLysSerLeuSerLeuSerProGly 447

RESULT 7  
US-10-226-435A-12  
; Sequence 12, Application US/10226435A  
; Publication No. US20040043418A1  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY and WASHINGTON UNIVERSITY  
; TITLE OF INVENTION: Humanized Antibodies that Sequester Amyloid Beta Peptide  
; FILE REFERENCE: 8792/293  
; CURRENT APPLICATION NUMBER: US/10/226.435A  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: PCT/US01/06191  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,601  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/254,465  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/254,498  
; PRIOR FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized antibodies  
US-10-226-435A-12

Alignment Scores:  
Pred. No.: 2,29e-133 Length: 442  
Score: 2183.00 Matches: 414  
Percent Similarity: 95.72% Conservative: 11  
Best Local Similarity: 93.24% Mismatches: 17  
Query Match: 90.77% Indels: 2  
DB: 12 Gaps: 1  
US-09-674-716B-18 (1-1335) x US-10-226-435A-12 (1-442)

QY 1 GAGGTGCGAGCTGCTGGAGCTTGGTAAAGCCGGGGCTCTAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
QY 61 TCCTGTGCGAGCTAGCGGATTCACTTTTCAGTGGCTACTGGATGCTCCTGGGTCCGCCAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrSerMetSerTrpValArgGlnAla 40  
QY 121 CCAGGAGAGGGCTCGAGTGGTCTGAAATAGATTGAATCTGATTAATTGCAACA 180  
DB 41 ProGlyLysGlyLeuGluLeuValAlaGlnLeu-----AsnSerValGlyAsnSerThr 58  
QY 181 CATTATGCGAGCTGTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240  
DB 59 TyrTyrProAspThrValLysGlyArgPheThrLysSerArgAspAsnAlaLysAsnThr 78  
QY 241 CTGTATCTGCAATGAACAGCTGAAACCCGAGGACAGCGGTGTATTACTGTACAGAT 300  
DB 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAlaSer 98  
QY 301 TTCATAGACTGGGGCCAGGACACTAGTTCACCGCTCTCTCAGCTCCACCAAGGGCCCA 360  
DB 99 GlyAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 118

QY 361 TCGGTCTTCCCTCGGCACCCCTCTCAAAGAGACACCTCTGGGGGCACACGGCCCTGGGC 420  
DB 119 SerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGly 138  
QY 421 TGCTGTGTCAGAGCTACTTCCCGGAAACCGGTGACGGTCTGTGGAACCTCAGCGCCCTG 480  
DB 139 CysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu 158  
QY 481 ACCAGCGGGTGCACACCTTCCCGGGTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGC 540  
DB 159 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSer 178  
QY 541 AGCGTGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCACGTTGAAT 600  
DB 179 SerValValThrValProSerSerLeuGlyThrGlnThrTyrIleCysAsnValAsn 198  
QY 601 CACAAGCCCAAGCAACACCAAGTGGACAGAAAGTGGAGCCCAATCTTGTGACAAAAC 560  
DB 199 HisLysProSerAsnThrLysValAspLysValGluProLysSerCysAspLysThr 218  
QY 661 CACACATGCCCCACCGTGGCCAGCACCTGAACTCGCGGGGGCCACCGTCAGTCTCTCTCTC 720  
DB 219 HisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPhe 238  
QY 721 CCCCCAAAACCAAGACACACCTCATGATCTCCCGGACCCCTGAGGTACATCGCTGGTG 780  
DB 239 ProProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCysValVal 258  
QY 781 GTGGAGCTGAGCCACCAAGACACCTGAGGTCAAGTTCAACTGGTACCTGACGACGCGTGGAG 840  
DB 259 ValAspValSerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGlu 278  
QY 841 GTGCATAATGCCAAGCAACAGCGCGGAGGAGCAGTACAACAGCAGTACCGTGTGGTC 900  
DB 279 ValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValVal 298  
QY 901 AGCGTCTCTACCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTC 960  
DB 299 SerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluLysCysLysVal 318  
QY 961 TCCACAAAAGCCCTCCCGACCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGACGCC 1020  
DB 319 SerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnPro 338  
QY 1021 CGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGACCAAGGTC 1080  
DB 339 ArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnVal 358  
QY 1081 AGCTGACCTGCTGCTCAAGGCTTCTATCCCGACGACATCCCGCTGGAGTGGGAGAGC 1140  
DB 359 SerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSer 378  
QY 1141 AATGGGAGCGCGAGAACAACTACAAGACACACCTCCCGTCTGCTGACTCCGACGCGCTCC 1200  
DB 379 AsnGlyGlnProGluAsnAsnTyrLysThrThrProProValLeuAspSerAspGlySer 398  
QY 1201 TTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTCGAGCGAGGGAACGCTTCTC 1260  
DB 399 PhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPhe 418  
QY 1261 TCATGTCTCGTGTGATGAGCTCTGCACAACCATACACGAGAGAGCCCTCTCCCTG 1320  
DB 419 SerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu 438  
QY 1321 TCTCCCGGTAAA 1332  
DB 439 SerProGlyLys 442

RESULT 8  
US-10-320-231A-79  
; Sequence 79, Application US/10320231A  
; Publication No. US20030194405A1  
; GENERAL INFORMATION:

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; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 79
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-79

Alignment Scores:
Pred. No.: 2,29e-133 Length: 445
Score: 2183.00 Matches: 415
Percent Similarity: 94.86% Conservative: 9
Best Local Similarity: 92.84% Mismatches: 15
Query Match: 90.77% Indels: 8
DB: 14 Gaps: 3

US-09-674-716B-18 (1-1335) x US-10-320-231A-79 (1-445)

QY 10 CTGGTGGTCTGGGGAGGCTGGTAAAGCCCGGGGGTCCCTAGACTCTCTGTGCA 69
Db 1 LeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSerCysAla 20
QY 70 GTAGCGGATTCACATTACAGTGGCTACTGGATGTCTGGTCCGCGAGGCTCCAGGAAG 129
Db 21 AlaSerGlyPheThrPheSerSerTyraMetSerTyrValArgGlnAlaProGlyLys 40
QY 130 GGGCTGAGTGGTGTCTGAATTAAGATTGAATCTGAATCTGAATTAATGAACACATTATCGG 189
Db 41 GlyLeuGluTrpValSerAlaIle-----SerGlySerGlyGlySerThrTyraAla 58
QY 190 GAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGACTGTATCTG 249
Db 59 AspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyraLeu 78
QY 250 CAATGAACAGCTGAAACACGAGACACAGCGGTGTATTACTGTACA-----GATTTC 303
Db 79 GlnMetAsnSerLeuArgAlaGluAspThrAlaValTyraValTyraCysAlaArgAspPhe 98
QY 304 ATAGAC-----TGGGGCCAGGAGAACACAGTACCGTCTCTCAGCTCCAGCTCCACC 351
Db 99 PheAlaHisPheAspValTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThr 118
QY 352 AAGGGCCCATCGGTCTTCCCTCGCACCTCTCTCCAAAGACACCTCTGGGGGACACGCG 411
Db 119 LysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAla 138
QY 412 GCCTGGGTCTGGTCTGACGACTACTTCCCGAACCGGTGACGGTCTGCTGGAATCA 471
Db 139 AlaLeuGlyCysLeuValLysAspTyraPheProGluProValThrValSerTrpAsnSer 158
QY 472 GCGGCCCTCAGCAGGGCGGTGACACACCTTCCCGGTGTCTACAGTCTCAGGACTCTAC 531
Db 159 GlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyra 178
QY 532 TCCTCAGCAGGTGGTGTACCGTCCCTCCAGCAGCTTGGGACCCACACCTACATCTGC 591
Db 179 SerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThrTyraCys 198
QY 592 AAGCTGAATCACAAGCCCAACCAACCAAGGTGGACAAGAAAGTGGAGCCCAATCTGT 651
Db 199 AsnValAsnHisLysProSerAsnThrLysValAspLysValGluProLysSerCys 218

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QY 652 GACAAAACCTCACATGTCGCCACCGTCCCGAGACCTGAACTCGCGGGGACCGCTCAGTC 711
Db 219 AspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSerVal 238
QY 712 TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTCAGGTACACA 771
Db 239 PheLeuPheProLysProLysAspThrLeuMetIleSerArgThrProGluValThr 258
QY 772 TGGGTGGTGGTGGACCTGAGCCACGAGACCTGAGTCAAGTTCACCTGAGTACGTTGGAC 831
Db 259 CysValValValAspValSerHisGluAspProGluValLysPheAsnTrpTyraValAsp 278
QY 832 GCGTGGAGTGTCAATATCCAAAGACAAAGCCCGGAGGAGCAGTACACAGCAGTAC 891
Db 279 GlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTrpAsnSerThrTyra 298
QY 892 CGTGTGGTCAAGCTCTCAGCTCCCTGACACGAGTGGCTGATGATGGCAAGGATACAG 951
Db 299 ArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyraLys 318
QY 952 TGCAAGGTCTTCCAAAGACCCCTCCCGAGCCCGCCCATCGAGAAACCATCTCCAAAGCCAAA 1011
Db 319 CysLysValSerAsnLysAlaLeuProAlaProLeuGluLysThrIleSerLysAlaLys 338
QY 1012 GGGCAGCCCGGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGTACCCCAAG 1071
Db 339 GlyGlnProArgGluProGlnValTyraThrLeuProProSerArgAspGluLeuThrLys 358
QY 1072 AACGAGTCAAGCTGACCTGCTGCTGCTCAAGGCTTATCCCGAGACATCGCGTGGAG 1131
Db 359 AsnGlnValSerLeuThrCysLeuValLysGlyPheTyraProSerAspIleAlaValGlu 378
QY 1132 TGGGAGAGCAATGGGAGCGGAGAGAACTCAAGACCAACCGCTCCCTCTGCTGACTCC 1191
Db 379 TrpGluSerAsnGlyGlnProGluAsnAsnTyraLysThrProProValLeuAspSer 398
QY 1192 GAGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1251
Db 399 AspGlySerPhePheLeuTyraSerLysLeuThrValAspLysSerArgTrpGlnGlnGly 418
QY 1252 AACGCTCTTCTCATGCTCCGCTGATGATGAGCTCTGACAAACCACTTACACGAGAGAGC 1311
Db 419 AsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyraThrGlnLysSer 438
QY 1312 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
Db 439 LeuSerLeuSerProGlyLys 445

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## RESULT 9

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US-09-736-371B-21
; Sequence 21, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
; CURRENT APPLICATION NUMBER: US/09/736,371B
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-371B-21

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Alignment Scores:

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Length:      449
Matches:     412
Conservative: 12
Mismatch:    18
Indels:      9
Gaps:        2

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454 ACAGTGTGCTGAACTCAGCGCCCTGACACGCGCGTGCACACCTTCCCGGCTGCTCTA 513
Db ThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeu 178
QY 514 CAGTCTCAGACTCTACTCCTCAGCAGCGTGTGTGACCGTGCCTCCAGCAGCTGGCC 573
Db GlnSerSerGlyLeuTySerLeuSerValValThrValProSerSerLeuGly 198
QY 574 ACCCAGACTCATCTGCAAGCTGAATCACAAGCCCAAGCAACCAAGGTGCACAAGAAA 633
Db ThrGlnThrTyIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLys 218
QY 634 GTGAGCCCAATCTGTGTGACAAACTCACAATGCCCGTGCCTGCCAGCCTGAATC 693
Db ValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeu 238
QY 694 GCGGGGGCAGCTGCTGCTCTCTCTCCCAAAACCAAGGACACCTCATGATCTCC 753
Db LeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIleSer 258
QY 754 CGGACCTCTGAGGTACATGCGTGTGTGTGACGCGTGCACGACGAGCCCTGAGGTCAAG 813
Db ArgThrProGluValThrCysValValValAspValSerHisGluAspProGluValLys 278
QY 814 TTCAACTGTGACGTGCGGCGTGTGTGTGATATGCAAGCAACCAAGCCCGGGAGGAG 873
Db PheAsnTrpTyValAspGlyValGluValHisAsnAlaLysThrLysProArgGluLeu 298
QY 874 CAGTCAACAGCAGCTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 933
Db GlnTyAsnSerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeu 318
QY 934 ATGCAAGAGTACAGTGCAGGTCTTCCAAAGCCCTCCAGCCCTCCAGCCCTCCAGGAAA 993
Db AsnGlyLysGluTyLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLys 338
QY 994 ACCATCTCCAAAGCCAAAGGGCAGCCCGGAGAACACAGAGTGTACACCTCGCCCTCCATCC 1053
Db ThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyThrLeuProProSer 358
QY 1054 CCGGATGAGTACCAAGAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113
Db ArgAspGluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyPro 378
QY 1114 ACAGCATCGCGTGGAGTGGAGAGCAATGGCAGCGGAGCAACAACTACAGACCCAGC 1173
Db SerAspIleAlaValGluTrpGlnSerAsnGlyGlnProGluAsnTyLysThrThr 398
QY 1174 CTTCCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1233
Db ProProValLeuAspSerAspGlySerPhePheLeuTySerLysLeuThrValAspLys 418
QY 1234 ACAGGTGCACAGCGGAGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1293
Db SerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsn 438
QY 1294 CACTACAGCAGAGAGCTCTCCCTGCTCCCGGTAA 1332
Db 439 HisTyThrGlnLysSerLeuSerLeuSerProGlyLys 451

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RESULT 12

US-09-848-832-3  
; Sequence 3, Application US/09848832  
; Publication No. US20030165507A1  
; GENERAL INFORMATION:  
; APPLICANT: Hooper, Douglas  
; APPLICANT: Dietzschold, Bernhard  
; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN  
; MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS  
; FILE REFERENCE: H0001.NP0002  
; CURRENT APPLICATION NUMBER: US/09/848,832  
; CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 60/204,518  
PRIOR FILING DATE: 2000-05-16  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 474  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-848-832-3

Alignment Scores:  
Pred. No.: 1,1e-132 Length: 474  
Score: 2172.50 Matches: 411  
Percent Similarity: 93.22% Conservative: 15  
Best Local Similarity: 89.93% Mismatches: 16  
Query Match: 90.33% Indels: 15  
DB: 10 Gaps: 2

US-09-674-716B-18 (1-1335) x US-09-848-832-3 (1-474)

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QY 1 GAGTCCAGCTGTGAGTCTGGGGAGGCTTGGTAAAGCCGGGGGGTCCCTTAGACTC 60
Db 20 GluValGlnLeuLeuGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
QY 61 TCCTGTGCAGCTAGCGATTCACTTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT 120
Db 40 SerCysAlaAlaSerGlyPheThrPheSerAsnTyAlaMetSerTrpValArgGlnAla 59
QY 121 CCAGGAGGGGCTCAGTGGGTGCTGAAATTTAGATTGAAATCTGATAATTATGCAACA 180
Db 60 ProGlyLysGlyLeuGluTrpValSerAlaIle-----SerAlaSerGlyHisSerThr 77
QY 181 CATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCATAATCTAGA 240
Db 78 TyrLeuAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 97
QY 241 CTGTATCTGCAATGAACAGCCCTGAAACCGAGGACACAGCCCTGTATTACTGTACA--- 297
Db 98 LeuTyLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyTyCysAlaLys 117
QY 298 -----GATTTCATAGACTCGGGCCAGGGA 321
Db 118 AspArgGluValThrMetIleValValLeuAsnGlyGlyPheAspTyTrpGlyGlnGly 137
QY 322 ACATAGTACCGTCTCTCAGCCTCCACCAAGGGGCCATCGGTCTTCCCTCCCTGGGACCC 381
Db 138 ThrArgValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaPro 157
QY 382 TCCTCCAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
Db 158 SerSerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyPhe 177
QY 442 CCCGAACCGGTGACGCTGCTGGAATCTCAGGCGCCCTGACCGCGCGTGCACACCTTC 501
Db 178 ProGluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhe 197
QY 502 CCGCTGTCTTACAGTCTCCTCAGGACTCTACTCCTCAGCAGCGTGTGTGACCGTCCCTCC 561
Db 198 ProAlaValLeuGlnSerSerGlyLeuTySerLeuSerSerValValThrValProSer 217
QY 562 AGCAGCTTGGCACCCAGACTCATCTCAACCTGAATCACAAGCCCAAGCCCAACCAAG 621
Db 218 SerSerLeuGlyThrGlnThrTyIleCysAsnValAsnHisLysProSerAsnThrLys 237
QY 622 GTGACCAAGAAAGTGGAGCCCAATCTGTGACAAAACTCACAATGCCCGTGCCTGCCCA 681
Db 238 ValAspLysArgValGluProLysSerCysAspLysThrHisThrCysProProCysPro 257
QY 682 GCACCTGACTCGCGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 741
Db 258 AlaProGluLeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThr 277
QY 742 CTCATGATCTCCCGGACCCCTGAGGTGCATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 801

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:29:27 ; Search time 16.4527 Seconds  
(without alignments)  
4852.647 Million cell updates/sec

Title: US-09-674-716B-1  
Perfect score: 753  
Sequence: 1 aagctttacagtactacgc.....tggggccaggacactagt 415

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cpn2.1/USPTO/spool\_p/US09674716/runat\_30092004\_070259\_25882/app.query.fasta\_1.3164  
-DB=PIR 78 -QFMT=fastn -SUFFIX=rpr -MINMATCH=0.1 -LOOCL=0 -LOOEXT=0  
-UNITS=Dits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-USER=US09674716 @CGN 1.152 @runat\_30092004\_070259\_25882 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 78:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	519	68.9	115	2	S38714	Ig heavy chain V r
2	518	68.8	139	2	PC1213	Ig heavy chain pre
3	518	68.8	139	2	G29380	Ig heavy chain pre
4	517.5	68.7	115	1	AVMS06	Ig heavy chain V-I
5	515.5	68.5	113	1	AVMSB	Ig heavy chain V-I
6	515.5	68.5	113	1	AVMSG1	Ig heavy chain V-I
7	514.5	68.3	125	2	S67945	Ig heavy chain BrE
8	510.5	67.8	115	2	A25803	Ig heavy chain V r
9	509.5	67.7	113	1	AVMSB7	Ig heavy chain V-I
10	507.5	67.4	113	1	AVMS7	Ig heavy chain V-I
11	506.5	67.3	115	1	AVMS82	Ig heavy chain V-I
12	505.5	67.1	113	1	AVMS09	Ig heavy chain V-I
13	498	66.1	106	2	S24521	Ig heavy chain V r
14	496.5	65.9	113	1	HVMSAM	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S38714  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S38714  
R:Cimanis, A.Y.  
submitted to the EMBL Data Library, November 1993  
A:Reference number: S38713  
A:Accession: S38714  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-115 <CIM>  
A:Cross-references: EMBL:X76014; NID:G416092; PIDN:CAA53601.1; PID:G1334076  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-99/Domain: immunoglobulin homology <IMV>

Alignment Scores:

Pred. No.:	2,31e-43	Length:	115
Score:	519.00	Matches:	99
Percent Similarity:	92.79%	Conservative:	4
Best Local Similarity:	89.19%	Mismatches:	2
Query Match:	68.92%	Indels:	6
DB:	2	Gaps:	2

US-09-674-716B-1 (1-415) x S38714 (1-115)

QY 90 GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGTCACACTGGAGGATCCATGAACCTCTCC 149

Db 1 ValLysLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetIysLeuSer 20

QY 150 TGTGTAGCTCTGGATTACTTTCAGTGGCTACTGATCTCTGGGTCGCCAGTCTCCA 209

Db 21 CysValAlaSerGlyPheThrPheSerSerTyrTrpMetSerTrpValArgInSerPro 40

QY 210 GAGAAGGGCTTGAGTGGGCTTGCTGAAATAGATTCAATCTGATAATATTCACACAT 269

Db 41 GluLysGlyLeuGluTrpIleAlaGluLeuArgLeuLysSerAspAsnTyrAlaThrHis 60  
 QY 270 TATGGGAGTCTGTGAAGGAGAGTCCACATCTCAAGAGATGATCCAAAGTGTCTTC 329  
 Db 61 TyrAlaGluSerValLysGlyPheThrIleSerArgAspSerLysSerArgLeu 80  
 QY 330 TACCTGCAATGACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA----- 383  
 Db 81 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrGlyIleTyrTyrCysThrAlaArg 100  
 QY 384 -----GATTTCATAGACTGGGGCCAAAGGACA 410  
 Db 101 LeuGlyAspTyr-----TrpGlyGlnGlyThr 109

## RESULT 2

PC1213

Ig heavy chain precursor V region (mAb H8) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Jul-1999  
 C:Accession: PC1213  
 R:Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim, Gene 121, 331-335, 1992  
 A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a monoclonal antibody  
 A:Reference number: PC1213; MUID:93077049; PMID:1446832  
 A:Accession: PC1213  
 A:Molecule type: mRNA  
 A:Residues: 1-139 <HON>  
 A:Cross-references: GB:M98041; NID:G195092; PIDN:AAA38159, 1; PID:G195093  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-139/Product: Ig heavy chain V region #status predicted <MAT>  
 F:134-119/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 2,92e-43 Length: 139  
 Score: 518.00 Matches: 101  
 Percent Similarity: 82.84% Conservative: 10  
 Best Local Similarity: 75.37% Mismatches: 15  
 Query Match: 68.79% Indels: 8  
 DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x PC1213 (1-139)

QY 36 ATGGATTTGGGCTG-----ATTTTATTATTGTTCTTTTAAAGGGTCCAGAGTCAA 89  
 Db 1 MetTyrLeuGlyLeuAsnTyrValPheIleValPheLeuLeuAsnGlyValGlnSerGlu 20  
 QY 90 GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGAACCTGGAGGATCCATGAAGTCTTCC 149  
 Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlySerMetLysLeuSer 40  
 QY 150 TGTGTAGCTCTGGATTACTTTTCACTGCTACTGATGCTTGGTCCGCGAGTCTCCA 209  
 Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60  
 QY 210 GAGAGGGGCTTGAGTGGTCTGAAATAGATTGAAATCTGATAATTATGCAACACAT 269  
 Db 61 GluLysGlyLeuGluTrpValGlyGlyLeuValGlnProGlySerMetLysLeuSer 80  
 QY 270 TATGGAGGCTTGAGTGGTCTGAGTGGTCTGAGTGGTCTGAGTGGTCTGAGTGGTCTC 329  
 Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60  
 QY 210 GAGAGGGGCTTGAGTGGTCTGAAATAGATTGAAATCTGATAATTATGCAACACAT 269  
 Db 61 GluLysGlyLeuGluTrpValGlyGlyLeuValGlnProGlySerMetLysLeuSer 80  
 QY 270 TATGGAGGCTTGAGTGGTCTGAGTGGTCTGAGTGGTCTGAGTGGTCTGAGTGGTCTC 329  
 Db 81 TyrAlaGluSerValLysGlyPheThrIleSerArgAspSerLysSerArgLeu 100  
 QY 330 TACCTGCAATGACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT--- 386  
 Db 101 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrGlyIleTyrTyrCysThrProIle 120  
 QY 387 -----TTTCATAGACTGGGGCCAAAGGACACTA 413  
 Db 121 ThrThrGlyAlaTrpPheAlaTyrTrpGlyGlnGlyThrLeu 134

## RESULT 3

G29380  
 Ig heavy chain precursor V region (BC-1004) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 16-Aug-1996  
 C:Accession: G29380  
 R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.  
 J. Biol. Chem. 262, 13579-13583, 1987  
 A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable  
 A:Reference number: A92612; MUID:8807592; PMID:3115981  
 A:Accession: G29380  
 A:Molecule type: mRNA  
 A:Residues: 1-139 <CHE>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:134-119/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 2,92e-43 Length: 139  
 Score: 518.00 Matches: 100  
 Percent Similarity: 82.84% Conservative: 11  
 Best Local Similarity: 74.63% Mismatches: 15  
 Query Match: 68.79% Indels: 8  
 DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x G29380 (1-139)

QY 36 ATGGATTTGGGCTG-----ATTTTATTATTGTTCTTTTAAAGGGTCCAGAGTCAA 89  
 Db 1 MetTyrLeuGlyLeuAsnTyrValPheIleValPheLeuLeuAsnGlyValGlnSerGlu 20  
 QY 90 GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGAACCTGGAGGATCCATGAAGTCTTCC 149  
 Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlySerMetLysLeuSer 40  
 QY 150 TGTGTAGCTCTGGATTACTTTTCACTGCTACTGATGCTTGGTCCGCGAGTCTCCA 209  
 Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60  
 QY 210 GAGAGGGGCTTGAGTGGTCTGAAATAGATTGAAATCTGATAATTATGCAACACAT 269  
 Db 61 GluLysGlyLeuGluTrpValGlyGlyLeuValGlnProGlySerMetLysLeuSer 80  
 QY 270 TATGGAGGCTTGAGTGGTCTGAGTGGTCTGAGTGGTCTGAGTGGTCTGAGTGGTCTC 329  
 Db 81 TyrThrGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerAsnVal 100  
 QY 330 TACCTGCAATGACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA----- 383  
 Db 101 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrGlyIleTyrTyrCysThrArgasp 120  
 QY 384 -----GATTTCATAGACTGGGGCCAAAGGACACTA 413  
 Db 121 TyrTyrGlyAlaGluPheAlaTyrTrpGlyGlnGlyThrLeu 134

## RESULT 4

AVMS06

Ig heavy chain V-III region (J606) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996  
 C:Accession: C92811; A02072  
 R:Johnson, N.; Slankard, J.; Paul, L.; Hood, L.  
 J. Immunol. 148, 302-307, 1992  
 A:Title: The complete V domain amino acid sequences of two myeloma inulin-binding protein  
 A:Reference number: A92811; MUID:82099361; PMID:6798111  
 A:Accession: C92811  
 A:Molecule type: protein  
 A:Residues: 1-115 <JOH>  
 C:Comment: This chain was isolated from a myeloma protein that binds inulin.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-100/Domain: immunoglobulin homology <IMM>  
 F:22-98/Disulfide bonds: #status predicted

Alignment Scores:  
 Pred. No.: 3,266-43 Length: 115  
 Score: 517.50 Matches: 97  
 Percent Similarity: 94.55% Conservative: 7  
 Best Local Similarity: 88.18% Mismatches: 5  
 Query Match: 68.73% Indels: 1  
 DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMS06 (1-115)

QY 87 GAAGTGAAGCTTGAGGAGCTGGAGAGGCTTGTTGCAACCTGGAGGATCCATGAATC 146  
 Db 1 GluValLysLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
 QY 147 TCCTGTGAGCTCTGGATTACTTTTCACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCT 206  
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40  
 QY 207 CCAGAGAGGGCTTGAGTGGTGGTCTGAATTAAGATTGAATCTGATTAATGCAACA 265  
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnAsnTyrAlaThr 60  
 QY 267 CATTATGCGAGCTCTGCAAGAGGAAGTTCCACATCTCAAGAGATGATTCCAAAAGTCGT 326  
 Db 61 HistyAlaGluSerValLysGlyArgPheThrIleSerA-GaspSerLysSerSer 80  
 QY 327 CTCTACCTGCAATGAACAGCTTAAGCTGAAGACAGCTGAGTGGAGTCTTATTACTGT---ACA 383  
 Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrCysThrThr 100  
 QY 384 GATTTCATAGACTGGGGCCAAAGGACACTA 413  
 Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 5

AVMSAB  
 Ig heavy chain V-III region (A4) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 24-Apr-1984 #sequence\_revision 30-Jun-1993 #text\_change 31-Mar-1997  
 C/Accession: A93818; A02072  
 R/Vrana, M.; Rudikoff, S.; Potter, M.  
 Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978  
 A/Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.  
 A/Reference number: A93818; MUID:78158406; PMID:417344  
 A/Molecule type: protein  
 A/Residues: 1-113 <VRA>  
 C/Comment: This chain was isolated from a myeloma protein that binds inulin.  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:15-100/Domain: immunoglobulin homology <IMM>  
 F:22-98/Disulfide bonds: #status predicted

Alignment Scores:  
 Pred. No.: 5,146-43 Length: 113  
 Score: 515.50 Matches: 97  
 Percent Similarity: 93.64% Conservative: 6  
 Best Local Similarity: 88.18% Mismatches: 6  
 Query Match: 68.46% Indels: 1  
 DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMSAB (1-113)

QY 87 GAAGTGAAGCTTGAGGAGCTGGAGAGGCTTGTTGCAACCTGGAGGATCCATGAATC 146  
 Db 1 GluValLysLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
 QY 147 TCCTGTGAGCTCTGGATTACTTTTCACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCT 206  
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40  
 QY 207 CCAGAGAGGGCTTGAGTGGTGGTCTGAATTAAGATTGAATCTGATTAATGCAACA 266

Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60  
 QY 267 CATTATGCGAGCTCTGAAAGGAGAGTTCACCATCTCAAGAGATGATTCACCAAGTCGT 326  
 Db 61 HistyAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80  
 QY 327 CTCTACCTGCAATGAACAGCTTAAGCTGAAGACAGCTGAGTGGAGTCTTATTACTGT---ACA 383  
 Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrCysThrThr 100  
 QY 384 GATTTCATAGACTGGGGCCAAAGGACACTA 413  
 Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 6

AVMS61  
 Ig heavy chain V-III region (U61) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996  
 C/Accession: B93818; A02072  
 R/Vrana, M.; Rudikoff, S.; Potter, M.  
 Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978  
 A/Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.  
 A/Reference number: A93818; MUID:78158406; PMID:417344  
 A/Molecule type: protein  
 A/Residues: 1-113 <VRA>  
 C/Comment: This chain was isolated from a myeloma protein that binds inulin.  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:15-100/Domain: immunoglobulin homology <IMM>  
 F:22-98/Disulfide bonds: #status predicted

Alignment Scores:

Pred. No.: 5,146-43 Length: 113  
 Score: 515.50 Matches: 97  
 Percent Similarity: 93.64% Conservative: 6  
 Best Local Similarity: 88.18% Mismatches: 6  
 Query Match: 68.46% Indels: 1  
 DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMS61 (1-113)

QY 87 GAAGTGAAGCTTGAGGAGCTGGAGAGGCTTGTTGCAACCTGGAGGATCCATGAATC 146  
 Db 1 GluValLysLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
 QY 147 TCCTGTGAGCTCTGGATTACTTTTCACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCT 206  
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40  
 QY 207 CCAGAGAGGGCTTGAGTGGTGGTCTGAATTAAGATTGAATCTGATTAATGCAACA 266  
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60  
 QY 267 CATTATGCGAGCTCTGAAAGGAGAGTTCACCATCTCAAGAGATGATTCACCAAGTCGT 326  
 Db 61 HistyAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80  
 QY 327 CTCTACCTGCAATGAACAGCTTAAGCTGAAGACAGCTGAGTGGAGTCTTATTACTGT---ACA 383  
 Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrCysThrThr 100

RESULT 7

S67945  
 Ig heavy chain BrE-3 - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 05-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
 C/Accession: S67945



QY 384 GATTTCATAGACTGGGGCCAAAGGACACTA 413  
Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 10  
AVMS57  
Ig heavy chain V-III region (T957) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996  
C:Accession: A92810; A02072  
R:Rudikoff, S.; Potter, M.  
J. Immunol. 127, 191-194, 1981  
A:Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a  
A:Reference number: A92810; MUID:81216632; PMID:6787122  
A:Accession: A92810  
A:Molecule type: protein  
A:Residues: 1-113 <RUD>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>  
F:22-98/Disulfide bonds: #status predicted

Alignment Scores:  
Pred. No.: 3,19e-42 Length: 113  
Score: 507.50 Matches: 96  
Percent Similarity: 91.82% Conservative: 5  
Best Local Similarity: 87.27% Mismatches: 8  
Query Match: 67.40% Indels: 1  
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMS57 (1-113)

QY 87 GAAGTGAAGCTTGAGGAGCTTGAGGAGCTTGTCGAACCTGGAGATCCATGAACCTC 146  
Db 1 GluValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20

QY 147 TCCTGTGTAGCTCTGGATTACTTTCAGTGGCTACTGATGCTTGGTCCGCGACTCT 206  
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40

QY 207 CCAGAGAAGGGCTTCAGTGGCTTGCTGAAATAGATTGAAATCTCTGATAATATGCAACA 266  
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60

QY 267 CATTTATCGGAGTCTCTGAAAGGAAAGTTCACCATCTCAAGAGATGATTCGAAAGTCTG 326  
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSerSer 80

QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT---ACA 383  
Db 81 ValTyrLeuArgMetAsnAsnLeuArgProGluAspThrGlyIleTyrCysThrThr 100

RESULT 11  
AVMS82  
Ig heavy chain V-III region (W3082) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996  
C:Accession: D92811; A02072  
R:Johnson, N.; Slankard, J.; Paul, L.; Hood, L.  
J. Immunol. 128, 302-307, 1982  
A:Title: The complete V domain amino acid sequences of two myeloma inulin-binding protei  
A:Reference number: A92811; MUID:8209361; PMID:6798111  
A:Accession: D92811  
A:Molecule type: protein  
A:Residues: 1-115 <JOH>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>  
F:22-98/Disulfide bonds: #status predicted

Alignment Scores:  
Pred. No.: 4.01e-42 Length: 115  
Score: 506.50 Matches: 95  
Percent Similarity: 92.73% Conservative: 7  
Best Local Similarity: 86.36% Mismatches: 7  
Query Match: 67.26% Indels: 1  
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMS82 (1-115)

QY 87 GAAGTGAAGCTTGAGGAGCTTGAGGAGCTTGTCGAACCTGGAGATCCATGAACCTC 146  
Db 1 GluValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20

QY 147 TCCTGTGTAGCTCTGGATTACTTTCAGTGGCTACTGATGCTTGGTCCGCGACTCT 206  
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40

QY 207 CCAGAGAAGGGCTTCAGTGGCTTGCTGAAATAGATTGAAATCTCTGATAATATGCAACA 266  
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60

QY 267 CATTTATCGGAGTCTCTGAAAGGAAAGTTCACCATCTCAAGAGATGATTCGAAAGTCTG 326  
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSerSer 80

QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT---ACA 383  
Db 81 ValTyrLeuArgMetAsnAsnLeuArgProGluAspThrGlyIleTyrCysThrThr 100

RESULT 12  
AVMS09  
Ig heavy chain V-III region (B109) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Aug-1996  
C:Accession: C93818; A02072  
R:Vrana, M.; Rudikoff, S.; Potter, M.  
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978  
A:Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.  
A:Reference number: A93818; MUID:78158406; PMID:417344  
A:Accession: C93818  
A:Molecule type: protein  
A:Residues: 1-113 <VRA>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>  
F:22-98/Disulfide bonds: #status predicted

Alignment Scores:  
Pred. No.: 5.03e-42 Length: 113  
Score: 505.50 Matches: 94  
Percent Similarity: 93.64% Conservative: 9  
Best Local Similarity: 85.45% Mismatches: 6  
Query Match: 67.13% Indels: 1  
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMS09 (1-113)

QY 87 GAAGTGAAGCTTGAGGAGCTTGAGGAGCTTGTCGAACCTGGAGATCCATGAACCTC 146  
Db 1 GluValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20

QY 147 TCCTGTGTAGCTCTGGATTACTTTCAGTGGCTACTGATGCTTGGTCCGCGACTCT 206  
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40

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QY 207 CCAGAGAGGGGCTTGAAGTGGTCTGCTGAAATAGATTGAATCTGATTAATATGCAACA 266
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuValGlnSerHisAsnTyrAlaThr 60
QY 267 CATTATGCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 326
Db 61 HistTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSer 80
QY 327 CTTCTACCTGCAAAATGAAAGCAGCTTAAGCTGAAGACAGCTGAGTGTATTACTGT---ACA 383
Db 81 ValPheLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleHisTyrCysThr 100
QY 384 GATTTTCATAGACTGGGGCCCAAGGGACACTA 413
Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 13
IG heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24521
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24521
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <XAA>
A:Cross-references: EMBL:X66664; NID:G51247; PIDN:CAA47226.1; PID:G51248
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-106/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,78e-41 Length: 106
Score: 498.00 Matches: 92
Percent Similarity: 96.19% Conservative: 9
Best Local Similarity: 87.62% Mismatches: 4
Query Match: 66.14% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-1 (1-415) x S24521 (1-106)
QY 69 TTAAGAGGGGCTCAGAGTGAAGTGAAGCTTGAGAGTCTGAGAGGCTTGGTGAACCT 128
Db 1 LeuLysGlyValGlnSerGluValLysLeuValGluSerGlyGlyLeuValGlnPro 20
QY 129 GGAGATCCATGAACCTCCCTGCTAGCTCTGATTTACTTTTTCAGTGGCTACTGGATG 188
Db 21 GlyGlySerMetLysLeuSerCysValAlaSerGlyPheThrPheAsnTyrTyrTrpMet 40
QY 189 TCTTGGGCTCCGCGCAGTCTCCAGAGAGGGGCTTGAGTGGTTCCTGAAATAGATTGAAA 248
Db 41 AsnTrpValArgGlnSerProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLys 60
QY 249 TGTGATAATTATGCAACACATTATCGGAGTCTGAAAGGAACTTCACCATCTCAGA 308
Db 61 SerAsnAsnTyrAlaThrHisTyrAlaGluSerValLysGlyArgPheThrIleSerArg 80
QY 309 GATGATTCCAAAGTCTGCTTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGA 368
Db 81 AspAspSerLysSerSerValTyrLeuGlnMetAsnAsnPheArgSerGluAspThrGly 100
QY 369 GTTATTACTGTACA 383
Db 101 IleTyrTyrCysThr 105

RESULT 14
HVM5AM
IG heavy chain V region (AMPC1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 31-Mar-1997
C:Accession: A02073
R:Rudikoff, S.; Potter, M.
J. Immunol. 127, 191-194, 1981
A:Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a ne
A:Reference number: A92810; MUID:81216632; PMID:6787122
A:Accession: A02073
A:Molecule type: protein
A:Residues: 1-113 <RUD>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 3,92e-41 Length: 113
Score: 496.50 Matches: 94
Percent Similarity: 90.91% Conservative: 6
Best Local Similarity: 85.45% Mismatches: 9
Query Match: 65.94% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x HVM5AM (1-113)
QY 87 GAAGTGAAGCTTGAGAGTCTGAGAGGCTTGGTGCACCTGGAGGATCCATGAACCTC 146
Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyArgSerMetLysLeu 20
QY 147 TCTGTGTAGCTCTGCTGATTTACTTTTCACTGCTGCTACTGATCTTGGTCCGCGAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAGGGGCTTGAAGTGGTCTGAAATAGATTGAATCTGATTAATATGCAACA 266
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60
QY 267 CATTATGCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCT 326
Db 61 HistTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSer 80
QY 327 CTTCTACCTGCAAAATGAAAGCAGCTTAAGCTGAAGACAGCTGAGTGTATTACTGT---ACA 383
Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThr 100

RESULT 15
IG heavy chain precursor V region (9-40) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 23-Jul-1999
C:Accession: D34903
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-react
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: D34903
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-137 <BED>
A:Cross-references: GB:M32378; GB:J05237; GB:J05238; NID:G639652; PIDN:AAA61587.1; PID:Gt
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-119/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 5,55e-41 Length: 137
Score: 495.00 Matches: 95
Percent Similarity: 82.58% Conservative: 14
Best Local Similarity: 71.97% Mismatches: 17
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Query Match:      65.74%      Indels:      6
DB:              2          Gaps:         2
US-09-674-716B-1 (1-415) x D34903 (1-137)

QY 36 ATCGATTTGGCTG-----ATTTTATTATTGTTCTTTTAAAGGGGTCCACAGTGAA 89
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MetTyrLeuGlyLeuSerCysValPheIleValPheLeuLeuLysGlyValGlnCysGlu 20
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 90 GTGAAGCTTGAGGAGCTCTGGAGGAGCTTGTCGAACCTGGAGGATCCATGAAACTCTCC 149
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 VallysLeuAspGluThrGlyGlyLeuValGlnProGlyArgProMetLysLeuSer 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 150 TGTGTAGCCTCTGGATTTACTTTAGTGGCTACTGGATGTCCTGGTCCGCCACTCTCCA 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41 CysValAlaSerGlyPheThrPheSerAspTyrTrpMetAsnTrpValArgGlnSerPro 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 210 GAGAGGGGCTTGAGTGGGTTGCTCAAAATTAGATTGAATCTGATTAATTATGCAACACAT 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GluLysGlyLeuGluTrpValAlaGlnIleArgAsnLysProTyrAsnTyrGluThrTyr 80
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 270 TATCGGAGTCTGTGAAAGGGAAGTTCAACATCTCAAGAGATGATTCAAAAGTCGTCTC 329
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 TyrSerAspSerValLysGlyArgPheThrIleSerArgAspSerLysSerSerVal 100
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 330 TACCTGCAATGAACAGCTTAAGAGCTGAACAGACAGAGTGGAGTTTATTACTGTACAGATTTC 389
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 101 TyrLeuGlnMetAsnAsnLeuArgAlaGluAspMetGlyIleTyrTyrCysThrSerTyr 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 390 -----ATAGACTGGGGCCAGGGACACTA 413
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GlyTyrHisGlyAlaTyrTyrGlyGlnGlyThrLeu 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: September 30, 2004, 08:56:59  
Job time : 18.4527 secs

Blank sheet



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:20:22 ; Search time 9.00395 Seconds  
(without alignments)  
4799.922 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 753

Sequence: 1 aagctttacagtactcagc.....tggggccaaaggacactagt 415

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2.1/USPto spool p/US09674716/runat 30092004 070257 25855/app query.fasta\_1.3164  
-DB=SwissProt\_42 -QFMT=fastan -SUFFIX=rs -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09674716 @CGN 1.1 82 @runat 30092004 070257 25855 -NCPU=6 -ICPU=3  
-NO.WMAP -LARGQQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	517.5	68.7	115	1 HV32_MOUSE	P01801 mus musculus
2	515.5	68.5	113	1 HV27_MOUSE	P01796 mus musculus
3	515.5	68.5	113	1 HV28_MOUSE	P01797 mus musculus
4	509.5	67.7	113	1 HV30_MOUSE	P01799 mus musculus
5	507.5	67.4	113	1 HV31_MOUSE	P01800 mus musculus
6	506.5	67.3	115	1 HV31_MOUSE	P01802 mus musculus
7	505.5	67.1	113	1 HV29_MOUSE	P01798 mus musculus
8	496.5	65.9	113	1 HV34_MOUSE	P01803 mus musculus
9	468	62.2	111	1 HV35_MOUSE	P01804 mus musculus
10	466.5	62.0	142	1 HV01_RAT	P01805 rattus norv
11	412	54.7	117	1 HV36_HUMAN	P01764 homo sapien
12	410.5	54.5	116	1 HV36_HUMAN	P01806 mus musculus
13	405	53.8	136	1 HV16_MOUSE	P01783 mus musculus
14	398.5	52.9	144	1 HV26_MOUSE	P01795 mus musculus
15	396	52.6	117	1 HV54_MOUSE	P01823 mus musculus
16	392.5	52.1	116	1 HV05_CARAU	P0181 carassius a
17	387	51.4	117	1 HV59_MOUSE	P018530 mus musculus
18	386.5	51.3	117	1 HV17_MOUSE	P01786 mus musculus

19	384	51.0	117	1 HV55_MOUSE	P18526 mus musculus
20	379	50.3	117	1 HV58_MOUSE	P18529 mus musculus
21	375	49.8	117	1 HV53_MOUSE	P18524 mus musculus
22	374	49.7	122	1 HV21_MOUSE	P01790 mus musculus
23	373.5	49.6	123	1 HV22_MOUSE	P01791 mus musculus
24	368.5	48.9	120	1 HV3E_HUMAN	P01766 homo sapien
25	368	48.9	122	1 HV20_MOUSE	P01789 mus musculus
26	368	48.9	122	1 HV3G_HUMAN	P01768 homo sapien
27	367.5	48.8	123	1 HV18_MOUSE	P01787 mus musculus
28	367.5	48.8	123	1 HV19_MOUSE	P01788 mus musculus
29	367.5	48.8	123	1 HV25_MOUSE	P01794 mus musculus
30	363.5	48.3	123	1 HV23_MOUSE	P01792 mus musculus
31	361	47.9	119	1 HV37_MOUSE	P01807 mus musculus
32	360	47.8	119	1 HV40_MOUSE	P01810 mus musculus
33	358.5	47.6	119	1 HV31_HUMAN	P01770 homo sapien
34	357	47.4	119	1 HV3N_HUMAN	P01775 homo sapien
35	356.5	47.3	123	1 HV24_MOUSE	P01793 mus musculus
36	355.5	47.2	121	1 HV3J_HUMAN	P01771 homo sapien
37	355	47.1	119	1 HV38_MOUSE	P01808 mus musculus
38	354.5	47.1	97	1 HV56_MOUSE	P18527 mus musculus
39	352	46.7	114	1 HV3B_HUMAN	P01763 homo sapien
40	352	46.7	119	1 HV3M_HUMAN	P01774 homo sapien
41	347.5	46.1	115	1 HV3D_HUMAN	P01765 homo sapien
42	347.5	46.1	117	1 HV41_MOUSE	P01811 mus musculus
43	346	45.9	98	1 HV57_MOUSE	P18528 mus musculus
44	345	45.8	116	1 HV3T_HUMAN	P01781 homo sapien
45	344.5	45.8	117	1 HV02_CANFA	P01785 canis famil

ALIGNMENTS

RESULT 1  
HV32\_MOUSE STANDARD; PRT; 115 AA.  
ID HV32\_MOUSE  
AC P01801;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE IG heavy chain V-III region J606.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=8209361; PubMed=6798111;  
RA Johnson N., Slankard J., Paul L., Hood L.;  
RT "The complete V domain amino acid sequences of two myeloma inulin-  
binding proteins."  
RL J. Immunol. 128:302-307(1982).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS INULIN.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; C92811; AVMS06.  
DR HSP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 114 IG-LIKE.  
FT DISULFID 22 98 BY SIMILARITY.  
FT NONTER 115 115  
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

Alignment Scores:  
Pred. No.: 2,37e-51 Length: 115  
Score: 517.50 Matches: 97  
Percent Similarity: 94.55% Conservative: 7  
Best Local Similarity: 88.18% Mismatches: 5  
Query Match: 88.73% Indels: 1  
DB: 1 Gaps: 1

```

US-09-674-716B-1 (1-415) x HV32_MOUSE (1-115)
QY 87 GAAGTGAAGCTTGGAGGCTGGAGAGGCTGGTGCACCTGGAGGATCCATGAATC 146
Db 1 GluValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTGTAGCCTCTGGATTACTTTTCAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGGAGGCTTCTGAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGGAGGCTTCTGAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnTyrAlaThr 60
QY 267 CATTATGGGAGCTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 326
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT 383
Db 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrThr 100
QY 384 GATTTCATAGACTGGGGCCCAAGGGACACTA 413
Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 2
HV27_MOUSE
ID HV27_MOUSE STANDARD; PRT; 113 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region A4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93818; AVMSAB.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;

Alignment Scores:
Pred. No.: 4,01e-51 Length: 113
Score: 515.50 Matches: 97
Percent Similarity: 93.64% Conservative: 6
Best Local Similarity: 88.18% Mismatches: 6
Query Match: 68.46% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x HV27_MOUSE (1-113)
QY 87 GAAGTGAAGCTTGGAGGCTGGAGAGGCTGGTGCACCTGGAGGATCCATGAATC 146
Db 1 GluValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTGTAGCCTCTGGATTACTTTTCAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGGAGGCTTCTGAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGGAGGCTTCTGAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnTyrAlaThr 60
QY 267 CATTATGGGAGCTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 326
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT 383
Db 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrThr 100
QY 384 GATTTCATAGACTGGGGCCCAAGGGACACTA 413
Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 3
HV28_MOUSE
ID HV28_MOUSE STANDARD; PRT; 113 AA.
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; B93818; AVMS61.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;

Alignment Scores:
Pred. No.: 4,01e-51 Length: 113
Score: 515.50 Matches: 97
Percent Similarity: 93.64% Conservative: 6
Best Local Similarity: 88.18% Mismatches: 6
Query Match: 68.46% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x HV28_MOUSE (1-113)
QY 87 GAAGTGAAGCTTGGAGGCTGGAGAGGCTGGTGCACCTGGAGGATCCATGAATC 146
Db 1 GluValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTGTAGCCTCTGGATTACTTTTCAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206

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Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40  
QY 207 CCAGAGAGGGCTGAGTGGTGGCTGAATAGATTGAATGAACTGATAATTATGCAACA 266  
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60  
QY 267 CATTTATCGGAGTCTGTGAAGAGGAGTTCACCACTCTCAAGAGATGATTCACAAAGTCGT 326  
Db 61 HistyXAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80  
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT--ACA 383  
Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrCysThrThr 100  
QY 384 GATTTCATAGACTGGGCCCAAGGACACTA 413  
Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110  
RESULT 4  
ID HV30\_MOUSE STANDARD; PRT; 113 AA.  
AC P01799;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-III region ABE-47N.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77134726; PubMed=402936;  
RA Vrana M., Rudikoff S., Potter M.;  
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma  
protein.";  
RL Biochemistry 16:1170-1175(1977).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC -!- BINDS INULIN.  
DR PIR; A30400; AVMSB7.  
DR HSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 >113 IG-LIKE.  
FT DISULFID 22 98 BY SIMILARITY.  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;  
Alignment Scores:  
Pred. No.: 1,966-50 Length: 113  
Score: 509.50 Matches: 96  
Percent Similarity: 92.73% Conservatives: 6  
Best Local Similarity: 87.27% Mismatches: 7  
Query Match: 67.66% Indels: 1  
DB: 1 Gaps: 1  
US-09-674-716B-1 (1-415) x HV30\_MOUSE (1-113)  
QY 87 GAAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAACCTC 146  
Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
QY 147 TCCTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTTGGGTCCGCCAGTCT 206  
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40  
QY 207 CCAGAGAGGGCTTGAGTGGTGGCTGAATAGATTGAATGAACTGATAATTATGCAACA 266  
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40  
QY 207 CCAGAGAGGGCTTGAGTGGTGGCTGAATAGATTGAATGAACTGATAATTATGCAACA 266

Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60  
QY 267 CATTTATCGGAGTCTGTGAAGAGGAGTTCACCACTCTCAAGAGATGATTCACAAAGTCGT 326  
Db 61 HistyXAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80  
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT--ACA 383  
Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrAlaIleTyrCysThrThr 100  
QY 384 GATTTCATAGACTGGGCCCAAGGACACTA 413  
Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110  
RESULT 5  
ID HV31\_MOUSE STANDARD; PRT; 113 AA.  
AC P01800;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-III region T957.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81216632; PubMed=6787122;  
RA Rudikoff S., Potter M.;  
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:  
evidence for a new heavy chain joining segment.";  
RL J. Immunol. 127:191-194(1981).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC -!- BINDS INULIN.  
DR PIR; A92810; AVMS57.  
DR HSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 >113 IG-LIKE.  
FT DISULFID 22 98 BY SIMILARITY.  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12732 MW; 26618F626B59859E CRC64;  
Alignment Scores:  
Pred. No.: 3,336-50 Length: 113  
Score: 507.50 Matches: 96  
Percent Similarity: 91.82% Conservatives: 5  
Best Local Similarity: 87.27% Mismatches: 8  
Query Match: 67.40% Indels: 1  
DB: 1 Gaps: 1  
US-09-674-716B-1 (1-415) x HV31\_MOUSE (1-113)  
QY 87 GAAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAACCTC 146  
Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
QY 147 TCCTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTTGGGTCCGCCAGTCT 206  
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40  
QY 207 CCAGAGAGGGCTTGAGTGGTGGCTGAATAGATTGAATGAACTGATAATTATGCAACA 266  
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrGluThr 60  
QY 267 CATTTATCGGAGTCTGTGAAGAGGAGTTCACCACTCTCAAGAGATGATTCACAAAGTCGT 326



```

Db 101 GlyPheAlaTyTrpGlyGlnGlyThrLeu 110
|||||
RESULT 8
HV34_MOUSE
ID HV34_MOUSE STANDARD; PRT; 113 AA.
AC P01803;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region AMPC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194 (1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02073; HVMSAM.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12691 MW; 7A6D906AAA966E9E CRC64;

Alignment Scores:
Pred. No.: 6.13e-49 Length: 113
Score: 496.50 Matches: 94
Percent Similarity: 90.91% Conservative: 6
Best Local Similarity: 85.45% Mismatches: 9
Query Match: 65.94% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x HV34_MOUSE (1-113)

QY 87 GAAGTGAAGCTGAGGAGCTTGGAGGAGCTTGGTGCACCTGGAGGATCCATGAACTC 146
Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyArgSerMetLysLeu 20
147 TCCTGTAGCTCTGGATTACTTTCAGTGGCTACTGGATGCTTGGTCCGCGCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAAGGGCTTGAGTGGTCTGCTGAATAGATTGAATCTGATAATTATGCAACA 266
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyAlaIle 60
QY 267 CATTTATGGGAGTCTGTAAGGGAAGTTCACCTCTCAAGAGATGATTCCAAAAGTCGT 326
Db 61 HisTyAlaGluSerValGlyGlyPheThrPheSerAsnTyTrpMetAsnTrpValArgGlnSer 80
QY 327 CTCCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT---ACA 383
Db 81 ValTyLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyTrpCysSerThr 100
QY 384 GATTTATAGACTGGGGCCAGGGCACTA 413
Db 101 GlyPheProSerTrpGlyProGlyThrLeu 110
|||||
RESULT 9

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HV35_MOUSE
ID HV35_MOUSE STANDARD; PRT; 111 AA.
AC P01804;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region HPC76 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81013937; PubMed=6251474;
RA Bernard O., Gough N.M.;
RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
between translocated VH and mu constant regions genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634 (1980).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE
CC CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02074; HVMS76.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT NON_TER 1 1 IG-LIKE.
FT DOMAIN <1 110
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12304 MW; 0EDE98EC7348056A CRC64;

Alignment Scores:
Pred. No.: 1.16e-45 Length: 111
Score: 468.00 Matches: 90
Percent Similarity: 89.81% Conservative: 7
Best Local Similarity: 83.33% Mismatches: 3
Query Match: 62.15% Indels: 8
DB: 1 Gaps: 3

US-09-674-716B-1 (1-415) x HV35_MOUSE (1-111)

QY 102 GAGTCTGGAGGAGCTTGGTGCACCTGGAGGATCCATGAACTCTCTGTGTAGCTCT 161
Db 1 GluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSerCysValAlaSer 20
162 GGATTTACTTTCAGTGGCTACTGAGTGTCTGGTCCGCGCAGTCTCCAGAGAAGGGCTT 221
Db 21 GlyPheThrPheSerAsnTyTrpMetAsnTrpValArgGlnSerProGluLysGlyLeu 40
QY 222 GAGTGGTGTCTGAAATTAGATTGAAATCTGATAATTATGCAACACATTATCGGAGTCT 281
Db 41 GluTrpValAlaGluLeuArgLeuLysSer---GlyTyAlaThrHisTyAlaGluSer 59
QY 282 GTGAAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAAGTCTCTTACCTGCAATG 341
Db 60 ValLysGlyArgPheThrIleSerArgAspSerLysSerValTyLeuGlnMet 79
QY 342 AACAGCTTAAGAGCTCAAGACAGTGGAGTTTATTACTGTACA-----GAT 386
Db 80 AsnAsnLeuArgAlaGluAspThrGlyIleTyTrpCysThrArgProGlyValProAsp 99
QY 387 TTCATAGACTGGGGCCAGGGGACA 410
Db 100 Tyr-----TrpGlyGlnGlyThr 105

RESULT 10
HV01_RAT
ID HV01_RAT STANDARD; PRT; 142 AA.
AC P01805;

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Db 79 TyrGlyAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
QY 330 TACCTGCAAAATGACAGCTTAAGAGCTGAACACAGCTGAGTTTATTACTGT 380
Db 99 TyrLeuGlnMetAsnSerLeuArgAlaGlnAspIlnrAlaValTyrCys 115
RESULT 12
HV36_MOUSE
ID HV36_MOUSE STANDARD; PRT; 116 AA.
AC P01806;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 441 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=82059449; PubMed=6795591;
RA Olio R., Auffray C., Sikorav J.-L., Rougeon F.;
RT "Mouse heavy chain variable regions: nucleotide sequence of a
  germ-line VH gene segment.";
RL Nucleic Acids Res. 9:4099-4109(1981).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; V00774; CAA24152.1; -.
DR PIR; A02076; HVMS44.
DR HSSP; P01810; 2FEJ.
DR MGB; MGI:96432; Igh-VX24.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 18 IG HEAVY CHAIN V REGION 441.
FT DOMAIN 19 >116 IG-LIKE.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12911 MW; 6B4FF3EF9A95D9F3 CRC64;
Alignment Scores:
Pred. No.: 4.77e-39 Length: 116
Score: 410.50 Matches: 80
Percent Similarity: 81.03% Conservative: 14
Best Local Similarity: 68.97% Mismatches: 19
Query Match: 54.52% Indels: 3
DB: 1 Gaps: 2
US-09-674-716b-1 (1-415) x HV36_MOUSE (1-116)
QY 36 ATGGATTTGGGCTGATTTTATTCTT---CTTTAAAGGGTCCAGAGTGAAGTG 92
Db 1 MetAspPheGlyLeuIlePhePheIleValAlaLeuLeuLysGlyValGlnCysGluVal 20
QY 93 AAGCTTGAGGAGCTCGGAGGGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTGT 152
Db 21 LysLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuLysLeuSerCys 40
QY 153 GTAGCTCTGGATTTACTTTTCAGTGGCTACCTGGATGTCTTGGGTCGGCAGTCTCCAGAG 212
Db 41 AlaAlaSerGlyPheAspPheSerArgTyrTrpMetSerTrpValArgGlnAlaProGly 60
```

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QY 213 AAGGGCTTGGGCTTGGTGAATTCGAAATCTGATAATCTGATAATTCGAAACACATTAT 272
Db 61 LysGlyLeuGluTrpIleGlyGluIle-----AsnProAspSerSerThrIleAsnTyr 78
QY 273 GCGAGCTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAGAGTCTCTCTAC 332
Db 79 ThrProSerLeuLysAspLysPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyr 98
QY 333 CTGCAAAATGAACAGCTTAAGAGCTGAAGACAGCTGAGTTTATTACTGT 380
Db 99 LeuGlnMetSerLysValArgSerGluAspThrAlaLeuTyrTyrCys 114
RESULT 13
HV16_MOUSE
ID HV16_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
  antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC
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CC
CC EMBL; J00522; AAD15290.1; -.
DR PIR; E90809; GIMS21.
DR PDB; 1IGC; 03-JUN-95.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT NON_TER 1 1
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 2276A98DBDBF7016 CRC64;
Alignment Scores:
Pred. No.: 2.12e-38 Length: 136
Score: 405.00 Matches: 79
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Percent Similarity: 74.81% Conservative: 19  
 Best Local Similarity: 60.31% Mismatches: 19  
 Query Match: 53.78% Indels: 14  
 DB: 1 Gaps: 3

US-09-674-716B-1 (1-415) x HV16\_MOUSE (1-136)

QY 48 CTGATTCTTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTCAGAGTCT 107  
 Db 4 LeuValPheLeuValLeuLeuValGlyValGlnCysAspValGlnLeuValGluSer 23  
 QY 108 GGAGAGGGTTCGTCGCAACTCGAGAGTCCATGAAGTCTCTCTGTGTAGCCCTCTGGATT 167  
 Db 24 GlyGlyGlyLeuValGlnProGlyGlySerArgLysLeuSerCysAlaAlaSerGlyPhe 43  
 QY 168 ACTTTCAGTGGTACTGATGCTTGGTCCGCGAGTCCAGAGAGGGGCTTCAGTGG 227  
 Db 44 ThrPheSerSerPheGlyMetHisTrpValArgGlnAlaProGluLysGlyLeuGluTrp 63  
 QY 228 GTTGCTGAATTTAGATTGAAATCTCATATTATGCAACACATTTATGCGAGTCTGTGAAA 287  
 Db 64 ValAlaTyrIle-----SerSerGlySerSerThrLeuHisTyrAlaAspThrValLys 81  
 QY 288 GGAAGTTCACCATCTCAAGAGATGATCCAAAGTCTCTACCTGCAATGAACAGC 347  
 Db 82 GlyArgPheThrIleSerArgAspAsnProLysAsnThrLeuPheLeuGlnMetThrSer 101  
 QY 348 TTAAGAGCTGAAGAGTGGAGTCTTATTACTGTACA----- 383  
 Db 102 LeuArgSerGluAspThrAlaMetTyrTyrCysAlaArgTrpGlyAsnTyrProTyrTyr 121  
 QY 384 -----GATTTCATAGATGGGGCCCAAGGACA 410  
 Db 122 AlaMetAspTyr-----TrpGlyGlnGlyThr 130

## RESULT 14

HV26\_MOUSE  
 ID HV26\_MOUSE STANDARD; PRT; 144 AA.  
 AC P1795;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region M167 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93358330; PubMed=6101208;  
 RA Kim S., Davis M., Sinn E., Patten P., Hood L.;  
 RT "Antibody diversity: somatic hypermutation of rearranged VH genes.";  
 RL Cell 27:573-581(1981).  
 RN [2]  
 RP SEQUENCE OF 20-142.  
 RX MEDLINE=7622762; PubMed=819932;  
 RA Rudikoff S., Potter M.;  
 RT "Size differences among immunoglobulin heavy chains from  
 RT phosphorylcholine-binding proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN  
 CC THAT BINDS PHOSPHORYLCHOLINE.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC  
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 CC  
 CC EMBL; J00516; AAC18867.2; ALT\_TERM.  
 CR

DR PIR; A90818; AVMS67.  
 DR HSP; P01789; IMCP.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 144 IG HEAVY CHAIN V REGION M167.  
 FT DOMAIN 20 133 IG-LIKE.  
 FT CONFLICT 125 125 N -> D (IN REF. 2).  
 FT NON\_TER 144 144  
 SQ SEQUENCE 144 AA; 16219 MW; BECB4A2C956CF769 CRC64;  
 Alignment Scores:  
 Pred. No.: 1,2e-37 Length: 144  
 Score: 398.50 Matches: 75  
 Percent Similarity: 70.99% Conservative: 18  
 Best Local Similarity: 57.25% Mismatches: 27  
 Query Match: 52.92% Indels: 11  
 DB: 1 Gaps: 1  
 US-09-674-716B-1 (1-415) x HV26\_MOUSE (1-144)  
 QY 51 ATTTTCTTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTCAGAGTCTGGA 110  
 Db 8 ValPheLeuLeuThrLeuLeuHisGlyIleGlnCysGluValLysValValGluSerGly 27  
 QY 111 GAGGGTTCGTCGCAACTCGAGAGTCCATGAAGTCTCTCTGTGTAGCCCTCTCGATTACT 170  
 Db 28 GlyGlyLeuValGlnProGlyGlySerLeuArgLeuSerCysAlaThrSerGlyPheThr 47  
 QY 171 TTCAGTGGCTACTGATGCTTGGTCCGCGAGTCCAGAGAGGGGCTTCAGTGGGT 230  
 Db 48 PheSerAspPheTyrMetGluTrpValArgGlnThrProGlyLysArgLeuGluTrpPile 67  
 QY 231 GCTGAAATAGATTGAATCTGATTAATGACACACATATGCGAGTCTGTGAAAGG 290  
 Db 68 AlaAlaSerArgSerLysAlaHisAspTyrArgThrGluTyrSerAlaSerValLysGly 87  
 QY 291 AGGTCACCATCTCAAGAGATGATCCAAAGTCTCTACCTGCAATGAACAGCTTA 350  
 Db 88 ArgPheIleValSerArgAspThrSerGlnSerValLeuTyrLeuGlnMetAsnAlaLeu 107  
 QY 351 AGAGCTGAGACAGTGGAGTTTATTCTTACAGATTTCATAGAC----- 395  
 Db 108 ArgAlaGluAspThrAlaThrTyrTyrCysThrArgAspAlaAspTyrGlyAsnSerTyr 127  
 QY 396 -----TGGGGCCCAAGGACA 410  
 Db 128 PheGlyTyrPheAspValTrpGlyAlaGlyThr 138  
 RESULT 15  
 HV54\_MOUSE  
 ID HV54\_MOUSE STANDARD; PRT; 117 AA.  
 AC P18526;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 5-84 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=BALB/cJ;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during  
 RT the primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 RL



- ! - MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

DR DR JTC0505; HVM584.  
DR HSP; P01a10; 2PB7.  
DR InterP; IPR007110; IG-like.  
DR InterP; IPR003596; IG\_v.  
DR P1am; PF00047; IG; 1.  
DR SMART; SMC0406; IGv; 1.  
DR PROSITE; PS50835; IG Like; 1.  
DR Immunoglobulin v region; Signal.  
KW

FT	1	IG HEAVY CHAIN V REGION 5-84.
CHAIN	19	FRAMEWORK-1.
DOMAIN	20	COMPLEMENTARITY-DETERMINING-1.
FT	49	FRAMEWORK-2.
FT	50	COMPLEMENTARITY-DETERMINING-2.
FT	54	FRAMEWORK-3.
FT	55	BY SIMILARITY.
FT	58	
FT	69	
FT	85	
FT	86	
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FT		

Alignment Scores:	
Pred. No.:	2,228-37
Score:	396.00
Percent Similarity:	82.91%
Best Local Similarity:	65.91%
Query Match:	52.59%
DB:	1
Gaps:	2
Indels:	4
Mismatches:	16
Conservative:	20
Matches:	77
Length:	117

US-09-674-716B-1 (1-415) x HV54 MOUSE (1-117)

36	ATGGATTGCG-----CTGATTTTTTTATCTCTCTTTTAAAGGGGTCACAGTGA	89	
QY			
1	MetAsnPheGlyLeuSerLeuIlePheLeuValLeuValLeuLysGlyValLeuCysGlu	20	
Db			
90	GTGAAGCTTGAGGAGCTCTGGAGGAGGCTTGCTGCACTGGAGAGTCATGAAC	149	
QY			
21	VallysLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuLysLeuSer	40	
Db			
150	TCTGTAGCCTCTGGATTTACTTTTCAGTGGCTACTGGATCTCTGGGTCGCCAGTCTCA	209	
QY			
41	CysAlaIleSerGlyPheThrPheSerSerTyrThrMetSerTrpValArgGlnThrPro	60	
Db			
210	GAGAAGGGCTTGAGTGGTGTCTGCAATTAGATTGAAATCTGATTAATTCAGACACAT	269	
QY			
61	GluLysArgLeuGluTrpValAlaTyrIle-----SerAsnGlyGlyGlySerThrTyr	78	
Db			
270	TATCGGAGCTCTGAAAGGAAGTTCACCATCTCAAGAGATGATTCCTCAAAAGCTGCTC	329	
QY			
79	TyrProAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnLeu	98	
Db			
330	TACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATCTACTCT	380	
QY			
99	TyrLeuGlnMetSerSerLeuLysSerGluAspThrAlaMetTyrTyrCys	115	
Db			

Search completed: September 30, 2004, 08:42:43  
Job time : 11.0039 secs

Blank sheet

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:27:18.; Search time 52.5503 Seconds  
(without alignments)  
4983.418 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 753  
Sequence: 1 aagttttacattactacgc.....tggggccaaaggacactagt 415

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+np.model -DEV=xl  
-Q=/cgn2\_1/USPTO\_spool\_p/US09674716/runat\_30092004\_070258\_25867/app\_query.fasta\_1.3.64  
-DB=SPTRMBL\_25 -QMT=fastan -SUFFIX=rpct -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=rpct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HSPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09674716@cgn\_1\_1\_499@runat\_30092004\_070258\_25867 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_ricent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriaph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	534.5	71.0	487	11 Q80Z17	Q80Z17 mus musculus

2	468	62.2	479	11 Q7TMK4	Q7tmk4 mus musculus
3	431	57.2	469	11 Q8R3V9	Q8r3v9 mus musculus
4	422.5	56.1	597	4 Q96BB9	Q96bb9 homo sapien
5	420	55.8	613	4 Q8WUK1	Q8wuk1 homo sapien
6	407.5	54.1	479	11 Q91WP5	Q91wp5 mus musculus
7	405	53.8	487	11 Q99KA4	Q99ka4 mus musculus
8	404	53.7	473	11 Q91Z05	Q91z05 mus musculus
9	400	53.1	494	4 Q86X68	Q86x68 homo sapien
10	395	52.5	573	4 Q8WU38	Q8wu38 homo sapien
11	394.5	52.4	113	4 Q9UL90	Q9ul90 homo sapien
12	393.5	52.3	480	11 Q91XE1	Q91xe1 mus musculus
13	391	51.9	484	11 Q8VEA0	Q8vea0 mus musculus
14	390.5	51.9	470	4 Q7ZSW1	Q7zsw1 homo sapien
15	390.5	51.9	486	11 Q91Z07	Q91z07 mus musculus
16	387.5	51.5	499	4 Q8NSK4	Q8nsk4 homo sapien
17	386	51.3	95	4 Q9ULB6	Q9ulb6 homo sapien
18	384.5	51.1	131	4 Q9UL88	Q9ul88 homo sapien
19	377.5	50.1	121	4 Q9UL71	Q9ul71 homo sapien
20	377	50.1	118	4 Q9UL91	Q9ul91 homo sapien
21	375.5	49.9	493	4 Q8NCL6	Q8nc16 homo sapien
22	375.5	49.9	521	4 Q8N4Y9	Q8n4y9 homo sapien
23	370	49.1	112	4 Q9HCC1	Q9hcc1 homo sapien
24	364.5	48.4	119	11 Q920E7	Q920e7 mus musculus
25	362.5	48.1	116	4 Q9UL93	Q9ul93 homo sapien
26	352	46.7	147	4 Q9Y509	Q9y509 homo sapien
27	351	46.6	122	4 Q9UL84	Q9ul84 homo sapien
28	350	46.5	298	11 Q9QIF0	Q9qif0 mus musculus
29	348	46.2	118	4 Q9UL72	Q9ul72 homo sapien
30	344.5	45.8	482	4 Q7Z351	Q7z351 homo sapien
31	332	44.1	437	11 Q9R1A4	Q9rla4 mus musculus
32	311	41.3	482	11 Q8K172	Q8k172 mus musculus
33	309	41.0	463	11 Q9SLC4	Q9slc4 mus musculus
34	304.5	40.4	634	11 Q7TMT6	Q7tmt6 mus musculus
35	304	40.4	278	11 Q921K1	Q921k1 mus musculus
36	304	40.4	613	11 Q8VCX7	Q8vcx7 mus musculus
37	303.5	40.3	168	11 Q8VDC9	Q8vdc9 mus musculus
38	303.5	40.3	473	11 Q9D8L4	Q9d8l4 mus musculus
39	302	40.1	143	11 Q924P9	Q924p9 mus musculus
40	299	39.7	488	11 Q8K0F2	Q8k0f2 mus musculus
41	295	39.2	143	11 Q91V67	Q91v67 mus musculus
42	294.5	39.1	112	4 Q9UGP3	Q9ugp3 homo sapien
43	291.5	38.7	470	11 Q7TMK1	Q7tmk1 mus musculus
44	291	38.6	137	11 Q924R6	Q924r6 mus musculus
45	289.5	38.4	117	11 Q9QXF0	Q9qxf0 mus musculus

## ALIGNMENTS

RESULT 1					
Q80Z17	Q80Z17	PRELIMINARY;	PRT;	487	AA.
AC	Q80Z17;				
DT	01-JUN-2003 (TREMREL. 24, Created)				
DT	01-JUN-2003 (TREMREL. 24, Last sequence update)				
DT	01-OCT-2003 (TREMREL. 25, Last annotation update)				
DE	Hypothetical protein.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=FVB/N; TISSUE=Colon;				
RA	Strausberg R.;				
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: BC049143; AAH49143.1; -				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003597; Ig-cl.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig_3.				
DR	SMART; SMC0409; IG; 3.				



DR PIR: B45837; B45837.  
 DR MGD; MGI: 96446; Igh-4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Hypothetical protein.  
 KW HYPOTHETICAL PROTEIN  
 SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Alignment Scores:  
 Pred. No.: 1.09e-39 Length: 469  
 Score: 431.00 Matches: 83  
 Percent Similarity: 72.93% Conservative: 14  
 Best Local Similarity: 62.41% Mismatches: 24  
 Query Match: 57.24% Indels: 12  
 DB: 11 Gaps: 1

US-09-674-716B-1 (1-415) x Q96BB9 (1-469)

QY 51 ATTTTATTTTATGTTCTTTTAAAGGGCTCCAGAGTGAAGCTTGAGAGCTCTGGA 110  
 DB 8 ILePheLeuValThrLeuLeuAsnGlyIleGlnCysGluValAlaSerGly 27  
 QY 111 GGAGCTTGCTGTCACACCTGGAGGATCCATGAATCTCTCTGTAGGCTCTGGAATTA 170  
 DB 28 GlyGlyLeuValGlnProGlySerLeuArgLeuSerCysAlaAlaSerGlyPheThr 47  
 QY 171 TTCAGTGGCTACTGATCTCTGGTCCGAGCTCCAGAGAGGGGCTTGAGTGGTT 230  
 DB 48 PheThrAspTyrTyrMetSerTrpValArgGlnProGlyLysAlaLeuGluTrpLeu 67  
 QY 231 GCTGAATATAGATTGAAATCTGATAATATGACACACATTTATGCGAGCTCTGTGAAGGG 290  
 DB 68 GlyPheIleArgAsnLysAlaAsnGlyTyrThrGluTyrSerAlaSerValLysGly 87  
 QY 291 AAGTTCACATCTCAAGAGATCAATCCAAAGTCTCTCTACCTGCAATCAAGAGCTTA 350  
 DB 88 ArgPheThrIleSerArgAspAsnSergInSerIleLeuTyrLeuGlnMetAsnAlaLeu 107  
 QY 351 ACAGCTGAAGACAGTGGAGTTTATTACTGT----- 380  
 DB 108 ArgAlaGluAspSerAlaThrTyrCysAlaArgAspArgSerTyrTyrTyr 127  
 QY 381 -----ACAGATTTCATAGCTGGGGCCCAAGGACACTA 413  
 DB 128 SerGlyThrSerPheAlaTyrTrpGlyGlnGlyThrLeu 140

RESULT 4  
 Q96BB9 PRELIMINARY; PRT; 597 AA.  
 AC Q96BB9  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC015760; AAH15760.1; -.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 5.  
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 DR Hypothetical protein.  
 KW HYPOTHETICAL PROTEIN  
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Alignment Scores:  
 Pred. No.: 1.03e-38 Length: 597  
 Score: 422.50 Matches: 85  
 Percent Similarity: 72.73% Conservative: 19  
 Best Local Similarity: 59.44% Mismatches: 18  
 Query Match: 56.11% Indels: 21  
 DB: 4 Gaps: 4

US-09-674-716B-1 (1-415) x Q96BB9 (1-597)

QY 36 ATGGAATTTGGGCTG-----ATTITTTTATGTTCTTTTAAAGGGTCCAGAGTGA 89  
 DB 1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyValGlnCysGlu 20  
 QY 90 GTGAAGCTTGAGGATCTGAGGAGGCTTGGTCCACCTGGAGGATCCATGAACCTCTCC 149  
 DB 21 ValGlnLeuLeuSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSer 40  
 QY 150 TGTGTAGCTCTGATTTTACTTTTCAGTGGCTACTGAGTCTTGGTCCGAGTCTCCA 209  
 DB 41 CysAlaAlaSerGlyPheSerPheSerTyrAlaMetAsnTrpValArgGlnAlaPro 60  
 QY 210 GAGAAGGGCTTGAGTGGTCTGCTGAAATAGATTGAAATCTGATAATATGCAACACAT 269  
 DB 61 GlyLysGlyLeuGluTrpValSerAlaIle-----SerGlySerGlyGlySerThrTyr 78  
 QY 270 TATGCGGAGTCTCTGAAAGGGAAGTTTCCACATCTCAAGAGATGATTCCTCAAGTCTCTC 329  
 DB 79 TyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerArgAspThrLeu 98  
 QY 330 TACTCTCAATGAACAGCTTAAAGCTGAAGAGTGAAGAGTGGAGTTTATTACTGTACA----- 383  
 DB 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAlaLysAsp 118  
 QY 384 -----GATTTCATAGACTGGGGCAA 404  
 DB 119 ProArgGlyTyrSerAlaSerGlyAsnTyrThrArgGluAspTyr-----TrpGlyGln 136  
 QY 405 GGGACACTA 413  
 DB 137 GlyThrLeu 139

RESULT 5  
 Q96BB9 PRELIMINARY; PRT; 613 AA.  
 AC Q96BB9  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Tonsil;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC020240; AAH20240.1; -.  
 DR PIR; P01200; P01200.  
 DR PIR; S15590; S15590.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 5.



36 ATGGATTTTGGG-----CTGATTTTATTTTATTTTATTTTAAAGGGGTCAGAGTCAA 89  
 1 MetAsnPheGlyLeuSerLeuValLeuValLeuValLeuValGlnCysGlu 20  
 90 GTGAAGCTTGGAGCTGTGGAGGAGGCTGTGGCAACTGAGGAGTCCATCAAACTCTCC 149  
 21 ValGlnLeuValGluSerGlyGlyLeuValValValValValValValValValVal 40  
 150 TGTGTAGCTCTGATTTTACTTTCAGTGGCTACTGGATGCTCTGGTCCGCGAGTCTCCA 209  
 41 CysAlaAlaSerGlyPheThrPheSerSerTyrrAlaMetSerTrpValArgGlnThrPro 60  
 210 GAGAGGGGCTGTAGTGGTGTCTGCTGAATTAAGTGAATTAAGTGAATTAAGTGAATTA 266  
 61 GluValArgLeuGluTrpValAlaThrIle-----SerAspGlyGlySerTyrrThr 77  
 267 CATATGCGGAGCTCTGTGAAGGAGGAGTCCACCTCTCAAGAGAGTGAATTAAGTGAATTA 326  
 78 TyrrTyrrProAspAsnValValValValValValValValValValValValValVal 97  
 327 CTCTACCTGCAATTAAGAGCTGTAGAGCTGAAGAGTGAAGTGAAGTGAAGTGAAGTGA 380  
 98 LeuTyrrLeuGlnMetSerHisLeuValSerGluAspThrAlaMetTyrrTyrrCysAlaArg 117  
 381 -----ACAGATTTTCATAGACTGGGGCCAGGGGACA 410  
 118 AspMetGlyGlySerProTyrrGlyGlyTyrrSerArgPheAspTyrrTrpGlyGlnGlyThr 137

RESULT 8  
 Q91Z05 PRELIMINARY; PRT; 473 AA.  
 ID Q91Z05  
 AC Q91Z05  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN AU04919.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC010327; AAH0327.1; -.  
 DR MGD; MGI:2144967; AU04919.  
 DR GO; GO:0005489; F:electron transporter activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR InterPro; IPR000345; Cyt c heme\_BS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00190; CYTOCHROME C; 1.  
 DR PROSITE; PS0835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AP12 CRC64;

Alignment Scores:  
 Pred. No.: 1,22e-36 Length: 473  
 Score: 404.00 Matches: 79  
 Percent Similarity: 76.74% Conservative: 20  
 Best Local Similarity: 61.24% Mismatches: 18  
 Query Match: 53.65% Indels: 12  
 DB: 11 Gaps: 3

US-09-674-716B-1 (1-415) x Q91Z05 (1-473)

48 CTGATTTTATTTTATTTTATTTTAAAGGGGTCAGAGTGAAGCTTCCAGAGTCT 107  
 1 MetAsnPheGlyLeuSerLeuValLeuValLeuValLeuValGlnCysGlu 20

7 LeuValPheLeuValLeuLeuLeuValGlnCysGluValGlnLeuValGluSer 26  
 108 GGAGGAGGCTTGGTGCACACTGAGGATCCATGAACCTCTCTGTGTAGCCTCTGGATTT 167  
 27 GlyGlyGlyLeuValValValValValValValValValValValValValValVal 46  
 168 ACTTTCAGTGGCTGTGGATGCTTGGGTCGCCAGTCTCCAGAGAGGGGCTTGGATGG 227  
 47 ThrPheSerAspTyrrGlyMethIstTrpValArgGlnAlaProGluValGlyLeuGluTrp 66  
 228 GTTGTCTGAATTAAGTGAATCTGATAATTAATGCAACACATTAATCGGAGTCTGTGAAA 287  
 67 ValAlaTyrrIle-----AsnSerGlySerThrThrIleTyrrAlaAspThrValLys 84  
 288 GGAAGTTCACCATCTCAAGAGAGTGAATCAAAAGTCTCTTCTCTCTCTCTCTCTCTCTCT 347  
 85 GlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuPheLeuGlnMetThrSer 104  
 348 TTAAGGCTGAACAGCAGTGGAGTTTATTACTGTACA----- 383  
 105 LeuArgSerGluAspThrAlaMetTyrrTyrrCysAlaArgGluLeuTrpLeuArgArgIle 124  
 384 GATTTCATAGACTGGGGCCAGGGGACA 410  
 125 AspTyrr-----TrpGlyGlnGlyThr 131

RESULT 9  
 Q96K68 PRELIMINARY; PRT; 494 AA.  
 ID Q96K68  
 AC Q96K68  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein FLJ14473.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE-Mammary gland;  
 RA ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
 RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Chiba Y., Ishida S., Murakami K., Ono Y., Takiguchi S.,  
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
 RA Nimomiyama K., Iwayanagi T.;  
 RL "NEDO human cDNA sequencing project."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK027379; BAB55072.1; -.  
 DR PIR; S21205; S21205.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; ig; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AEE4C0E CRC64;

Alignment Scores:  
 Pred. No.: 3,48e-36 Length: 494  
 Score: 400.00 Matches: 79  
 Percent Similarity: 72.46% Conservative: 21  
 Best Local Similarity: 57.25% Mismatches: 24  
 Query Match: 53.12% Indels: 14  
 DB: 4 Gaps: 3

US-09-674-716B-1 (1-415) x Q96K68 (1-494)

36 ATGGATTTTGGGCTG-----ATTTTATTTTATTTTATTTTAAAGGGGTCAGAGTCAA 89





QY 333 CTGCAATGAACAGCTTAGAGCTGAAGACAGTGGAGTTATTACTGTACAGAT----- 386  
 Db 99 LeuLglnMetThrSerLeuAsnSerGluAspThrAlaValTyrCysThrArgGlyAsp 118  
 QY 387 -----TTCATAGCTGGGCCCAAGGACA 410  
 Db 119 TyrTrpTyrPheAspValTrpGlyAlaGlyThr 129

### RESULT 13

ID	Q8VEA0	PRELIMINARY;	PRT;	484 AA.
AC	Q8VEA0;			
DT	01-MAR-2002	(T-EMBLrel. 20, Created)		
DT	01-MAR-2002	(T-EMBLrel. 20, Last sequence update)		
DT	01-OCT-2003	(T-EMBLrel. 25, Last annotation update)		
DE	Hypothetical protein.			
GN	IGH-VJ558 OR A1893585.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC019425; AAH19425.1; -			
DR	MGI; J96486; Igh-VJ558.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig_4.			
DR	SMART; SMO0406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 4.			
DR	PROSITE; PS00290; IG_MHC; 2.			
KW	Hypothetical protein_N			
SQ	SEQUENCE 484 AA; 52859 MW; P2522DF5ED6288A6 CRC64;			

  

Alignment Scores:			
Pred. No.:	3.6e-35	Length:	484
Score:	391.00	Matches:	75
Percent Similarity:	73.02%	Conservative:	17
Best Local Similarity:	59.52%	Mismatches:	28
Query Match:	51.93%	Indels:	6
DB:	11	Gaps:	1

  

US-09-674-716B-1 (1-415) x Q8VEA0 (1-484)

QY	51	ATTTTTTTTATTGTTCTTTTAAAGGGTC	CAGAGTGAAAGCTTGAGGAGTCTCGA	110
Db	8	IlePheLeuValThrLeuLeuAsnGlyPheGlnCysGluVallysLeuValGluSerGly		27
QY	111	GGAGGCTGTGTGCACCTGGAGGATCCATGAAACTCTCCTGTGTAGCCCTCTGGATTACT		170
Db	28	GlyGlyLeuValGlnProGlyThrSerLeuThrLeuSerCysAlaThrSerGlyPheThr		47
QY	171	TTCAGTGGCTACTCGATGTCCTTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGT		230
Db	48	PheThrGluTyrTyrMetSerIrpValArgGlnProGlyValArgAlaLeuGluTrpLeu		67
QY	231	GCTCAAATTAGATTGCAATCTGTAATTATTCACACACATTTATGCGGAGTCTGTGAAAGGG		290
Db	68	GlyPheIleArgAsnArgAlaAsnGlyTyrThrProGluTyrSerAlaSerValGlnGly		87
QY	291	AAGTTCACCATCTCAAGAGATGATCCAAAAGTCGTCTCTACCTGCAATGAACAGCTTA		350
Db	88	ArgPheThrIleSerArgAspAsnSerGlnAsnLeuTyrLeuGlnMetAsnThrLeu		107
QY	351	AGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT-----TTCATA		392
Db	108	ArgAlaGluAspSerAlaThrTyrTyrCysAlaArgAlaTyrSerAsnTyrTyrPheAsp		127
QY	393	GACTGGGCCCAAGGACA 410		

```

Db      128 AsnTrpGlyGlnGlyThr 133
RESULT 14
Q725W1
ID      Q725W1
AC      Q725W1
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Spleen;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Strausberg R.L., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Xie H.F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Sapotnick M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzyvinski M.I., Skalska U., Smallos J.E., Scherch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Spleen;
RA      Strausberg R.;
RL      Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RW      EMBL; BC053984; AAHS3984.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE 470 AA; 51204 MW; 778CF34521483B1A CRC64;

Alignment Scores:
Pred. No.:      4,08e-35      Length:      470
Score:          390.50      Matches:      80
Percent Similarity: 70.29%      Conservative: 17
Best Local Similarity: 57.97%      Mismatches: 26
Query Match:    51.86%      Indels:      15
DB:             4      Gaps:        3

US-09-674-716B-1 (1-415) x Q725W1 (1-470)

QY      36 ATGAGTTTGGGTG-----ATTTTATTTTATTTTAAAGGGGTCAGAGTGAA 89
Db      1 MetGluLeuSerTrpValPheLeuValValIleLeuGluGlyValGlnCysGlu 20

QY      90 GTCAAGCTTGAGAGCTCGAGAGGCTGGTGGCACTGGAGGAGTCCATGAATCTCC 149
Db      21 ValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSer 40

QY      150 TGTGTAGCTCTGGATTTACTTTCTAGTGGCTACTGGATGCTTGGTCCGCCAGTCTCCA 209
Db      41 CysValAlaSerGlyPheThrLeuAsnAspMetHisTrpValArgGlnGlyIle 60

QY      210 GAGAGGGCTTCAGTGGGCTCTCGAATAGATTGAATCTGAATATTCACACAT 269
Db      61 GlyLysGlyLeuGlnTrpValSerLysIleGlyThrAlaGlyAspArgTyr----- 77

US-09-674-716B-1 (1-415) x Q91207 (1-486)

QY      36 ATGAGTTTGGGTG-----CTGATTTTATTTTATTTTAAAGGGGTCAGAGTGAA 89
Db      1 MetAsnPheGlyLeuArgLeuLeuPheLeuValLeuAlaLeuLysGlyValGlnCysGlu 20

QY      90 GTCAAGCTTGAGAGCTCGAGAGGCTGGTGGCACTGGAGGAGTCCATGAATCTCC 149
Db      21 ValHisLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuLysLeuSer 40

QY      150 TGTGTAGCTCTGGATTTACTTTCTAGTGGCTACTGGATGCTTGGTCCGCCAGTCTCCA 209
Db      41 CysValValSerGlyPheSerPheThrSerTyrAspMetSerTrpValArgGlnThrPro 60

QY      210 GAGAGGGGCTTCAGTGGGCTTCGTAATAGATTGAATCTGAATATTCACACAT 269
Db      61 GluArgGluLeuGlnTrpValAlaIle-----ThrSerGlyGlyAsnThrTyr 77

QY      270 TATGCGGAGTCTGTGAAGGAGAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGCTC 329
Db      78 TyrProAspAsnValLysGlyArgPheThrValSerArgAspAsnAlaLysTyrThrLeu 97

QY      330 TACTGCAATGAACAGCTTAAGAGCTCAAGACAGTGGAGTTTATTACTGTACA----- 383
Db      98 TyrLeuGlnMetAsnSerLeuArgValGlyAspAlaValTyrCysAlaArgGly 117

QY      384 -----GATTTATAGATGGGGCCCAAGGACACTA 413
Db      118 AlaGlyArgTrpAlaProLeuGlyAlaPheAspIleTrpGlyGlnGlyThrMet 135

RESULT 15
Q91207
ID      Q91207
AC      Q91207;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Strausberg R.;
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RW      EMBL; BC010324; AAH10324.1; -.
DR      InterPro; IPR007110; Ig-Like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig_4.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS00835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 2.
KW      Hypothetical protein.
SQ      SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Alignment Scores:
Pred. No.:      4.1e-35      Length:      486
Score:          390.50      Matches:      78
Percent Similarity: 72.66%      Conservative: 23
Best Local Similarity: 56.12%      Mismatches: 21
Query Match:    51.86%      Indels:      17
DB:             11      Gaps:        3.

US-09-674-716B-1 (1-415) x Q91207 (1-486)

QY      36 ATGAGTTTGGGTG-----CTGATTTTATTTTATTTTAAAGGGGTCAGAGTGAA 89
Db      1 MetAsnPheGlyLeuArgLeuLeuPheLeuValLeuAlaLeuLysGlyValGlnCysGlu 20

QY      90 GTCAAGCTTGAGAGCTCGAGAGGCTGGTGGCACTGGAGGAGTCCATGAATCTCC 149
Db      21 ValHisLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuLysLeuSer 40

QY      150 TGTGTAGCTCTGGATTTACTTTCTAGTGGCTACTGGATGCTTGGTCCGCCAGTCTCCA 209
Db      41 CysValValSerGlyPheSerPheThrSerTyrAspMetSerTrpValArgGlnThrPro 60

QY      210 GAGAGGGGCTTCAGTGGGCTTCGTAATAGATTGAATCTGAATATTCACACAT 269
Db      61 GluArgGluLeuGlnTrpValAlaIle-----ThrSerGlyGlyAsnThrTyr 77

QY      270 TATGCGGAGTCTGTGAAGGAGAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGCTC 329
Db      78 TyrProAspAsnValLysGlyArgPheThrValSerArgAspAsnAlaLysTyrThrLeu 97

QY      330 TACTGCAATGAACAGCTTAAGAGCTCAAGACAGTGGAGTTTATTACTGT----- 380
Db      98 TyrLeuGlnMetSerLeuLysSerGluAspThrAlaMetTyrTyrCysValArgPro 117

```

QY 381 -----ACAGATTTCATAGACTGGGGCCAGGGACA 410  
Db 118 GluileProIleTyrTyrSerGlySerTyrPheAspSerTipGlyGlnGlyThr 136  
:::  
|||

Search completed: September 30, 2004, 08:53:35  
Job time : 57.5503 secs

Blank sheet

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:19:42 ; Search time 49.4398 Seconds  
(without alignments)  
4743.430 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 753

Sequence: 1 aagctttacagttactcagc.....tggggcccaaggacactagt 415

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DB=frame+ n2p model -DEV=xlp

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-DB=A\_Geneseq\_29Jan04 -CFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09674716 @CN 1.1 475 @runat\_30092004\_070257\_25848 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THRAIDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_29Jan04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	715	95.0	137	3 AAY32260	Mouse ant
2	573.5	76.2	151	4 AAB35292	Mouse hea
3	573.5	76.2	151	4 AAB35292	Mouse PS
4	561.5	74.6	142	2 AAW06212	MAB Br-3
5	561.5	74.6	142	2 AAW85059	Mouse Br-
6	561.5	74.6	142	6 ABUS5893	Mouse ant
7	561.5	74.6	143	2 AAR09423	Br-3 Heavy
8	553.5	73.5	160	2 AAR70829	MAB 4197X
9	531.5	70.6	134	2 AAR12358	Heavy cha
10	531.5	70.6	134	2 AAR12236	Mouse MAB

11	531	70.5	444	3 AAY32263	Humanised
12	524.5	69.7	134	2 AAR52771	Murine Br
13	524.5	69.7	134	2 AAR52789	Murine Br
14	521.5	69.3	570	2 AAY39451	Antibody
15	518.5	68.9	123	6 ABO10742	Variable
16	518.5	68.9	123	6 ABR44686	Murine Mu
17	518	68.8	139	2 AAR30484	VH region
18	511.5	67.9	119	2 AAW46958	Amino aci
19	511.5	67.9	554	2 AAR70827	Anti-cata
20	507	67.3	120	2 AAW01589	Lead bind
21	503.5	66.9	116	2 AAY03869	SM3 heavy
22	503	66.8	114	2 AAR25410	Heavy cha
23	500.5	66.5	134	2 AAR52807	Humanised
24	500	66.4	286	4 AAB50426	Antibody
25	498.5	66.2	119	2 AAW01588	Lead bind
26	497.5	66.1	136	2 AAR12326	Heavy cha
27	497.5	66.1	503	5 AAU72874	3B10P5-2
28	495	65.7	100	4 AAE06973	Mouse ger
29	493	65.5	256	5 AAU72866	PS-3 sing
30	491	65.2	114	3 AAY90816	113F1 hyb
31	490	65.1	122	3 AAY90812	2G3 hybri
32	489.5	65.0	123	6 ABO10743	Consensus
33	489.5	65.0	123	6 ABR44687	Murine J4
34	488	64.8	299	4 AAB50425	Mouse ant
35	483.5	64.2	129	2 AAR85908	Monoclonal
36	483	64.2	255	5 AAU72870	PS-23 sin
37	481	63.9	133	6 ABO10730	Variable
38	481	63.9	133	6 ABR44674	Murine J4
39	480.5	63.8	253	2 AAR72599	Anti-gans
40	480	63.7	116	6 ABO10726	Variable
41	480	63.7	116	6 ABR44670	Murine J4
42	476	63.2	116	6 ABO10728	Variable
43	476	63.2	116	6 ABR44672	Murine J4
44	475	63.1	507	5 ABG71552	Murine sc
45	473	62.8	116	6 ABO10734	Consensus

#### ALIGNMENTS

RESULT 1

AAAY32260  
ID AAAY32260 standard; protein; 137 AA.

XX AC AAAY32260;

XX AC 15-FEB-2000 (first entry)

XX DE Mouse anti-CD23 MAB C11 heavy chain variable region.

XX KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.

XX OS Mus musculus.

XX Key	Location/Qualifiers
FT Region	59..63
FT Region	/note= "CDR H1"
FT Region	78..96
FT Region	/note= "CDR H2"
FT Region	129..131
FT Region	/note= "CDR H3"

PN WO9958679-A1.

PD 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.  
 XX 09-MAY-1998; 98GB-00009839.  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 DR WPI; 2000-053101/04.  
 DR N-PSDB; AAZ34745.  
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.  
 XX Claim 8; Fig 1; 81pp; English.  
 XX This sequence represents the heavy chain variable region (VH) of murine  
 CC anti-CD23 (FCER1I) monoclonal antibody C11. The invention provides  
 CC altered antibodies, such as chimeric or humanised antibodies (see  
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions (see AAY32254-59) to render them capable of binding to the CD23  
 CC type II molecule expressed on haematopoietic cells. The antibodies are  
 CC used to block soluble CD23 formation in human therapy, for the treatment  
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents  
 XX SQ Sequence 137 AA;  
 Alignment Scores:  
 Pred. No.: 3.67e-70 Length: 137  
 Score: 715.00 Matches: 137  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 94.95% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-674-716B-1 (1-415) x AAY32260 (1-137)  
 QY 3 GCTTACGTTACTACGACACAGGACCTCACCATGGATTGGCGGATTTTATTTATT 62  
 DB 1 AlaLeuGlnLeuSerThrGlnAspLeuThrMetAspPheGlyLeuIlePhePhe 20  
 QY 63 GTTCTTTAAAGGGCTCCAGAGTGAAGTGAAGCTTGAGAGCTCGGAGGCGCTGGTG 122  
 DB 21 ValLeuLeuLysGlyValGlnSerGluValLysLeuGluLysSerGlyGlyLeuVal 40  
 QY 123 CACCTGGAGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTTTTCAGTGGCTAC 182  
 DB 41 GlnProGlyGlySerMetLysLeuSerCysValAlaSerGlyPheThrPheSerGlyTyr 60  
 QY 183 TGGATGCTTGGTTCGCGCAGTCTCCAGAGAGGGGCTTGAGTGGCTTGCCTCAAAATTAGA 242  
 DB 61 TrpMetSerTrpValArgGlnSerProGluLysGlyLeuGluTrpValAlaGluLeuArg 80  
 QY 243 TTGAATCTGATTAATATGCAACATTAATGCGAGCTCTGTGAAGGGAGGATCCACATC 302  
 DB 81 LeuLysSerAspSerTrpAlaThrHisTrpAlaGluSerValLysGlyLysPheThrIle 100  
 QY 303 TCAGAGATGATTCGAAAGTCTCTCTACCTGCAATCAAGCTTAGAGCTGAAGAC 362  
 DB 101 SerArgAspSerLysSerArgLeuTrpLeuGlnMetAsnSerLeuArgAlaGluasp 120  
 QY 363 AGTGGAGTTTATTCTGTACAGATTTTCATAGACTGGGCGCAAGGACACTA 413

Db 121 SerGlyValTyrTyrCysThrAspPheIleAspTrpGlyGlnGlyThrLeu 137  
 RESULT 2  
 AAU76696  
 ID AAU76696 standard; protein; 151 AA.  
 XX AAU76696;  
 AC AAU76696;  
 XX 21-MAY-2002 (first entry)  
 DT Mouse heavy chain variable domain region of PSCA antibody 2H9 protein.  
 DE  
 XX Mouse; prostate stem cell antigen; PSCA; antibody; immunogen;  
 KW prostate cancer; bladder cancer; pancreatic cancer; immunconjugate;  
 KW PSCA-associated cancer; heavy chain variable domain region; PSCA antigen;  
 KW PSCA antibody 2H9.  
 XX Mus sp.  
 OS  
 XX Key Location/Qualifiers  
 FH 45..54  
 FT Region /note= "Complementarity determining region 1 (CDR1)"  
 FT Region 69..87  
 FT Region /note= "Complementarity determining region 2 (CDR2)"  
 FT Region 120..125  
 FT Region /note= "Complementarity determining region 3 (CDR3)"  
 XX US2001055751-A1.  
 XX 27-DEC-2001.  
 XX 03-MAY-2000; 2000US-00564329.  
 PR 10-MAR-1997; 97US-0228816P.  
 PR 12-JAN-1998; 98US-0071141P.  
 PR 13-FEB-1998; 98US-0074675P.  
 PR 10-MAR-1998; 98US-00038261.  
 PR 02-DEC-1998; 98US-0020939.  
 PR 21-DEC-1998; 98US-0113230P.  
 PR 17-FEB-1999; 99US-00251835.  
 PR 17-FEB-1999; 99US-0120536P.  
 PR 16-MAR-1999; 99US-0124858P.  
 PR 25-MAY-1999; 99US-00318503.  
 PR 20-JUL-1999; 99US-00359326.  
 XX (REIT/) REITER R E.  
 PA (WITT/) WITTE O N.  
 PA (SAFF/) SAFFRAN D C.  
 PA (JAKO/) JAKOBOVITS A.  
 XX Reiter RE, Witte ON, Saffran DC, Jakobovits A;  
 XX WPI; 2001-159478/16.  
 DR N-PSDB; ABK09984.  
 XX Antibodies binding to prostate stem cell antigen inhibit the growth of  
 PT cancer cells and are used to detect and treat prostate, pancreatic or  
 FT bladder cancers.  
 XX Example 21; Fig 60; 127pp; English.  
 PS The present invention relates to new antibodies that specifically bind a  
 CC novel prostate stem cell antigen (PSCA), which is widely over-expressed  
 CC across all stages of prostate cancer. The antibodies of the invention are  
 CC useful to kill tumour cells expressing PSCA and as PSCA expression is  
 CC observed in prostate tumour cells and in other human cancers,  
 CC particularly bladder and pancreatic carcinomas, the antibodies are useful  
 CC therapeutically to treat these diseases. In particular, monoclonal  
 CC antibodies can be administered to subjects suffering from PSCA-associated  
 CC cancers, e.g. prostate, bladder or pancreatic cancer or metastatic  
 CC prostate, bladder or pancreatic cancer, to inhibit the cancer and prolong  
 CC the subject's life. The antibodies can be combined with a therapeutic  
 CC agent in immunconjugates useful to treat subjects suffering from



```

XX DE MAb Br-3 heavy chain variable region.
XX KW Chimeric antibody; monoclonal antibody; Br-3; antibody engineering;
XX KW tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;
XX KW ovary carcinoma; cancer; diagnosis; therapy; heavy chain.
XX OS Mus sp.
XX PN US5576184-A.
XX PD 19-NOV-1996.
XX PF 27-DEC-1994; 94US-00364001.
XX PR 06-SEP-1988; 88US-00240624.
XX PR 08-SEP-1988; 88US-00241744.
XX PR 13-SEP-1988; 88US-00243739.
XX PR 04-OCT-1988; 88US-00253002.
XX PR 19-JUN-1989; 89US-00367641.
XX PR 21-JUL-1989; 89US-00382768.
XX PR 06-MAY-1991; 91US-00659401.
XX PA (XOMA ) XOMA CORP.
XX PI Chang CP, Lei S, Better MD, Robinson RR, Horwitz AH;
XX KW WPI; 1997-011249/01.
XX DR N-PSDB; AAT43437.
XX FT Chimeric mouse-human antibodies - recognise a human tumour antigen, used
XX PT for the treatment and diagnosis of human cancers.
XX PS Example 3; Fig 15; 102pp; English.
XX CC The heavy chain variable region (AAW06212) of mouse monoclonal antibody
XX CC Br-3 is the product of a cDNA clone (AAT43437) isolated from a Br-3
XX CC hybridoma cDNA library. MAb Br-3 (IgG1) binds to an antigen that is
XX CC expressed on the surface of human lung, breast, colon and ovary
XX CC carcinomas, but not on most normal adult tissues. The heavy chain and
XX CC light chain variable regions (see also AAW06211) of B38-1 can be linked
XX CC to human constant regions and expressed in transformed host cells. Novel
XX CC mouse-human chimeric antibodies (see also AAW06209-10 and AAW06213-18)
XX CC can be produced that have specificity to human tumour antigens and can be
XX CC used for the treatment and diagnosis of human cancer. (Updated on 25-MAR-
XX CC 2003 to correct PF field.)
XX SQ Sequence 142 AA;

Alignment Scores:
Pred. No.: 3,42e-53 Length: 142
Score: 561.50 Matches: 108
Percent Similarity: 89.31% Conservative: 9
Best Local Similarity: 82.44% Mismatches: 9
Query Match: 74.57% Indels: 5
DB: Gaps: 2

US-09-674-716B-1 (1-415) x AAW06212 (1-142)
QY 36 ATGAGTTTGGGTG-----ATTGTTTATGTTCTTTTAAAGGGTCCAGAGTGAA 89
D 1 MetTyrLeuGlyLeuAsnGlyValPheLeuValPheLeuLeuGlyValGlnSerGlu 20
QY 90 GTCAAGCTTCAGAGCTCGAGGAGCTGGTGGCAACCTGGAGGATCCATGAATCTCC 149
D 21 ValTyrLeuGlyLeuGlyGlyGlyLeuValGlnProGlyGlySerMetTyrLeuSer 40
QY 150 TGTGAGCTCTGGATTTACTTTTCAGTGGCTACTGGATCTCTGGGTCGGCAGTCTCA 209
D 41 CysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSerPro 60
QY 210 GAGAGGGCTTCAGTGGTCTGTAATTAGATTGAAATGATTAATATGACACAT 269

```

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Db 61 GlulysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnAsnTyrAlaThrHis 80
QY 270 TATCGGAGTCTGTGAAGGGAAGTTCCACCATCTCAGAGATGATTCCTCAAAAGTCGCTC 329
D 81 TyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerVal 100
QY 330 TACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGCTTTTACTGTACA----- 383
D 101 TyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrCysThrPheGly 120
QY 384 ---GATTTCATAGACTGGGCCCAAGGACACTA 413
D 121 AsnGlnPheAlaTyrTrpGlyGlnGlyThrLeu 131
RESULT 5
AAW85059
ID AAW85059 standard; protein; 142 AA.
AC AAW85059;
XX 20-MAR-2003 (revised)
XX 16-APR-1999 (first entry)
XX Mouse Br-3 heavy chain variable region.
XX Heavy chain variable region; murine antibody Br-3; antibody ING-1;
XX KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;
XX KW treatment; human cancer.
XX OS Mus sp.
XX PN US5843685-A.
XX PD 01-DEC-1998.
XX PF 06-JUN-1995; 95US-00466034.
XX PR 06-SEP-1988; 88US-00240624.
XX PR 08-SEP-1988; 88US-00241744.
XX PR 13-SEP-1988; 88US-00243739.
XX PR 04-OCT-1988; 88US-00253002.
XX PR 19-JUN-1989; 89US-00367641.
XX PR 21-JUL-1989; 89US-00382768.
XX PR 06-SEP-1989; 89WO-US003852.
XX PR 06-MAY-1991; 91US-00659401.
XX PR 27-DEC-1994; 94US-00364001.
XX PA (XOMA ) XOMA CORP.
XX PI Horwitz AH, Lei S, Chang CP, Better MD, Robinson RR;
XX KW WPI; 1999-044574/04.
XX DR N-PSDB; AAV71155.
XX Chimeric antibody specific for human tumour antigen - useful as
XX PT immunoassay, imaging or antitumour agent.
XX PS Example 3; Fig 15; 92pp; English.
XX CC The present sequence represents the heavy chain variable region of murine
XX CC antibody Br-3. The sequence was used to create chimeric mouse-human
XX CC immunoglobulins which recognise the human tumour antigen bound by
XX CC antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The
XX CC chimeric antibodies also have an antigen-binding site that competitively
XX CC inhibits the binding of antibody ING-1 and mediate complement-dependent
XX CC cytolysis of target cells or antibody-dependent cellular cytotoxicity to
XX CC target cells. The chimeric antibodies can be used for therapeutic
XX CC purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to
XX CC correct PR field.)
XX SQ Sequence 142 AA;

Alignment Scores:

```



Pred. No.: 3,42e-53 Length: 142  
 Score: 561.50 Matches: 108  
 Percent Similarity: 89.31% Conservative: 9  
 Best Local Similarity: 82.44% Mismatches: 9  
 Query Match: 74.57% Indels: 5  
 DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x AAW85059 (1-142)

QY	36	ATGGATTGGGCTG-----ATTTTATTTATGTTCTTTTAAAGGGGTCCAGAGTGAA	89
DB	1	MetTyrLeuGlyLeuAsnCysValPheIleValPheLeuLeuLysGlyValGlnSerGlu	20
QY	90	GTGAAGCTTGAGAGCTCGGAGGCTGGTGGCAACCTGGAGGATCCATGAAGCTCTCC	149
DB	21	ValLysLeuGluGlnSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer	40
QY	150	TGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGGATGTCCTTGGTCCGCCAGTCTCCA	209
DB	41	CysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSerPro	60
QY	210	GAGAGGGCTTGAGTGGTCTGCAATAGATTGAATCTGATATTAATGCAACACAT	269
DB	61	GluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnAsnTyrAlaThrHis	80
QY	270	TATGGGAGCTCTGCAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCTCTC	329
DB	81	TyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerVal	100
QY	330	TACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTATTACTGTACA-----	383
DB	101	TyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrCysThrPheGly	120
QY	384	---GATTTCATAGCTGGGGCCCAAGGACACTA	413
DB	121	AsnGlnPheAlaTyrTrpGlyGlnGlyThrLeu	131

RESULT 6  
 ABUS8893  
 ID ABUS8893 standard; protein; 142 AA.  
 XX AC ABUS8893;  
 XX AC  
 DT 16-APR-2003 (first entry)  
 XX DE  
 DE Mouse antibody heavy chain variable region #2.  
 KW Mouse; human tumour antigen; anti-human tumour antigen-antibody;  
 KW ING-1 antibody; cell line H9812; immunoassay; imaging; tumour diagnosis;  
 KW tumour therapy; cytostatic; heavy chain variable region.  
 XX OS  
 XX Mus sp.  
 XX US6461824-B1.  
 XX PD  
 XX 08-OCT-2002.  
 XX PF  
 XX 06-JUN-1995; 95US-00467142.  
 XX PR  
 XX 06-SEP-1988; 88US-00240624.  
 XX PR  
 XX 08-SEP-1988; 88US-00241744.  
 XX PR  
 XX 13-SEP-1988; 88US-00243739.  
 XX PR  
 XX 04-OCT-1988; 88US-00253002.  
 XX PR  
 XX 19-JUN-1989; 89US-00367641.  
 XX PR  
 XX 21-JUL-1989; 89US-00382768.  
 XX PR  
 XX 06-SEP-1989; 89NO-US003852.  
 XX PR  
 XX 06-MAY-1991; 91US-00659401.  
 XX PR  
 XX 27-DEC-1994; 94US-00364001.  
 XX  
 (XOMA ) XOMA TECHNOLOGY LTD.  
 XX PA  
 XX Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;

WPI: 2003-196707/19.  
 N-PSDB; ABK79231.  
 Antibody for detecting antigen in animal or killing cells carrying antigen comprises human constant region and variable region having specificity for human tumor antigen bound by ING-1 antibody.  
 Example 3; Fig 15; 101pp; English.  
 The invention describes an antibody comprising a human constant region and a variable region having specificity for the human tumour antigen bound by the ING-1 antibody, where the ING-1 is produced by cell line H9812 as deposited with ATCC, and the antibody has the same affinity as the ING-1 for the human tumour antigen. The antibody is useful in an immunoassay method for detecting an antigen in a sample by contacting a label-detectable antigen in the sample with the antibody, detecting the label and relating the detected label to the presence of the antigen; for use in an imaging method for revealing the presence of a label-detectable antigen in an animal by contacting the antibody with a part of the animal suspected of containing the antigen, detecting the label and relating the detected label to the presence of the antigen; and for killing cells carrying an antigen by contacting the cells with the antibody and allowing the killing to occur. The antibodies are useful in tumour diagnosis and therapy. The chimeric antibodies bind to the surface of human tumour cells but do not bind detectably to normal cells, e.g., fibroblasts, endothelial cells or epithelial cells in the major organs. The high biological activity of the chimeric antibodies against human tumour cell lines combined with minimal reactivity with normal tissues imply that these antibodies may mediate selective destruction of malignant tissue. The presence of human rather than murine antigenic determinants on the chimeric antibodies increases their resistance to rapid clearance from the body relative to the original murine mAbs. The resistance to clearance enhances the potential utility of these chimeric antibodies, as well as their derivatives, in tumour diagnosis and therapy. This is the amino acid sequence of a mouse antibody heavy chain variable region used in the creation of an anti-human tumour antigen-antibody

Sequence 142 AA;  
 Alignment Scores:  
 Pred. No.: 3,42e-53 Length: 142  
 Score: 561.50 Matches: 108  
 Percent Similarity: 89.31% Conservative: 9  
 Best Local Similarity: 82.44% Mismatches: 9  
 Query Match: 74.57% Indels: 5  
 DB: 2 Gaps: 2  
 US-09-674-716B-1 (1-415) x ABUS8893 (1-142)  
 QY 36 ATGGATTGGGCTG-----ATTTTATTTATGTTCTTTTAAAGGGGTCCAGAGTGAA 89  
 DB 1 MetTyrLeuGlyLeuAsnCysValPheIleValPheLeuLeuLysGlyValGlnSerGlu 20  
 QY 90 GTGAAGCTTGAGAGCTCGGAGGCTGGTGGCAACCTGGAGGATCCATGAAGCTCTCC 149  
 DB 21 ValLysLeuGluGlnSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40  
 QY 150 TGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGGATGTCCTTGGTCCGCCAGTCTCCA 209  
 DB 41 CysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSerPro 60  
 QY 210 GAGAGGGCTTGAGTGGTCTGCAATAGATTGAATCTGATATTAATGCAACACAT 269  
 DB 61 GluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnAsnTyrAlaThrHis 80  
 QY 270 TATGGGAGCTCTGCAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCTCTC 329  
 DB 81 TyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerVal 100  
 QY 330 TACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTATTACTGTACA----- 383  
 DB 101 TyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrCysThrPheGly 120  
 QY 384 ---GATTTCATAGCTGGGGCCCAAGGACACTA 413  
 DB 121 AsnGlnPheAlaTyrTrpGlyGlnGlyThrLeu 131



CC to ricin-A. cDNAs encoding the VL and VH regions of 4197X (AAQ85387-88, CC respectively) were obtained from hybridoma mRNA, amplified by PCR, and CC engineered for inclusion in the immunotoxin construct (AAQ85386). CC (Updated on 25-MAR-2003 to correct FN field.) XX  
SQ Sequence 160 AA;

Alignment Scores:  
Pred. No.: 2,696-52 Length: 160  
Score: 553.50 Matches: 106  
Percent Similarity: 88.64% Conservative: 11  
Best Local Similarity: 80.30% Mismatches: 10  
Query Match: 73.51% Indels: 5  
DB: 2 Gaps: 2  
US-09-674-716B-1 (1-415) x AAR70829 (1-160)

QY 33 ACCATGGATTGGGCTG-----ATTGTTTATTGTTCTTTTAAAGGGTCCAGAGT 86  
DB 19 ThrMetTyrLeuGlyLeuAsnCysValPheLeuValPheValLeuGlyValGlnSer 38  
QY 87 GAAGTGAAGCTTTGAGGAGTCTGGAGGAGCTTGGTCAACCTGGAGGATCCATGAATC 146  
DB 39 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 58  
QY 147 TCCTGTGAGCTCTGGATTACTTTTCACTGCTACTGATGCTTGGTGGCGAGTCT 206  
DB 59 SerCysValAlaSerGlyPheThrPheSerAsnPheTrpMetAsnTrpValArgGlnSer 78  
QY 207 CCAGAGAGGGGCTTGAGTGGCTTCTGAAATAGATTGAATCTGATAATTATGCAACA 266  
DB 79 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnAsnTyrProThr 98  
QY 267 CATTATGGGAGTCTGTGAAGGAGTTCACCTCTCAAGAGATGATTCGAAAGTCTG 326  
DB 99 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 118  
QY 327 CACTACCTGCAATGAACAGCTTAAGAGCTGAAGAGTGGAGTTTATTACTGTACA--- 383  
DB 119 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrCysThrThr 138  
QY 384 -----GATTTCATAGACTGGGGCCCAAGGGACACTA 413  
DB 139 AspSerProPheAlaTyrTrpGlyGlnGlyThrLeu 150

RESULT 9  
AAR12358  
ID AAR12358 standard; protein; 134 AA.  
XX  
AC AAR12358;  
DT 25-MAR-2003 (revised)  
DT 15-AUG-1991 (first entry)  
XX  
DE Heavy chain variable region of murine 1C11 immunoglobulin.  
XX  
KW Chimeric antibodies; immunoconjugates; HIV; AIDS.  
XX  
OS Mus musculus.  
XX  
PN WO9107493-A.  
XX  
PD 30-MAY-1991.  
XX  
PF 13-NOV-1989; 89US-00433730.  
XX  
PR 13-NOV-1989; 89US-00433730.  
XX  
PA (XOMA ) XOMA CORP.  
PA (GEC ) GREEN CROSS CORP.  
XX  
PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;

DR WPI; 1991-178105/24.  
DR N-PSDB; AAQ12060.  
XX  
PT New chimeric mouse-human antibodies - used to detect, kill and remove HIV  
XX -1 antigen from sample.  
XX  
PS Disclosure; Fig 12; 107pp; English.

XX This is the heavy-chain variable (V) region of a mouse mono- clonal  
CC antibody (MAB), 1C11, and is specific for an HIV-1 viral antigen. It is  
CC used in the construction of a chimeric MAB comprising heavy and light  
CC chains having murine V regions and human C regions. The chimeric MABs are  
CC more effective than murine MAB 1C11 since they have an increased  
CC compatibility in humans. The heavy and light chain V-regions are joined  
CC by manipulating their respective joining (J) regions, to generate  
CC restriction enzyme recognition sites. The chimeric MABs can be used as  
CC immunoconjugates, in association with e.g. toxins for HIV treatment. They  
CC can also be used in diagnosis of HIV. See also AAQ12056-59 and AAQ12061-  
CC 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003  
CC to correct FI field.) (Updated on 25-MAR-2003 to correct DR field.)  
XX

SQ Sequence 134 AA;  
Alignment Scores:  
Pred. No.: 7e-50 Length: 134  
Score: 531.50 Matches: 103  
Percent Similarity: 87.60% Conservative: 10  
Best Local Similarity: 79.84% Mismatches: 13  
Query Match: 70.58% Indels: 3  
DB: 2 Gaps: 2  
US-09-674-716B-1 (1-415) x AAR12358 (1-134)

QY 36 ATGATTTTGGGCTG-----ATTGTTTATTGTTCTTTTAAAGGGTCCAGAGTGA 89  
DB 1 MetTyrLeuGlyLeuAsnTyrValPheValPheLeuLeuAsnGlyValGlnSerGlu 20  
QY 90 GTGAAGCTTCAGGAGTCTGGAGGAGCTTGGTCAACCTGGAGGATCCATGAATCTCC 149  
DB 21 ValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40  
QY 150 TGTGATGCTCTGATTTACTTTTCAGTGGCTACTGATGCTCTGGTCCGCCAGTCTCCA 209  
DB 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60  
QY 210 GAGAGGGGCTTGAGTGGTGTCTGAATAGATTGAATCTGATTAATTATGCAACAT 269  
DB 61 GluLysGlyLeuGluTrpValAlaGluLeuArgSerLysAlaAsnAsnHisAlaThrTyr 80  
QY 270 TATCGGAGTCTGTGAAGGAGGAGTTCACCATCTCAAGAGATGATTCGAAAGTGGTCTC 329  
DB 81 TyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSerVal 100  
QY 330 TACCTGCAATGAACAGCTTAAGAGCTGAAGAGTGGAGTGGATTTATTACTGTACAGAT--- 386  
DB 101 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrGlyIleTyrCysThrAspTrp 120  
QY 387 TTCATAGACTGGGGCCCAAGGGACACTA 413  
DB 121 PheAlaTyrTrpGlyGlnGlyThrLeu 129

RESULT 10  
AAR12236  
ID AAR12236 standard; protein; 134 AA.  
XX  
AC AAR12236;  
XX  
DT 25-MAR-2003 (revised)  
DT 19-AUG-1991 (first entry)  
XX  
DE Mouse MAB 1C11 H chain V region.  
XX  
KW HIV-1; chimera.

XX Mus sp.  
 OS  
 PN WO9107494-A.  
 XX  
 PD 30-MAY-1991.  
 XX  
 XX 13-NOV-1989; 89US-00433703.  
 XX  
 XX 13-NOV-1989; 89US-00433703.  
 PR  
 XX (XOMA ) XOMA CORP.  
 PA (GREC ) GREEN CROSS CORP.  
 PA (ZOMA-) ZOMA CORP.  
 XX  
 PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;  
 XX  
 XX WPI; 1991-178106/24.  
 DR N-PSDB; AAQ12106.  
 XX  
 XX New chimeric mouse human antibodies - used in treatment, diagnosis and  
 PT prophylaxis of HIV infections.  
 PT  
 PS Disclosure; Fig 12; 108pp; English.  
 XX  
 CC The mouse VH gene product may be used to produce chimeric mouse- human  
 CC Abs against HIV-1 comprising human Ig constant regions and murine  
 CC variable regions. These novel sequence are useful in treatment, diagnosis  
 CC and prophylaxis of HIV infections, and may be produced by a bacterial,  
 CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct  
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)  
 CC  
 SQ Sequence 134 AA;  
 Alignment Scores:  
 Pred. No.: 7e-50 Length: 134  
 Score: 531.50 Matches: 103  
 Percent Similarity: 87.60% Conservative: 10  
 Best Local Similarity: 79.84% Mismatches: 13  
 Query Match: 70.58% Indels: 3  
 DB: 2 Gaps: 2  
 US-09-674-716B-1 (1-415) x AAR12236 (1-134)  
 QY 36 ATCGATTGGGGTG-----ATTGTTTATGTTCTTTTAAAGGGTCCAGAGTGAA 89  
 Db 1 MetTyLeuGlyLeuAsnTyValPheLeuLeuAsnGlyValGlnSerGlu 20  
 QY 90 GTGAAGCTTGAGGAGTCTGGAGGAGCTTGGTGCACCTGGAGGATCCATGAACTCTCC 149  
 Db 21 ValLysLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40  
 QY 150 TGTGTAGCTCTGGATTACTTTTCACTGCTACTGATCTCTGGTCCGCGAGTCTCA 209  
 Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60  
 QY 210 GAGAAGGGGCTTCAGTGGGTGTCTGAATTCAGATTGAAATTCAGATTATTCACACAT 269  
 Db 61 GluLysGlyLeuGluTrpValAlaGluLeuArgSerLysAlaAsnHisAlaThrTy 80  
 QY 270 TATCGGAGTCTGTGAAGGAGTTCACATCTCAAGAGATGATTCACAAAGTCTGTC 329  
 Db 81 TyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerVal 100  
 QY 330 TACTCTCAATGACAGCTTAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT--- 386  
 Db 101 TyLeuGlnMetAsnSerLeuArgAlaGluAspThrGlyIleTyrcysThrAspTrp 120  
 QY 387 TTCATAGCTGGGGCCCAAGGGACACTA 413  
 Db 121 PheAlaTyTrpGlyGlnGlyThrLeu 129  
 RESULT 11

AAV32263  
 ID AAY32263 standard; protein; 444 AA.  
 XX  
 AC AAY32263;  
 XX  
 DT 15-FEB-2000 (first entry)  
 XX  
 XX Humanised anti-CD23 MAb C11 heavy chain.  
 DE  
 XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT Region 1..30  
 FT /note= "framework region 1"  
 FT Region 31..35  
 FT /note= "CDR 1"  
 FT Region 36..49  
 FT /note= "framework region 2"  
 FT Region 50..68  
 FT /note= "CDR 2"  
 FT Region 69..100  
 FT /note= "framework region 3"  
 FT Region 101..103  
 FT /note= "CDR 3"  
 FT Region 104..111  
 FT /note= "framework region 4"  
 FT Region 112..444  
 FT /note= "constant region"  
 XX  
 PN WO9958679-A1.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PF 07-MAY-1999; 99WO-GB001434.  
 XX  
 PR 09-MAY-1998; 98GB-00009839.  
 XX  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 XX  
 DR WPI; 2000-053101/04.  
 DR N-PSDB; AAZ34748.  
 XX  
 PT Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.  
 XX  
 PS Claim 9; Fig 4; 81pp; English.  
 XX  
 CC This amino acid sequence represents the heavy chain of humanised anti-  
 CC CD23 (FCERII) monoclonal antibody C11, composed of a human framework  
 CC (HIGKVI) and the heavy chain complementarity determining regions (see  
 CC AAY32257-59) of murine antibody C11. The DNA was constructed by splice  
 CC overlap PCR. The invention provides altered antibodies, such as chimeric  
 CC or humanised antibodies, which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions to render them capable of binding to the CD23 type II molecule  
 CC expressed on haematopoietic cells. The antibodies are used to block  
 CC soluble CD23 formation in human therapy, for the treatment of arthritis,  
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,  
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,

CC glomerulonephritis, inflammatory bowel disease, ulcerative colitis,  
CC Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
CC malignancies (claimed). They are also useful for studying interactions  
CC between CD23 and various ligands and determining the binding agents  
XX  
SQ Sequence 444 AA;

Alignment Scores:  
Pred. No.: 1.03e-49 Length: 444  
Score: 531.00 Matches: 97  
Percent Similarity: 95.41% Conservativeness: 7  
Best Local Similarity: 88.93% Mismatches: 5  
Query Match: 70.52% Indels: 0  
DB: 3 Gaps: 0

US-09-674-716B-1 (1-415) x AAY32263 (1-444)

QY 87 GAAGTGAAGCTTGAGGAGCTGAGGAGGCTTGTCACCTGGAGGATCCATGAACCTC 146  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20  
QY 147 TCTGTGTAGCTCTGGATTACTTTTCAGTGCTACTCGATGTCTTGGTCCGCCAGTCT 206  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerGlyTyrTrpMetSerTrpValArgGlnAla 40  
QY 207 CCAGAGAGGGCTTGAGTGGCTTCTGTAATAGATTCGAATCTGATAATTATGCAACA 266  
Db 41 ProGlySerGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAspAsnTyrAlaThr 60  
QY 267 CATTATGCGAGTCTGTGAAGGAGGAGTTCCACCTCAAGAGATGATTCACAAAGTGGT 326  
Db 61 HisTyrAlaGluSerValLysGlyLysPheThrLeSerArgAspSerLysSerArg 80  
QY 327 CTCTACCTCCAAATGAACAGCTAGAGCTGAAGACAGAGTGGAGTTATATCTGACAGAT 386  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrAsp 100  
QY 387 TTCATAGACTGGGCCCAAGGGACACTA 413  
Db 101 PheLeuAspTrpGlyGlnGlyThrLeu 109

RESULT 12  
AAR52771  
ID AAR52771 standard; protein; 134 AA.  
XX  
AC AAR52771;

XX 25-MAR-2003 (revised)  
DT 24-JAN-1995 (first entry)  
XX  
DE Murine BrE-3 immunoglobulin heavy chain variable domain.  
XX  
KW Immunoglobulin variable domain; primer; polymerase chain reaction;  
KW Chimeric antibody; human milk fat globule; BrE-3 VH-chain.  
XX

OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Protein 20..134  
FT Region /label= BrE-3\_VH-chain  
FT Region 50..54 /label= CDR1  
FT Region 69..87 /label= CDR2  
FT Region 120..123 /label= CDR3

XX WO9411508-A2.  
PN  
XX  
PD 26-MAY-1994.

XX 15-NOV-1993; 93WO-US011316.  
PF  
XX 13-NOV-1992; 92US-00977706.  
PR 13-NOV-1992; 92US-00977707.  
PR 28-SEP-1993; 93US-00128015.  
XX  
XX (CANC-) CANCER RES FUND CONTRA COSTA.  
XX  
XX WPI; 1994-183509/22.  
DR N-PSDB; AAQ62750.  
XX  
XX Chimeric human-murine polypeptide(s) specific for human mammary fat  
XX globule antigen - for imaging, diagnosing and treating neoplasia, with  
XX less undesirable immunogenic response.  
XX  
XX Example 10; Page 32; 54pp; English.  
XX  
XX Primers JO2, JO3, JO4, JO14 and VH1BACK (AAQ62740-Q62744) were all used  
XX to prepare cDNAs that encode the BrE-3 mouse Ig variable domains. The  
XX amplified V-regions lacked constant regions so as to produce less  
XX immunogenic polypeptides. A hybrid polypeptide was prepared using human  
XX constant regions with the murine V regions. The chimeric polypeptide  
XX retained the binding affinity of BrE-3 for human milk fat globule.  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 134 AA;

Alignment Scores:  
Pred. No.: 4.16e-49 Length: 134  
Score: 524.50 Matches: 102  
Percent Similarity: 88.37% Conservativeness: 12  
Best Local Similarity: 79.07% Mismatches: 12  
Query Match: 69.65% Indels: 3  
DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x AAR52771 (1-134)

QY 36 ATGATTTTGGCTG-----ATTTTTTATTTGTTCTTTTAAAGGGTCCAGAGTGAA 89  
Db 1 MetTyrLeuGlyLeuAsnTyrValPheLeuLeuLeuLysGlyValGlnSerGlu 20  
QY 90 GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGTCACCTGGAGATCCATGAACCTCTCC 149  
Db 21 ValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40  
QY 150 TGTGTACCTCTGTGATTACTTTTTCAGTGGTCTGATGTTCTGGTCCGCCAGTCTCCA 209  
Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60  
QY 210 GAGAAGGGCTTGAGTGGTCTGCTGAATAGATTGAATCTGATATATTATGCAACACAT 269  
Db 61 GluLysGlyLeuGluTrpValAlaGluLeuArgAsnLysAlaAsnHisAlaThrTyr 80  
QY 270 TATCGGAGTCTGTGAAGGAGGAGTTCACCATCTCAAGAGATGATTCAAAAGTCGTCTC 329  
Db 81 TyrAspGluSerValLysGlyArgPheThrLysSerArgAspSerLysSerArgVal 100  
QY 330 TACCTGCAATGAACACCTTAAGAGCTGAACAGAGTGGAGTTTATTACTGTACH---GAT 386  
Db 101 TyrLeuGlnMetLysSerLeuArgAlaGluAspThrGlyLeuTyrTyrCysThrGlyGlu 120  
QY 387 TTCATAGACTGGGCCCAAGGGACACTA 413  
Db 121 PheAlaAsnTrpGlyGlnGlyThrLeu 129

RESULT 13  
AAR52789  
ID AAR52789 standard; protein; 134 AA.  
XX  
AC AAR52789;  
XX  
DT 25-MAR-2003 (revised)

DT 24-JAN-1995 (first entry)  
 XX Murine BrE-3 immunoglobulin heavy chain variable domain.  
 XX  
 XX Immunoglobulin variable domain; primer; polymerase chain reaction;  
 XX chimeric antibody; human milk fat globule; BrE-3 VH-chain.  
 XX  
 XX Mus musculus.

Key Location/Qualifiers  
 FT Protein 20..134  
 FT /label= BrE-3\_VH-chain  
 FT Region 50..54  
 FT /label= CDR1  
 FT Region 69..87  
 FT /label= CDR2  
 FT Region 120..123  
 FT /label= CDR3

XX WO9411509-A2.

XX 26-MAY-1994.

XX 16-NOV-1993; 93WO-US011445.

XX 16-NOV-1992; 92US-00977696.

XX 30-SEP-1993; 93US-00129930.

XX 08-OCT-1993; 93US-00134346.

XX (CANC-) CANCER RES FUND CONTRA COSTA.

XX Do Couto FJR, Ceriani RL, Peterson JA, Padlan EA;

XX WPI; 1994-183510/22.

XX New analogue peptide(s) comprising antibody variable regions - used to  
 develop prods. for use in the detection, diagnosis, therapy and  
 prevention of neoplasms.

XX Example 11; Page 48; 109pp; English.

XX Primers J02, J03, J04, J014 and VHBACK (AA062765-Q62769) were all used  
 to prepare cDNAs that encode the BrE-3 mouse Ig variable domains. The  
 amplified V-regions lacked constant regions so as to produce less  
 immunogenic polypeptides. A hybrid polypeptide was prepared using human  
 constant regions with the murine V regions. The chimeric polypeptide  
 retained the binding affinity of BrE-3 for human milk fat globule.  
 CC (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 134 AA;

Alignment Scores:  
 Pred. No.: 4,156-49 Length: 134  
 Score: 524.50 Matches: 102  
 Percent Similarity: 88.37% Conservative: 12  
 Best Local Similarity: 79.07% Mismatches: 12  
 Query Match: 69.65% Indels: 3  
 DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x AAR52789 (1-134)

QY 36 ATGATTTGGGTG-----ATTATTTATGTTCTTTAAAGGGTCCAGACTGAA 89  
 Db 1 MetTyrLeuGlyLeuAsnTyrValPheLeuValPheLeuLeuGlyValGlnSerGlu 20  
 QY 90 GTCAAGCTTGAGAGCTGGAGAGGCTTGGTGCAACTGGAGGATCCATGAAGACTCTCC 149  
 Db 21 ValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40  
 QY 150 TGTGTAGCTCTGGATTTACTTTCACTGGCTACTGGATCTCTGGTCCGCCAGTCTCCA 209  
 Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60

QY 210 GAGAAAGGGCTTGAGTGGTGGTGAATAGATTGAATCTGATTAATTATGCAACACAT 269  
 Db 61 GluLysGlyLeuGluTrpValAlaGluLeuLeuArgAsnLysAlaAsnHisAlaThrTyr 80  
 QY 270 TATCGGAGTCTGTGAAGGGAAGTTCCACCATCTCAAGAGATGATTCCAAAGCTCTCTC 329  
 Db 81 TyrAspGluSerValLysGlyArgPheThrLysSerArgAspSerLysSerArgVal 100  
 QY 330 TACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA--GAT 386  
 Db 101 TyrLeuGlnMetLysSerLeuArgAlaGluAspThrGlyLeuTyrTyrCysThrGlyGlu 120  
 QY 387 TTCATAGACTGGGCGCCAGGACACTA 413  
 Db 121 PheAlaAsnTrpGlyGlnGlyThrLeu 129

RESULT 14

AA39451

ID AAY39451 standard; protein; 570 AA.

XX AAY39451;

XX 19-NOV-1999 (first entry)

DE Antibody ABX-CBL heavy chain sequence.

XX Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
 KW organ transplant rejection disease; lymphoma; pancreatic disease;  
 KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Homo sapiens.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

XX 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LI, Hales J;  
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX N-PSDB; AAZ20419.

XX New monoclonal antibody, used for treating e.g. graft versus host  
 disease, cancers, autoimmune diseases and inflammatory diseases.

XX Disclosure; Page 58; 245pp; English.

XX This sequence represents the heavy chain of the antibody ABX-CXL. The  
 invention relates to a monoclonal antibody (mAb) with an isotype that  
 fixes complement and a variable region that binds to the epitope on CD147  
 bound by the IGM mAb ABX-CBL, providing that the antibody is not CBL1.  
 CC The mAb can selectively kill activated T-cells, activated B-cells or  
 CC resting or activated monocytes. The products and methods can be used for  
 CC treating diseases involving activated T-cells or B-cells or monocytes,  
 CC e.g. graft versus host disease (GVHD), organ transplant rejection  
 CC diseases (e.g. renal transplant, ocular transplant), cancers (e.g.  
 CC cancers of the blood (e.g. leukaemia's and lymphomas) and pancreatic),  
 CC autoimmune diseases (e.g. lupus), and inflammatory diseases (e.g.  
 CC arthritis)

XX Sequence 570 AA;

Alignment Scores:

Pred. No.: 1,22e-48 Length: 570  
 Score: 521.50 Matches: 97

Percent Similarity: 95.45% Conservative: 8  
 Best Local Similarity: 88.18% Mismatches: 4  
 Query Match: 69.26% Indels: 1  
 DB: 2 Gaps: 1

US-09-674-716B-1 (1-415) x AAY39451 (1-570)

QY 87 GAAGTGAAGCTTGAGAGTCTGGAGAGCTTGGTGAACCTGGAGAGTCCATGAATC 146  
 Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
 QY 147 TCCTGTGTAGCTCTGGATTACTTTTCACTGCTACTGATGCTTGGTCCGCCAGTCT 206  
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40  
 QY 207 CCAGAGAAGGGCTTCACTGGTCTGCTGAATAGATTCAATCTGATAATTATGCAACA 266  
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnTyrAlaThr 60  
 QY 267 CATTATGGGAGTCTGGAAGGAGTTCACATCTCAAGAGATGATCCAAAGTCGT 326  
 Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgASPSPSerLysSer 80  
 QY 327 CTTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGCTGGAGTTTATTCTGTACAGAT 386  
 Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyr-Tyr-CysThrAsp 100  
 QY 387 TTC---ATAGACTGGGCGCAAGGACACTA 413  
 Db 101 TyrAspAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 15  
 ABO10742  
 ID ABO10742 standard; protein; 123 AA.  
 XX AC ABO10742;  
 XX DT 20-AUG-2003 (first entry)  
 XX DE Variable region of murine antibody MuVHIIC.  
 XX KW Modified antibody; deimmunised antibody; anti-PSMA antibody;  
 KW prostate specific membrane antigen; immunogenic; CDR; murine;  
 KW complementarity determining region; J591; J415; J533; E99; mouse;  
 KW prostatic disorder; cancerous disorder; genitourinary inflammation;  
 KW prostatitis; benign enlargement; prostatic cancer; testicular cancer;  
 KW solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;  
 KW antiinflammatory; cystostatic; framework region; variable heavy chain;  
 KW variable light chain; VH; VL; variable region.  
 XX OS Mus musculus.  
 XX PN WO200298897-A2.  
 XX PD 12-DEC-2002.  
 XX PF 30-MAY-2002; 2002WO-US017068.  
 XX PR 01-JUN-2001; 2001US-0295214P.  
 PR 20-SEP-2001; 2001US-0323585P.  
 PR 08-MAR-2002; 2002US-0362810P.  
 XX PA (CORR ) CORNELL RES FOUND INC.  
 XX PI Bander N, Carr FU, Hamilton A;  
 XX DR WPI; 2003-156839/15.  
 XX PT New modified anti-prostate specific membrane antigen (PSMA)  
 PT immunoglobulins, useful for treating or preventing a prostatic or  
 PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or  
 PT prostatic or testicular cancer.

PS Disclosure; Fig 7C; 254pp; English.  
 XX The present invention relates to modified (e.g. deimmunised) antibodies  
 CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA  
 CC antibodies are less immunogenic compared to the unmodified anti-PSMA  
 CC antibodies. The modified antibodies comprise complementarity determining  
 CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,  
 CC J533 or E99), and framework sequences that are less immunogenic in humans  
 CC (e.g. less antigenic than the murine frameworks in which a murine CDR  
 CC naturally occurs). The modified antibodies bind with PSMA, preferably  
 CC human PSMA, with high affinity and specificity. The anti-PSMA antibodies  
 CC are useful for treating or preventing a prostatic or cancerous disorder,  
 CC e.g. genitourinary inflammation, prostatitis, benign enlargement,  
 CC prostatic cancer or testicular cancer, or solid tumours, soft tissue  
 CC tumours or metastatic lesions, and its associated pain. The present  
 CC sequence represents a variable region from a murine antibody  
 XX Sequence 123 AA;

Alignment Scores:  
 Pred. No.: 1.88e-48 Length: 123  
 Score: 518.50 Matches: 98  
 Percent Similarity: 88.14% Conservative: 6  
 Best Local Similarity: 83.05% Mismatches: 5  
 Query Match: 68.86% Indels: 9  
 DB: 6 Gaps: 1

US-09-674-716B-1 (1-415) x ABO10742 (1-123)

QY 87 GAAGTGAAGCTTGAGAGTCTGGAGAGCTTGGTGAACCTGGAGATCCATGAATC 146  
 Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
 QY 147 TCCTGTGTAGCTCTGGATTACTTTTCACTGCTACTGATGCTTGGTCCGCCAGTCT 206  
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40  
 QY 207 CCAGAGAAGGGCTTCACTGGTCTGCTGAATAGATTCAATCTGATAATTATGCAACA 266  
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnTyrAlaThr 60  
 QY 267 CATTATGGGAGTCTGGAAGGAGTTCACATCTCAAGAGATGATCCAAAGTCGT 326  
 Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgASPSPSerLysSer 80  
 QY 327 CTTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGCTGGAGTTTATTCTGTACAGAT 386  
 Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyr-Tyr-CysThrThr 100  
 QY 387 -----TTCATAGACTGGGCGCAAGGACACTA 413  
 Db 101 GlyGlyTyrGlyGlyArgGSerTrpPheAlaTyrTrpGlyGlnGlyThrLeu 118

Search completed: September 30, 2004, 08:40:50  
 Job time : 54.4398 secs

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; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
; US-09-564-329A-15

Alignment Scores:
Pred. No.: 5,19e-51 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 9 Gaps: 2

US-09-674-716B-1 (1-415) X US-09-564-329A-15 (1-151)
QY 39 GATTTCGGCTG-----ATTTCCTTATGTCCTTTTAAAGGGTCGAGTGAAGTG 92
Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGAGTCTCGAGAGGCTTGGTGCACCTGGAGGATCCATGAACTCTCCGT 152
Db 22 ArgLeuGluGlySerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCTGGATTTACTTTCAGTGGCTACTGATGTCCTGGTCCGCGAGTCTCCAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTCAGTGGCTTCTGAAATGAGTGAATCTGAATCTGATAATTCACACATTAT 272
Db 62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGlyLeuTyrCysThrAspGlyLeu 81
QY 273 GCGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGTCTTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
QY 333 CTGCAATGAACAGCTTAGAGCTAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----CACTGGGGCCCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 2
US-09-855-153-15
; Sequence 15, Application US/09855153
; Patent No. US20020102666A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSICA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855,153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279

; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
; US-09-855-153-15

Alignment Scores:
Pred. No.: 5,19e-51 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 9 Gaps: 2

US-09-674-716B-1 (1-415) X US-09-855-153-15 (1-151)
QY 39 GATTTCGGCTG-----ATTTCCTTATGTCCTTTTAAAGGGTCGAGTGAAGTG 92
Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGAGTCTCGAGAGGCTTGGTGCACCTGGAGGATCCATGAACTCTCCGT 152
Db 22 ArgLeuGluGlySerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCTGGATTTACTTTCAGTGGCTACTGATGTCCTGGTCCGCGAGTCTCCAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTCAGTGGCTTCTGAAATGAGTGAATCTGAATCTGATAATTCACACATTAT 272
Db 62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGlyLeuTyrCysThrAspGlyLeu 81
QY 273 GCGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGTCTTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
QY 333 CTGCAATGAACAGCTTAGAGCTAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----CACTGGGGCCCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 3
US-09-854-811-15
; Sequence 15, Application US/09854811
; Patent No. US20020119157A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
```

; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/854,811
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-854-811-15

Alignment Scores:
Pred. No.: 5,19e-51 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 9 Gaps: 2

US-09-674-716B-1 (1-415) x US-09-854-811-15 (1-151)
QY 39 GATTTGGGCTG-----ATTTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGT 92
Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGGACTCGGAGGAGCTTGGTGCACCTGGAGGATCCATGAACTCTCCNGT 152
Db 22 ArgLeuGluGluSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCTCTGGATTACTTTCAGTGGTCTACTGGATGCTTGGGTCCCGCAGTCTCCAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTGAGTGGTCTGCTCAATAGATTGAATCTGATAATATGCAACATTAT 272
Db 62 LysGlyLeuGluTrpValAlaGluLeuArgLeuArgSerGluAsnTyAlaThrHisTy 81
QY 273 GCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTy 101
QY 333 CTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyTrpCysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGCACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 4
US-09-934-773-15
; Sequence 15, Application US/09934773
; Patent No. US20020136689A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/934,773
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141

; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-934-773-15

Alignment Scores:
Pred. No.: 5,19e-51 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 9 Gaps: 2

US-09-674-716B-1 (1-415) x US-09-934-773-15 (1-151)
QY 39 GATTTGGGCTG-----ATTTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGT 92
Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGGACTCGGAGGAGCTTGGTGCACCTGGAGGATCCATGAACTCTCTCTGT 152
Db 22 ArgLeuGluGluSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCTCTGGATTACTTTCAGTGGTCTACTGGATGCTTGGGTCCCGCAGTCTCCAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTGAGTGGTCTGCTCAATAGATTGAATCTGATAATATGCAACATTAT 272
Db 62 LysGlyLeuGluTrpValAlaGluLeuArgLeuArgSerGluAsnTyAlaThrHisTy 81
QY 273 GCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTy 101
QY 333 CTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyTrpCysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGCACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 5
US-09-963-620-15
; Sequence 15, Application US/09963620
; Patent No. US20020141941A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14

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; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-963-620-15

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Alignment Scores:
Pred. No.: 151
Score: 573.50
Percent Similarity: 92.31%
Best Local Similarity: 83.85%
Query Match: 76.16%
DB: 9
Length: 151
Matches: 109
Conservative: 11
Mismatches: 5
Indels: 5
Gaps: 2

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US-09-674-716B-1 (1-415) X US-09-963-620-15 (1-151)

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QY 39 GATTGGGCTG-----ATTGTTTATTGTTCTTTTAAAGGGGTCAGAGTGAAGTG 92
DB 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGAGTCTGGAGAGGCTTGGTGCAACCTGGAGGATCCATGAACTCTCCTGT 152
DB 22 ArgLeuGluSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCTGGATTACTTTCAGTGCTACTGGATGCTTGGTCCGCGAGTCCAGAG 212
DB 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTCAGTGGCTTCTGTAATAGATTGAAATCTGAAATCTGATTAATTCACACATTAT 272
DB 62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGlyLeuAsnTyrAlaThrHisTyr 81
QY 273 GCGAGTCTGTGAAGGGAAGTTCCACATCTCAAGAGATGATTCCAAAGTCTCTCTAC 332
DB 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
QY 333 CTCGAAATGACAGCTTAGAGCTGAAGACAGTGGAGTTTATCTACTGACACATTTCATA 392
DB 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGACACTA 413
DB 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

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US-09-855-632-15
; Sequence 15, Application US/09855632
; Publication No. US20030113818A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435,54US14
; CURRENT APPLICATION NUMBER: US/09/855,632
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-632-15

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Alignment Scores:
Pred. No.: 151
Score: 573.50
Percent Similarity: 92.31%
Best Local Similarity: 83.85%
Query Match: 76.16%
DB: 10
Length: 151
Matches: 109
Conservative: 11
Mismatches: 5
Indels: 5
Gaps: 2

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US-09-674-716B-1 (1-415) X US-09-855-632-15 (1-151)

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QY 39 GATTGGGCTG-----ATTGTTTATTGTTCTTTTAAAGGGGTCAGAGTGAAGTG 92
DB 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGAGTCTGGAGAGGCTTGGTGCAACCTGGAGGATCCATGAACTCTCCTGT 152
DB 22 ArgLeuGluSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCTGGATTACTTTCAGTGCTACTGGATGCTTGGTCCGCGAGTCCAGAG 212
DB 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTCAGTGGCTTCTGTAATAGATTGAAATCTGAAATCTGATTAATTCACACATTAT 272
DB 62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGlyLeuAsnTyrAlaThrHisTyr 81
QY 273 GCGAGTCTGTGAAGGGAAGTTCCACATCTCAAGAGATGATTCCAAAGTCTCTCTAC 332
DB 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101

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Db      62  LysGlyLeuGluTrpValAlaGluLeuArgSerGluAsnTyrAlaThrHisTyr  81
QY      273  GCGAGTCTGTGAAGAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCTCTCTAC  332
Db      82  AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr  101
QY      333  CTCGAAATGACACGCTTAAGAGCTGAAGACAGTGGAGTTATTACTGTACAGATTTCATA  392
Db      102  LeuGlnMetAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu  121
QY      393  -----GACTGGGGCCCAAGGGACACTA  413
Db      122  GlyArgProAsnTrpGlyGlnGlyThrLeu  131

RESULT 8
US-10-224-720-15
; Sequence 15, Application US/10224720
; Publication NO. US20030147806A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USBS THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/224,720
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US/09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-224-720-15

Alignment Scores:
Pred. No.: 5,19e-51 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 14 Gaps: 2

US-09-674-716B-1 (1-415) x US-10-224-720-15 (1-151)

QY      39  GATTTTGGGCTG-----ATTTTTTTTATTGTTCTTTTAAAGGGGTCCAGAGTGAAGTG  92
Db      2  AspPheGlyLeuSerTrpValPheIleIleValLeuLeuLysGlyValArgSerGluVal  21
QY      93  AGCTTGAGGAGTCTGGAGGAGGCTTGTCGAACCTGGAGGATCCATGAACCTCTCTGT  152
Db      22  ArgLeuGluGluSerGlyGlyGlyTrpValGlnProGlyGlySerValLysSerCys  41

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DB: 15 Gaps: 2

US-09-674-716B-1 (1-415) x US-10-374-381-15 (1-151)

QY 39 GATTTCGGCTG-----ATTTCCTTTTAAAGGGTCCAGAGTGAAGTG 92

Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21

QY 93 AAGCTTGAGGAGCTCGGAGGAGCTTGGTCAACCTGGAGGATCCATGAAGTCTCCTGT 152

Db 22 ArgLeuGluGlySerGlyGlyGlyTrpValGlnProGlySerMetLysLeuSerCys 41

QY 153 GTAGCCTCGGATTTACTTCAGTGGCTACTGGATGCTTGGGTCCGCCAGTCTCCAGAG 212

Db 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu 61

QY 213 AAGGGCTTGAGTGGTCTGCTGAATAGATTGAATCTGATAATTATGCAACACATTAT 272

Db 62 LysGlyLeuGluTrpValAlaGluLeuArgLeuArgLeuArgLeuArgLeuArgLeu 81

QY 273 GCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCAAAAGTCTCTCTAC 332

Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101

QY 333 CTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTACTGTACAGATTTCATA 392

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QY 393 -----GACTGGGGCCCAAGGACACTA 413

Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 11

US-10-446-542-15

; Sequence 15, Application US/10446542

; Publication No. US20040018571A1

; GENERAL INFORMATION:

; APPLICANT: Reiter, Robert E.

; APPLICANT: Witte, Owen N.

; APPLICANT: Saffran, Douglas C.

; TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

; FILE REFERENCE: 30435.54US14

; CURRENT APPLICATION NUMBER: US/10/446,542

; CURRENT FILING DATE: 2003-05-27

; PRIOR APPLICATION NUMBER: US/09/855,153

; PRIOR FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: 09/564,329

; PRIOR FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: 09/359,326

; PRIOR FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: 08/814,279

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: 60/071,141

; PRIOR FILING DATE: 1998-01-12

; PRIOR APPLICATION NUMBER: 60/074,675

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: 60/113,230

; PRIOR FILING DATE: 1998-12-21

; PRIOR APPLICATION NUMBER: 60/120,536

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: 60/124,658

; PRIOR FILING DATE: 1999-03-16

; PRIOR APPLICATION NUMBER: 09/038,261

; PRIOR FILING DATE: 1998-03-10

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15

; LENGTH: 151

; TYPE: PRT

; ORGANISM: SCID Mice

US-10-446-542-15

Alignment Scores:

Pred. No.: 5,19e-51 Length: 151

Score: 575.50 Matches: 109

Percent Similarity: 92.31% Conservative: 11

Best Local Similarity: 83.85% Mismatches: 5

Query Match: 76.16% Indels: 5

DB: 15 Gaps: 2

US-09-674-716B-1 (1-415) x US-10-446-542-15 (1-151)

QY 39 GATTTCGGCTG-----ATTTCCTTTTAAAGGGTCCAGAGTGAAGTG 92

Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21

QY 93 AAGCTTGAGGAGCTCGGAGGAGCTTGGTCAACCTGGAGGATCCATGAAGTCTCCTGT 152

Db 22 ArgLeuGluGlySerGlyGlyGlyTrpValGlnProGlySerMetLysLeuSerCys 41

QY 153 GTAGCCTCGGATTTACTTCAGTGGCTACTGGATGCTTGGGTCCGCCAGTCTCCAGAG 212

Db 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu 61

QY 213 AAGGGCTTGAGTGGTCTGCTGAATAGATTGAATCTGATAATTATGCAACACATTAT 272

Db 62 LysGlyLeuGluTrpValAlaGluLeuArgLeuArgLeuArgLeuArgLeuArgLeu 81

QY 273 GCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCAAAAGTCTCTCTAC 332

Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101

QY 333 CTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTACTGTACAGATTTCATA 392

Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121

QY 393 -----GACTGGGGCCCAAGGACACTA 413

Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 12

US-09-947-839-13

; Sequence 13, Application US/09947839

; Publication No. US20030138428A1

; GENERAL INFORMATION:

; APPLICANT: do Couto Dr., Fernando J.R.

; Ceriani Dr., Roberto L.

; Peterson Dr., Jerry A.

; Padlan Dr., Eduardo A.

; TITLE OF INVENTION: Analogue Peptides With Broad

; Carcinoma Specificity, and Kit and

; Diagnostic Vaccination and

; Therapeutic Methods

; NUMBER OF SEQUENCES: 96

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pretty, Schroeder & Poplawski

; STREET: 444 South Flower St., 19th Floor

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/947,839

; FILING DATE: 06-Sep-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/976,288

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 07/977,696

; FILING DATE: No. US20030138428A1ember 16, 1992

ATTORNEY/AGENT INFORMATION:  
 NAME: Viviana Amzel Ph.D.  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: P6639938  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 622-7700  
 TELEFAX: (213) 489-4210  
 TELEX: n.a.  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 134 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 US-09-947-839-13

Alignment Scores:  
 Pred. No.: 6 53e-46 Length: 134  
 Score: 524.50 Matches: 102  
 Percent Similarity: 88.37% Conservative: 12  
 Best Local Similarity: 79.07% Mismatches: 12  
 Query Match: 69.65% Indels: 3  
 DB: 10 Gaps: 2

US-09-674-716B-1 (1-415) X US-09-947-839-13 (1-134)

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QY 36 ATGGATTGGGTG-----ATTGTTTATTGTTCTTTTAAAGGGTCCAGAGTGAA 89
Db 1 MetTyrLeuGlyLeuAsnTyrValPheIleValPheLeuLeuLysGlyValGlnSerGlu 20
QY 90 GTCAAGCTTGAGAGCTGGAGAGGCTGGTGCACCTGGAGGATCCATGAAGTCTCC 149
Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
QY 150 TGTGACCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTTGGTCCGCCAGTCTCCA 209
Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTyrMetAspTyrValArgGlnSerPro 60
QY 210 GAGAGGGCTTACAGGGTGTGGAATAGATTGAATTCGAATTCGAATTCGAACACAT 269
Db 61 GluLysGlyLeuGluTyrValAlaGluIleArgAsnLysAlaAsnHisAlaThrTyr 80
QY 270 TATCGGAGTCTGTAAAGGGAAGTTCCACATCTCAAGAGATGATTCCAAAGTCTCTC 329
Db 81 TyrAspGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerArgVal 100
QY 330 TACTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTATTACTGTACA---GAT 386
Db 101 TyrLeuGlnMetIleSerLeuArgAlaGluAspThrGlyLeuTyrTyrCysThrGlyGlu 120
QY 387 TTCATAGACTGGGGCCCAAGGACACTA 413
Db 121 PheAlaAsnTyrGlyGlnGlyThrLeu 129

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RESULT 13  
 US-10-160-506-69  
 ; Sequence 69, Application US/10160506  
 ; Publication No. US20030161832A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bander, Neil H.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING  
 ; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR  
 ; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN  
 ; FILE REFERENCE: 10448-162001  
 ; CURRENT APPLICATION NUMBER: US/10/160,506  
 ; CURRENT FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: 60/324,100  
 ; PRIOR FILING DATE: 2001-09-20  
 ; PRIOR APPLICATION NUMBER: 60/362,612  
 ; PRIOR FILING DATE: 2002-03-08  
 ; NUMBER OF SEQ ID NOS: 128  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0

; SEQ ID NO 69  
 ; LENGTH: 123  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-160-506-69

Alignment Scores:  
 Pred. No.: 2.72e-45 Length: 123  
 Score: 518.50 Matches: 98  
 Percent Similarity: 88.14% Conservative: 6  
 Best Local Similarity: 83.05% Mismatches: 5  
 Query Match: 68.86% Indels: 9  
 DB: 14 Gaps: 1

US-09-674-716B-1 (1-415) X US-10-160-506-69 (1-123)

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QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTCGAGGATCCATGAACCTC 146
Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTyrMetAsnTyrValArgGlnSer 40
QY 207 CCAGAGAAGGGCTTGAGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266
Db 41 ProLysGlyLeuGluTyrValAlaGluIleArgLeuLysSerAspAsnTyrAlaThr 60
QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 326
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTATTACTGTACAGAT 386
Db 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrThr 100
QY 387 -----TTCATAGACTGGGGCCCAAGGACACTA 413
Db 101 GlyGlyTyrGlyArgSerTyrPheAlaTyrTyrGlyGlnGlyThrLeu 118

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RESULT 14  
 US-10-449-379-69  
 ; Sequence 69, Application US/10449379  
 ; Publication No. US20040120958A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bander, Neil H.  
 ; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC  
 ; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF  
 ; FILE REFERENCE: 10448-163002  
 ; CURRENT APPLICATION NUMBER: US/10/449,379  
 ; CURRENT FILING DATE: 2003-05-30  
 ; PRIOR APPLICATION NUMBER: 10/160,505  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: 60/323,585  
 ; PRIOR FILING DATE: 2001-09-20  
 ; PRIOR APPLICATION NUMBER: 60/362,810  
 ; PRIOR FILING DATE: 2002-03-08  
 ; PRIOR APPLICATION NUMBER: 60/295,214  
 ; PRIOR FILING DATE: 2001-06-01  
 ; NUMBER OF SEQ ID NOS: 128  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0  
 ; SEQ ID NO 69  
 ; LENGTH: 123  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-449-379-69

Alignment Scores:  
 Pred. No.: 2.72e-45 Length: 123  
 Score: 518.50 Matches: 98  
 Percent Similarity: 88.14% Conservative: 6  
 Best Local Similarity: 83.05% Mismatches: 5  
 Query Match: 68.86% Indels: 9



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DB: 16 Gaps: 1
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DB 1 GluValLysLeuGluGlnSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTAGCTCTGGATTTACTTTTCAGTCTAGTCTGATGCTTGGTCCGCGAGTCT 206
DB 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGAGTGGTCTGCAATAGATTGAATCTGATAATTATGCAACA 266
DB 41 ProGluLysGlyLeuGlnTrpValAlaGluLeuArgLeuLysSerAspAsnTyrAlaThr 60
QY 267 CATTATGGGAGCTGTGAAAGGAGTTCACCATCTCAAGAGATGATTCAAAAGTCGT 326
DB 61 HistyAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
QY 327 CTCCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGACAGAT 386
DB 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrCysThrThr 100
QY 387 -----TTCATAGACTGGGGCCAAAGGACACTA 413
DB 101 GlyGlyTyrGlyArgSerTrpPheAlaTyrTrpGlyGlnGlyThrLeu 118
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## RESULT 15

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US-10-688-015-69
; Sequence 69, Application US/10688015
; Publication No. US20040136998A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: INSULIN-RELATED DISORDERS USING BINDING AGENTS SPECIFIC FOR
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-196001
; CURRENT APPLICATION NUMBER: US/10/688,015
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/422,396
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-688-015-69
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Best Local Similarity:	83.05%	Mismatches:	5
Query Match:	68.86%	Indels:	9
DB:	16	Gaps:	1

US-09-674-716B-1 (1-415) x US-10-688-015-69 (1-123)

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DB 1 GluValLysLeuGluGlnSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTAGCTCTGGATTTACTTTTCAGTCTAGTCTGATGCTTGGTCCGCGAGTCT 206
DB 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGAGTGGTCTGCAATAGATTGAATCTGATAATTATGCAACA 266
DB 41 ProGluLysGlyLeuGlnTrpValAlaGluLeuArgLeuLysSerAspAsnTyrAlaThr 60
QY 267 CATTATGGGAGCTGTGAAAGGAGTTCACCATCTCAAGAGATGATTCAAAAGTCGT 326
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DB 61 HistyAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
QY 327 CTCCTACCTGCAATGAACAGCTTAAAGAGCTGAAGACAGTGGAGTTTATTACTGACAGAT 386
DB 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrCysThrThr 100
QY 387 -----TTCATAGACTGGGGCCAAAGGACACTA 413
DB 101 GlyGlyTyrGlyArgSerTrpPheAlaTyrTrpGlyGlnGlyThrLeu 118
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Search completed: September 30, 2004, 09:48:28

Job time : 57.4329 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:41:28 ; Search time 10.1499 Seconds  
(without alignments)  
4221.672 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 753

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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6: /cgn2\_6/prodata/2/iaa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	524.5	69.7	134	1	US-07-977-696C-13
3	524.5	69.7	134	1	US-08-129-930B-13
4	524.5	69.7	134	4	US-08-976-288A-13
5	507	67.3	120	3	US-08-767-128-28
6	500	66.4	285	3	US-09-318-661-4
7	500	66.4	285	4	US-09-883-758-4
8	498.5	66.2	119	3	US-08-767-128-26
9	491	65.2	114	3	US-08-483-749A-10
10	480	65.1	122	3	US-08-483-749A-2
11	488	64.8	298	3	US-09-318-661-2
12	488	64.8	298	4	US-09-883-758-2

13	463	61.5	119	1	US-08-192-102-5	Sequence 5, Appl
14	463	61.5	119	1	US-08-324-799-5	Sequence 5, Appl
15	463	61.5	119	2	US-08-192-861A-5	Sequence 5, Appl
16	463	61.5	119	3	US-09-133-119-5	Sequence 5, Appl
17	463	61.5	119	3	US-08-192-093A-5	Sequence 5, Appl
18	458.5	60.9	227	1	US-08-681-432-2	Sequence 6, Appl
19	452	60.0	139	3	US-09-136-315-6	Sequence 6, Appl
20	452	60.0	139	4	US-09-767-888-6	Sequence 6, Appl
21	451	59.9	242	2	US-08-224-591-14	Sequence 14, Appl
22	451	59.9	242	2	US-08-392-338A-23	Sequence 23, Appl
23	451	59.9	242	2	US-08-926-789-14	Sequence 14, Appl
24	451	59.9	242	3	US-09-166-750-23	Sequence 23, Appl
25	451	59.9	242	3	US-09-166-093-23	Sequence 23, Appl
26	451	59.9	242	3	US-09-172-019-23	Sequence 23, Appl
27	451	59.9	242	3	US-09-166-094-23	Sequence 23, Appl
28	451	59.9	242	4	US-09-443-213-23	Sequence 23, Appl
29	451	59.9	244	5	PCT-US93-11138-14	Sequence 14, Appl
30	450	59.8	115	1	US-08-468-661-1	Sequence 1, Appl
31	450	59.8	115	1	US-08-466-272A-1	Sequence 1, Appl
32	450	59.8	115	1	US-08-478-857-1	Sequence 1, Appl
33	450	59.8	115	2	US-08-471-771-1	Sequence 1, Appl
34	450	59.8	115	3	US-09-130-783-1	Sequence 13, Appl
35	450	59.8	244	2	US-08-392-338A-13	Sequence 13, Appl
36	450	59.8	244	3	US-09-166-750-13	Sequence 13, Appl
37	450	59.8	244	3	US-09-166-093-13	Sequence 13, Appl
38	450	59.8	244	3	US-09-172-019-13	Sequence 13, Appl
39	450	59.8	244	3	US-09-166-094-13	Sequence 13, Appl
40	450	59.8	244	4	US-09-443-213-13	Sequence 13, Appl
41	447	59.4	250	2	US-08-392-338A-15	Sequence 15, Appl
42	447	59.4	250	3	US-09-166-750-15	Sequence 15, Appl
43	447	59.4	250	3	US-09-166-093-15	Sequence 15, Appl
44	447	59.4	250	3	US-09-172-019-15	Sequence 15, Appl
45	447	59.4	250	3	US-09-166-094-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-564-329A-15  
; Sequence 15, Application US/09564329A  
; Patent No. 6541212  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; FILE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 30435.540S14  
; CURRENT APPLICATION NUMBER: US/09/564,329A  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/359,326  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/113,230  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/120,536  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 60/124,658  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/038,261  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 09/203,939  
; PRIOR FILING DATE: 1998-12-02  
; PRIOR APPLICATION NUMBER: 09/251,835  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 09/308,503  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-15

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Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 4 Gaps: 2

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Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGAGTCTGGAGGAGCTTGTGCAACCTGGAGGATCCATGAAACTCTCTGT 152
Db 22 ArgLeuGluSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCTGGATTACTTTCAGTGGCTACTGATGCTTGGTCCGCGAGTCTCCAGAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTGAGTGGCTTGTGAAATAGATTGAAATCTGAAATATGCAACACATTAT 272
Db 62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGluAsnTrpAlaThrHis 81
QY 273 GCGAGTCTGTGAAGAGGAGTTCACCATCTCAAGAGATGATCCAAAGTCTCTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTrp 101
QY 333 CTCCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTrpCysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 2
US-07-977-696C-13
; Sequence 13, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6668
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-696C-13

Alignment Scores:
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Score: 524.50 Matches: 102
Percent Similarity: 88.37% Conservative: 12
Best Local Similarity: 79.07% Mismatches: 12
Query Match: 69.65% Indels: 3
DB: 1 Gaps: 2

US-09-674-716B-1 (1-415) x US-07-977-696C-13 (1-134)
QY 36 ATGATTTTGGCTG-----ATTGTTTATTGTTCTTTTAAAGGGTCCAGAGTGAA 89
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QY 90 GTGAAGCTTCAGAGAGTCTGGAGGAGCTTGGTCAACCTGGAGGATCCATGAAACTCTCC 149
Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
QY 150 TGTGTAGCCTCTGGATTACTTTCAGTGGCTACTGATGCTTTGGTCCGCGAGTCTCCA 209
Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60
QY 210 GAGNAGGGCTTCAGTGGTTCGTAATAGATTGAAATCTGAAATCTGAAATCTGAAACAT 269
Db 61 GluLysGlyLeuGluTrpValAlaGluIleArgAsnLysAlaAsnAsnHisAlaThrTrp 80
QY 270 TATCGCGAGTCTGTGAAGGAAAGTTCCACCATCTCAAGAGATGATTCCAAAGTCTCTC 329
Db 81 TyrAspGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerArgVal 100
QY 330 TACTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTGGAGTTTATTACTGTACA---GAT 386
Db 101 TyrLeuGlnMetIleSerLeuArgAlaGluAspThrGlyLeuTrpCysThrGlyGlu 120
QY 387 TTCATAGACTGGGCGCAAGGACACTA 413
Db 121 PheAlaAsnTrpGlyGlnGlyThrLeu 129

RESULT 3
US-08-129-930B-13
; Sequence 13, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
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COUNTRY: USA  
ZIP: 94596  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/129,930B  
FILING DATE: September 30, 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel Ph.D., Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: CRFCC-008A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 521-1333  
TELEFAX: (510) 521-3541  
TELEX: n.a.  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 134 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-129-930B-13

Alignment Scores:  
Pred. No.: 2,86e-56 Length: 134  
Score: 524.50 Matches: 102  
Percent Similarity: 88.37% Conservative: 12  
Best Local Similarity: 79.07% Mismatches: 12  
Query Match: 69.65% Indels: 3  
DB: 1 Gaps: 2

US-09-674-716B-1 (1-415) x US-08-129-930B-13 (1-134)

QY 36 ATGGATTGGCTG-----ATTTTATTGTTCTTTAAAGGGTCCAGAGTGAA 89  
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QY 90 GTGAAGCTTGAGAGCTCTGGAGAGGCTTGTCACCTGGAGGATCCATGAACTCTCC 149  
Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40  
QY 150 TGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGTGATGTCTTGGTCCGCCAGTCTCCA 209  
Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTyrMetAspTyrValArgGlnSerPro 60  
QY 210 GAGAAGGGGCTTGAGTGGGTTCTGAAATTAGATTGAAATCTGATAATTATGCAACACAT 269  
Db 61 GluLysGlyLeuGluTyrValAlaGluLeuArgAsnLysAlaAsnHisAlaThrTyr 80  
QY 270 TATCGCGAGCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGTCTC 329  
Db 81 TyrAspGluSerValLysGlyValGlyArgPheThrLysSerArgAspSerLysSerArgVal 100

US-09-674-716B-1 (1-415) x US-08-976-288A-13 (1-134)

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QY 90 GTGAAGCTTGAGAGCTCTGGAGAGGCTTGTCACCTGGAGGATCCATGAACTCTCC 149  
Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40  
QY 150 TGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGTGATGTCTTGGTCCGCCAGTCTCCA 209  
Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTyrMetAspTyrValArgGlnSerPro 60  
QY 210 GAGAAGGGGCTTGAGTGGGTTCTGAAATTAGATTGAAATCTGATAATTATGCAACACAT 269  
Db 61 GluLysGlyLeuGluTyrValAlaGluLeuArgAsnLysAlaAsnHisAlaThrTyr 80  
QY 270 TATCGCGAGCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGTCTC 329  
Db 81 TyrAspGluSerValLysGlyValGlyArgPheThrLysSerArgAspSerLysSerArgVal 100

RESULT 4  
US-08-976-288A-13  
Sequence 13, Application US/08976288A  
Patent No. 6315997  
GENERAL INFORMATION:  
APPLICANT: do Couto Dr., Fernando J.R.  
APPLICANT: Ceriani Dr., Roberto L.  
APPLICANT: Peterson Dr., Jerry A.

QY 330 TACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA---GAT 386  
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Db 101 TyrLeuGlnMetIleSerLeuArgAlaGluAspThrGlyLeuTyrcysThrGlyGlu 120  
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QY 387 TTCATAGACTGGGGCCCAAGGCACCTA 413  
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Db 121 PheAlaAsnTrpGlyGlnGlyThrLeu 129  
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## RESULT 5

US-08-767-128-28  
; Sequence 28, Application US/08767128  
; Patent No. 6111079  
; GENERAL INFORMATION:  
; APPLICANT: WYLIE, DWANE E.  
; APPLICANT: LOPEZ, OSVALDO  
; APPLICANT: MURRAY, PETER JOSEPH  
; APPLICANT: GORBEL, PETER  
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
; NUCLEOTIDES CODING THEREFORE  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. 6111079west Center, 90 South Seventh St  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/767,128  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 05-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/09258  
; FILING DATE: 05-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/541,373  
; FILING DATE: 10-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/462,798  
; FILING DATE: 05-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.49USF1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/371-5278  
; TELEFAX: 612/332-9081  
; TELEX:

; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-08-767-128-28

Alignment Scores: 3.96e-54 Length: 120  
Pred. No.:

Score: 507.00 Matches: 95  
Percent Similarity: 89.57% Conservative: 8  
Best Local Similarity: 82.61% Mismatches: 6  
Query Match: 67.33% Indels: 6  
DB: 3 Gaps: 1  
US-09-674-716B-1 (1-415) x US-08-767-128-28 (1-120)  
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Db 1 GluValIysThrGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
|||||  
QY 147 TCCTGTAGCCTCTGGATTACTTTTCAGTGGGTACTGGATGCTTGGTCCGCCAGTCT 206  
|||||  
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrrpMetAsnTrpValArgGlnSer 40  
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QY 207 CCAGAGAAGGGCTTGAGTGGGTCTGCTGAAATAGATTGAAATCTGATAATTATGCAACA 266  
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Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnAsnTyrrAlaThr 60  
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QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCCCATCTCAAGAGATGATCCAAAAGTCGT 326  
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Db 61 HisTyrrAlaGluSerValLysGlyA:GpheThrIleSerArgAspAspSerLysSerSer 80  
|||||  
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGAGTGGAGTTTATTACTGTACA--- 383  
|||||  
Db 81 ValTyrrLeuGlnMetAsnAsnLeuA:GalaGluAspThrGlyIleTyrrCysThrArg 100  
|||||  
QY 384 -----GATTTCATAGACTGGGGCCCAAGGCACACTA 413  
|||||  
Db 101 TyrGlyArgGluGlyGlyPheAlaTyrrTrpGlyGluGlyThrLeu 115  
|||||

## RESULT 6

US-09-318-661-4  
; Sequence 4, Application US/09318661  
; Patent No. 6268488  
; GENERAL INFORMATION:  
; APPLICANT: Barbas III, Carlos F.  
; APPLICANT: Shabat, Doron  
; APPLICANT: Rader, Christoph  
; APPLICANT: List, Benjamin  
; APPLICANT: Lerner, Richard A.  
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
; FILE REFERENCE: PLF00115  
; CURRENT APPLICATION NUMBER: US/09/318,661  
; CURRENT FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 285  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
; OTHER INFORMATION: residue sequence of catalytic fragment  
US-09-318-661-4

## Alignment Scores:

Pred. No.: 4.01e-53 Length: 285  
Score: 500.00 Matches: 96  
Percent Similarity: 87.61% Conservative: 3  
Best Local Similarity: 84.96% Mismatches: 10  
Query Match: 66.40% Indels: 4  
DB: 3 Gaps: 1  
US-09-674-716B-1 (1-415) x US-09-318-661-4 (1-285)

QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACCTC 146  
|||||  
Db 154 GluValMetLeuValGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 173  
|||||  
QY 147 TCCTGTAGCCTCTGGATTACTTTTCAGTGGGTACTGGATGCTTGGTCCGCCAGTCT 206  
|||||

Alignment Scores: 3.96e-54 Length: 120  
Pred. No.:

Db 174 SerCysValValSerGlyLeuThrPheSerArgPheTrpMetSerTrpValArgGlnSer 193  
QY 207 CCAGAGAGGGGCTGAGTGGCTGCTGAAATAGATTGAATCTGATTAATATCAACA 266  
Db 194 ProGluLysGlyLeuGluTrpValAlaGluLeuLeuSerAspAsnTyrAlaThr 213  
QY 267 CATTATGCGGAGTCTGTGAAGGGAGTTCACCATCTCAAGAGATGATCCAAAAGTCGT 326  
Db 214 HisTyrAlaGluSerValLysGlyLysPheThrIleSerArgAspSerLysSerArg 233  
QY 327 CTTACTCTCAATGAACAGCTTAAGAGCTGAAGCAGTGGAGTTATTACTGTACA--- 383  
Db 234 LeuTyrLeuGlnMetAsnSerLeuArgThrGluAspThrGlyIleTyrCysLysile 253  
QY 384 -----GATTTCATAGACTGGGCCCAAGGACACTA 413  
Db 254 TyrPheTyrSerPheSerTyrTrpGlyGlnGlyThrLeu 266  
RESULT 7  
US-09-883-758-4  
; Sequence 4, Application US/09883758  
; Patent No. 6677435  
; GENERAL INFORMATION:  
; APPLICANT: Barbas III, Carlos F.  
; APPLICANT: Shabat, Doron  
; APPLICANT: Rader, Christoph  
; APPLICANT: List, Benjamin  
; APPLICANT: Lerner, Richard A.  
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
; FILE REFERENCE: PLF00115  
; CURRENT APPLICATION NUMBER: US/09/883,758  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US/09/318,661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 285  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
; OTHER INFORMATION: residue sequence of catalytic fragment  
US-09-883-758-4  
Alignment Scores:  
Pred. No.: 4,01e-53 Length: 285  
Score: 500.00 Matches: 96  
Percent Similarity: 87.61% Conservative: 3  
Best Local Similarity: 84.96% Mismatches: 10  
Query Match: 66.40% Indels: 4  
DB: 4 Gaps: 1  
US-09-674-716B-1 (1-415) x US-09-883-758-4 (1-285)  
QY 87 GAAGTGAAGCTTGAGGAGTCTGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACCTC 146  
Db 154 GluValMetLeuValGluSerGlyGlyLeuValGlnProGlySerMetLysLeu 173  
QY 147 TCCTGTGTAGCTCGGATTTACTTTCAGTGCTACTGAGTCTTGGTCCGCCAGTCT 206  
Db 174 SerCysValValSerGlyLeuThrPheSerArgPheTrpMetSerTrpValArgGlnSer 193  
QY 207 CCAGAGAGGGGCTGAGTGGGTTGCTGAAATAGATTGAATCTGATTAATATCAACA 266  
Db 194 ProGluLysGlyLeuGluTrpValAlaGluLeuLeuSerAspAsnTyrAlaThr 213  
QY 267 CATTATGCGGAGTCTGTGAAGGGAGTTCACCATCTCAAGAGATGATCCAAAAGTCGT 326  
Db 214 HisTyrAlaGluSerValLysGlyLysPheThrIleSerArgAspSerLysSerArg 233  
QY 327 CTTACTCTCAATGAACAGCTTAAGAGCTGAAGCAGTGGAGTTATTACTGTACA--- 383

Db 234 LeuTyrLeuGlnMetAsnSerLeuArgThrGluAspThrGlyIleTyrCysLysile 253  
QY 384 -----GATTTCATAGACTGGGCCCAAGGACACTA 413  
Db 254 TyrPheTyrSerPheSerTyrTrpGlyGlnGlyThrLeu 266  
RESULT 8  
US-08-767-128-26  
; Sequence 26, Application US/08767128  
; Patent No. 6111079  
; GENERAL INFORMATION:  
; APPLICANT: WYLIE, DWANE E.  
; APPLICANT: LOPEZ, OSVALDO  
; APPLICANT: MURRAY, PETER JOSEPH  
; APPLICANT: GOEBEL, PETER  
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. 6111079west Center, 90 South Seventh St  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/767,128  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/09258  
; FILING DATE: 05-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/541,373  
; FILING DATE: 10-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/462,798  
; FILING DATE: 05-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.49USF1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/371-5278  
; TELEFAX: 612/332-9081  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-08-767-128-26  
Alignment Scores:  
Pred. No.: 4,43e-53 Length: 119  
Score: 498.50 Matches: 95  
Percent Similarity: 89.57% Conservative: 8  
Best Local Similarity: 82.61% Mismatches: 5

Query Match: 66.20% Indels: 7  
DB: 3 Gaps: 2

US-09-674-716B-1 (1-415) x US-08-767-128-26 (1-119)

QY 87 GAAGTGAAGCTTCAGGAGTCTGGAGGAGGCTGGTGCACACCTGGAGGATCCATGAATC 146  
DB 1 GluValylsLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
QY 147 TCGTGTAGCTCTCGATTTACTTTTCAGTGGCTACTGATGTTGGTCCGCCAGTCT 206  
DB 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40  
QY 207 CCAGAGAAGGGCTTCAGTGGTTCGTAATTCAGATTCGAAATTCGATTAATTCACA 266  
DB 41 ProGluylsGlyLeuGluTrpValAlaGluValylsLeuLysSerAsnTyrAlaThr 59  
QY 267 CATTATCGGAGTCTGTGAAGGAAAGTTCACCATCTCAAGAGATGATTCGAAAGTCTGT 326  
DB 60 HisTyrAlaGluSerVallylsGlyArgPheThrIleSerArgAspSerLysSerSer 79  
QY 327 CTCTACTGCAATGACACAGCTTAAGAGCTGAAGCAGTGGAGTTTATTACTGTACAGAT 386  
DB 80 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrArg 99  
QY 387 TTC-----ATAGACTGGGGCCAGGACACTA 413  
DB 100 TyrGlyArgGluGlyGlyValAlaTyrTrpGlyGlnGlyThrLeu 114

## RESULT 9

US-08-483-749A-10  
; Sequence 10, Application US/08483749A  
; Patent No. 6054561  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
; CITY: EMERYVILLE  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,749A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL B.  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0508.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-749A-10

Alignment Scores:  
Pred. No.: 3 67e-52 Length: 114  
Score: 491.00 Matches: 89  
Percent Similarity: 92.59% Conservative: 11

Best Local Similarity: 82.41% Mismatches: 8  
Query Match: 65.21% Indels: 0  
DB: 3 Gaps: 0

US-09-674-716B-1 (1-415) x US-08-483-749A-10 (1-114)

QY 87 GAAGTGAAGCTTCAGGAGTCTGGAGGAGGCTGGTGCACACCTGGAGGATCCATGAATC 146  
DB 1 GluValylsLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
QY 147 TCGTGTAGCTCTCGATTTACTTTTCAGTGGCTACTGATGTTGGTCCGCCAGTCT 206  
DB 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40  
QY 207 CCAGAGAAGGGCTTCAGTGGTTCGTAATTCAGATTCGAAATTCGATTAATTCACA 266  
DB 41 ProGluylsGlyLeuGluTrpValAlaGluValylsLeuLysSerAsnTyrProThr 60  
QY 267 CATTATCGGAGTCTGTGAAGGAAAGTTCACCATCTCAAGAGATGATTCGAAAGTCTGT 326  
DB 61 HisTyrAlaGluSerVallylsGlyArgPheThrAlaSerArgAspSerLysSerSer 80  
QY 327 CTCTACTGCAATGACACAGCTTAAGAGCTGAAGCAGTGGAGTTTATTACTGTACAGAT 386  
DB 81 IleTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrPheCysThrPhe 100  
QY 387 TTCATAGACTGGGGCCAGGACACTA 410  
DB 101 TrpAspTyrTrpGlyArgGlyThr 108

## RESULT 10

US-08-483-749A-2  
; Sequence 2, Application US/08483749A  
; Patent No. 6054561  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
; CITY: EMERYVILLE  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,749A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL B.  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0508.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-749A-2

Alignment Scores:  
Pred. No.: 5e-52 Length: 122  
Score: 490.00 Matches: 93



```
Percent Similarity: 86.44% Conservative: 9
Best Local Similarity: 78.81% Mismatches: 4
Query Match: 65.07% Indels: 12
DB: 3 Gaps: 2

US-09-674-716B-1 (1-415) x US-08-483-749A-2 (1-122)

QY 87 GAAGTGAAGCTTGGAGGCTGCGAGGAGCTTGGTGCACCTGGAGGATCCATGAACTC 146
Db 1 GluValLysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyArgSerMetLysLeu 20
QY 147 TCCTGTAGCTCTGGATTACTTTACTTTCAGTGCTACTGATGCTCTGGTCCGCGAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAAGGGCTTGGAGTGGTCTGCTGAAATAGATTCAAACTGATAATTATGCAACA 266
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuLeuValLysSerAsnAsnTyrAlaThr 60
QY 267 CATTATGGGAGCTCTGTAAGGAGGAGTTCACCATCTCAAGAGATGATCCAAAAGTCGT 326
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTATTACTGTACA--- 383
Db 81 ValTyrLeuGlnLeuAsnAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysAlaArg 100
QY 384 -----GATTTCATAGACTGGGCGCAAGGGACA 410
Db 101 GluArgTyrLeuTyrTyrTyrThrMetAspTyr-----TrpGlyGlnGlyThr 116

RESULT 11
US-09-318-661-2
; Sequence 2, Application US/09318661
; Patent No. 6288488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-318-661-2

Alignment Scores:
Pred. No.: 1,238-51 Length: 298
Score: 488.00 Matches: 93
Percent Similarity: 85.84% Conservative: 4
Best Local Similarity: 82.30% Mismatches: 12
Query Match: 64.81% Indels: 4
DB: 3 Gaps: 1

US-09-674-716B-1 (1-415) x US-09-318-661-2 (1-298)

QY 87 GAAGTGAAGCTTGGAGGCTGCGAGGAGCTTGGTGCACCTGGAGGATCCATGAACTC 146
Db 156 GluValMetLeuValGluSerGlyGlyLeuValGlnProGlyGlyThrMetLysLeu 175
QY 147 TCCTGTAGCTCTGGATTACTTTACTTTCAGTGCTACTGATGCTCTGGTCCGCGAGTCT 206
Db 176 SerCysGluLeuSerGlyLeuThrPheArgAsnTyrTrpMetSerTrpValArgGlnSer 195
QY 207 CCAGAGAAGGGCTTGGAGTGGTCTGCTGAAATAGATTCAAACTGATAATTATGCAACA 266
Db 196 ProGluLysGlyLeuGluTrpValAlaGluLeuLeuValLysSerAsnTyrAlaThr 215
QY 267 CATTATGGGAGCTCTGTAAGGAGGAGTTCACCATCTCAAGAGATGATCCAAAAGTCGT 326
Db 216 HisTyrAlaGluSerValLysGlyLysPheThrIleSerArgAspSerLysSerArg 235
QY 327 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTATTACTGTACA--- 383
Db 236 LeuTyrLeuGlnMetAsnSerLeuArgThrGluAspThrGlyIleTyrTyrCysLysThr 255
QY 384 -----GATTTCATAGACTGGGCGCAAGGGACA 413
Db 256 TyrPheTyrSerPheSerTyrTrpGlyGlnGlyThrLeu 268

RESULT 13
```

US-08-192-102-5  
; Sequence 5, Application US/08192102  
; Patent No. 5656272  
; GENERAL INFORMATION:  
; APPLICANT: Le, Junming  
; APPLICANT: Vilcek, Jan  
; APPLICANT: Daddona, Peter E.  
; APPLICANT: Grayeb, John  
; APPLICANT: Knight, David M.  
; APPLICANT: Siegel, Scott A.  
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING  
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/192,102  
; FILING DATE: 04-FEB-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/192,093  
; FILING DATE: 04-FEB-1994  
; APPLICATION NUMBER: US 08/013,413  
; FILING DATE: 02-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/010,406  
; FILING DATE: 29-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,852  
; FILING DATE: 11-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/853,606  
; FILING DATE: 18-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/670,827  
; FILING DATE: 18-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: NY093-01M3  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-192-102-5

Alignment Scores:	Length:	119
Pred. No.:	1.07e-48	
Score:	463.00	90
Percent Similarity:	83.62%	Conservative: 7
Best Local Similarity:	77.59%	Mismatches: 9
Query Match:	61.49%	Indels: 10
DB:	1	Gaps: 2

US-09-674-716B-1 (1-415) x US-08-192-102-5 (1-119)

87 GAAGTGAAGTTCGAGGAGTCTGGTGCACACCTGGAGGATCCATGAATC 146  
|||||

Db . 1 GluVallylsLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
Qy 147 TCCTGTGTACCTCTGATTTACTTTCAGTGGTACTGATGCTCTGGTCCGCCAGTCT 206  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 21 SerCysValAlaSerGlyPheIlePheSerAsnHisTrpMetAsnTrpValArgGlnSer 40  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 207 CCAGAGAAGGGCTTGAGTGGTGTCTGAAATAGATTGAATCTGATTAATATGCAACA 266  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 41 ProGlnLysGlyLeuGlnTrpValAlaGluIleArgSerLysSerIleAsnSerAlaThr 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 267 CATTATCGGAGTCTGTGAAAGGAAAGTTCAACCATCTCAAGAGATGATCCAAAAGTCGT 326  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 HistyAlaGluSerVallylsGlyA:GpheThrIleSerArgAspSerLysSerAla 80  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA--- 383  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 81 ValTyrLeuGlnMetThrAspLeuA:GThrGluAspThrGlyValTyrCysSerArg 100  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 384 -----GATTTTCATAGACTGGGGCCCAAGGGACA 410  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 101 AsnTyrTyrGlySerThrTyrAspTyr-----TipGlyGlnGlyThr 114  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
RESULT 14  
US-08-324-799-5  
; Sequence 5, Application US/08324799  
; Patent No. 5698195  
; GENERAL INFORMATION:  
; APPLICANT: Le, Junming  
; APPLICANT: Vilcek, Jan  
; APPLICANT: Daddona, Peter E.  
; APPLICANT: Grayeb, John  
; APPLICANT: Knight, David M.  
; APPLICANT: Siegel, Scott A.  
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND PEPTIDES  
; TITLE OF INVENTION: OF HUMAN TUMOR NECROSIS FACTOR  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/324,799  
; FILING DATE: 18-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/192,093  
; FILING DATE: 04-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/192,102  
; FILING DATE: 04-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/192,861  
; FILING DATE: 04-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/013,413  
; FILING DATE: 02-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/010,406  
; FILING DATE: 29-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,852  
; FILING DATE: 11-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/853,606  
; FILING DATE: 18-MAR-1992  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/670,827  
FILING DATE: 18-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: NYU93-01M4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-324-799-5

Alignment Scores:  
Pred. No.: 1,07e-48 Length: 119  
Score: 463.00 Matches: 90  
Percent Similarity: 83.62% Conservative: 7  
Best Local Similarity: 77.59% Mismatches: 9  
Query Match: 61.49% Indels: 10  
DB: 1 Gaps: 2

US-09-674-716B-1 (1-415) x US-08-324-799-5 (1-119)

QY 87 GAAGTGAAGCTTGAAGAGCTTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAATC 146  
Db 1 GluValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
QY 147 TCCTGTGAGCTCTGGATTACTTTTCAGTGCTACTGATCTGTGGTCCGCCAGTCT 206  
Db 21 SerCysValAlaSerGlyPheIlePheSerAsnHisTrpMetAsnTrpValArgGlnSer 40  
QY 207 CCAGAGAAGGGCTTGAAGGAGTTCACCATCTCAAGAGATGATTCGAATATGATCAACA 266  
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgSerLysSerIleAsnSerAlaThr 60  
QY 267 CATTATCGGAGTCTGTGAAGGAGGAGTTCACCATCTCAAGAGATGATTCGAATATGATCAACA 326  
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerAla 80  
QY 327 CTCTACTGCAATGAACAGCTTAAGAGCTGAACAGCTGAACAGCTGAATTTACTGTACA--- 383  
Db 81 ValTyrLeuGlnMetThrAspLeuArgThrGluAspThrGlyValTyrTyrCysSerArg 100  
QY 384 -----GATTTCATAGACTGGGCCCAAGGACA 410  
Db 101 AsnTyrTyrGlySerThrTyrAspTyr-----TrpGlyGlnGlyThr 114

Search completed: September 30, 2004, 09:31:33

APPLICATION NUMBER: US 07/670,827  
FILING DATE: 18-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: NYU93-01M4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-324-799-5

Alignment Scores:  
Pred. No.: 1,07e-48 Length: 119  
Score: 463.00 Matches: 90  
Percent Similarity: 83.62% Conservative: 7  
Best Local Similarity: 77.59% Mismatches: 9  
Query Match: 61.49% Indels: 10  
DB: 1 Gaps: 2

US-09-674-716B-1 (1-415) x US-08-324-799-5 (1-119)

QY 87 GAAGTGAAGCTTGAAGAGCTTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAATC 146  
Db 1 GluValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
QY 147 TCCTGTGAGCTCTGGATTACTTTTCAGTGCTACTGATCTGTGGTCCGCCAGTCT 206  
Db 21 SerCysValAlaSerGlyPheIlePheSerAsnHisTrpMetAsnTrpValArgGlnSer 40  
QY 207 CCAGAGAAGGGCTTGAAGGAGTTCACCATCTCAAGAGATGATTCGAATATGATCAACA 266  
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgSerLysSerIleAsnSerAlaThr 60  
QY 267 CATTATCGGAGTCTGTGAAGGAGGAGTTCACCATCTCAAGAGATGATTCGAATATGATCAACA 326  
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerAla 80  
QY 327 CTCTACTGCAATGAACAGCTTAAGAGCTGAACAGCTGAACAGCTGAATTTACTGTACA--- 383  
Db 81 ValTyrLeuGlnMetThrAspLeuArgThrGluAspThrGlyValTyrTyrCysSerArg 100  
QY 384 -----GATTTCATAGACTGGGCCCAAGGACA 410  
Db 101 AsnTyrTyrGlySerThrTyrAspTyr-----TrpGlyGlnGlyThr 114

RESULT 15  
US-08-192-861A-5  
Sequence 5, Application US/08192861A  
Patent No. 5919452  
GENERAL INFORMATION:  
APPLICANT: Le, Junming  
APPLICANT: Vilcek, Jan  
APPLICANT: Daddona, Peter E.  
APPLICANT: Grayeb, John  
APPLICANT: Knight, David M.  
APPLICANT: Siegel, Scott A.  
TITLE OF INVENTION: METHODS OF TREATING TNF-MEDIATED DISEASE USING  
TITLE OF INVENTION: CHIMERIC ANTI-TNF ANTIBODIES (As Amended)  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:

Thu Sep 30 13:18:40 2004

us-09-674-716b-1.ra1

Page 10

Job time : 13.1499 secs

GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:29:27; Search time 17.3249 Seconds  
(without alignments)  
4852.647 Million cell updates/sec

Title: US-09-674-716B-2

Perfect score: 785

Sequence: 1 aagctttacagtactacgc.....agttggaataaaacgtacg 437

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cnp2.1/USPTO.spool.p/US09674716/runat.30092004.070259.25882/app.query.fasta\_1.3164  
-DB=PIR\_78 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODES=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09674716 @CNP 1.152 @runat.30092004.070259.25882 -NCPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	601	76.6	120	1 KVM567	Ig kappa chain pre
2	558	71.1	120	2 A29775	Ig kappa chain pre
3	542	69.0	113	1 KVM516	Ig kappa chain v r
4	539	68.7	113	1 KVM551	Ig kappa chain v r
5	522	66.5	120	2 B29775	Ig kappa chain pre
6	503	64.1	136	2 S40357	Ig kappa chain v-j
7	492	62.7	131	2 S40372	Ig kappa chain v-j
8	489	62.3	132	2 S26882	Ig kappa chain v r
9	487	62.0	133	2 S23230	Ig kappa chain pre
10	486	61.9	142	2 S22902	Ig kappa chain v r
11	485	61.8	135	2 S40342	Ig kappa chain - h
12	483	61.5	197	2 S29593	Ig kappa chain (MM
13	479	61.0	133	1 K2HURP	Ig kappa chain pre
14	479	61.0	133	2 S40324	Ig kappa chain v r

15 477.5 60.8 130 2 S40321 Ig kappa chain - h  
16 476 60.6 135 2 S40356 Ig kappa chain - h  
17 475 60.5 133 2 S42611 HUNK protein prec  
18 473.5 60.3 140 2 S22658 Ig kappa chain pre  
19 469.5 59.8 126 2 S40339 Ig kappa chain - h  
20 466 59.4 120 2 D29775 Ig kappa chain pre  
21 466 59.4 136 2 S40312 Ig kappa chain - h  
22 465 59.2 133 1 A24452 Ig kappa chain pre  
23 464 59.1 132 2 S40322 Ig kappa chain - h  
24 456.5 58.2 127 2 S40323 Ig kappa chain v r  
25 451 57.5 112 2 FL0275 Ig kappa chain pre  
26 448.5 57.1 131 2 B30577 Ig kappa chain pre  
27 447.5 57.0 131 2 D34904 Ig kappa chain pre  
28 446.5 56.9 131 2 B32513 Ig kappa chain pre  
29 446 56.8 120 2 C29775 Ig kappa chain pre  
30 444 56.6 112 2 T26317 Ig kappa chain v r  
31 443 56.4 128 2 S40373 Ig kappa chain - h  
32 442.5 56.4 131 2 B34904 Ig kappa chain pre  
33 442 56.3 112 2 F26317 Ig kappa chain v r  
34 442 56.3 122 2 S40338 Ig kappa chain - h  
35 441 56.2 112 2 D26317 Ig kappa chain v r  
36 439.5 56.0 132 2 PH0106 anti-digoxin trans  
37 439 55.9 112 2 B26317 Ig kappa chain v r  
38 439 55.9 112 2 A26317 Ig kappa chain v r  
39 438.5 55.9 131 2 C34904 Ig kappa chain pre  
40 438 55.8 112 2 G26317 Ig kappa chain v r  
41 437.5 55.7 126 2 S40341 Ig kappa chain - h  
42 437.5 55.7 131 2 G34903 Ig kappa chain pre  
43 436.5 55.6 131 2 B39276 Ig light chain pre  
44 435 55.4 113 1 K2HUTM Ig kappa chain v-i  
45 433.5 55.2 121 2 S24205 Ig kappa chain v r

#### ALIGNMENTS

##### RESULT 1

KVM567

Ig kappa chain precursor V region (VK167) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 21-Jan-2000

C:Accession: A01909

R:Selsing, E.; Storb, U.

Cell 25, 47-58, 1981

A>Title: Somatic mutation of immunoglobulin light-chain variable-region genes.

A:Reference number: A01909; MUID:82002223; PMID:6791832

A:Accession: A01909

A:Molecule type: DNA

A:Residues: 1-120 <SEL>

A>Note: the sequence was determined from the germline gene

C:Genetics: 17/1

A:Introns: 17/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>

F:136-115/Domain: immunoglobulin homology <IMM>

F:143-113/Disulfide bonds: #status predicted

Alignment Scores:  
Pred. No.: 1.31e-51 Length: 120  
Score: 601.00 Matches: 117  
Percent Similarity: 99.17% Conservative: 2  
Best Local Similarity: 97.50% Mismatches: 1  
Query Match: 76.56% Indels: 0  
DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KVM567 (1-120)

Qy 36 ATGAGGTCCTGTCAGTTCTGGGGTCTTATGTCCTGATCTCTGGAGTCAGTGGG 95

Db 1 MetArgCysSerLeuGlnPheLeuGlyValIleuMetPheIrrIleSerGlyValSerCly 20

```
QY 96 GATATTGTGATACCCAGGATGAACCTCAATCCTGTCTCACTTCTGGAGAAATCAGTTTCC 155
Db 21 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 40

QY 156 ATCTCTGCAGGCTCTAGTAAAGATCTCTGTATAGATGGGAAGACATACCTGTAATGG 215
Db 41 IleSerCysArgSerSerLysLeuLeuTyLysAspGlyLysThrTyLysLeuAsnTrp 60

QY 216 TTCTCTCAGAGACCCAGACATCTCTCAGCTCCTCATGATGATTTAGTGTCCACCGTGCA 275
Db 61 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80

QY 276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTCAAGGACAGATTTCCACCTGGAAATC 335
Db 81 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle 100

QY 336 ACTAGAGTGAAGCTGAGGATGGGTGTGTTACTCTCAACACTTGTAGAGTATCCA 395
Db 101 SerArgValLysAlaGluAspValGlyValTyLysCysGlnGlnLeuValGluTyPro 120

RESULT 2
A29775
Ig kappa chain precursor V region (mouse 24.2) - shrew mouse
C:Species: Mus pahari
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C:Accession: A29775
R:Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A:Title: Evolution of a V-kappa gene family.
A:Reference number: A91751; MUID:87006895; PMID:3093373
A:Accession: A29775
A:Molecule type: DNA
A:Residues: 1-120 <JOU>
A:Cross-references: GB:M15552; NID:g197468; PIDN:AAA39036.1; PID:g197469
A:Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region 24.2 #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,45e-47 Length: 120
Score: 558.00 Matches: 107
Percent Similarity: 96.67% Conservative: 9
Best Local Similarity: 89.17% Mismatches: 4
Query Match: 71.08% Indels: 0
DB: Gaps: 0

US-09-674-716B-2 (1-437) x A29775 (1-120)

QY 36 ATGAGTCTCTCTTCTCAGTTCTCTGGGGTCTTATGTTCTGATCTCTGAGTCAAGTGG 95
Db 1 MetArgHisSerLeuGlnPheLeuGlyLeuLeuLeuPheCysIleSerGlyValSerGly 20

QY 96 GATATTGTGATACCCAGGATGAACCTCAATCCTGTCTCACTTCTGGAGAAATCAGTTTCC 155
Db 21 AspValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 40

QY 156 ATCTCTGCAGGCTCTAGTAAAGATCTCTGTATAGATGGGAAGACATACCTGTAATGG 215
Db 41 IleSerCysArgSerSerLysLeuLeuTyLysAspGlyLysThrTyLysLeuAsnTrp 60

QY 216 TTCTCTCAGAGACCCAGACATCTCTCAGCTCCTCATGATGATTTAGTGTCCACCGTGCA 275
Db 61 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80

QY 276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTCAAGGACAGATTTCCACCTGGAAATC 335
Db 81 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle 100

QY 336 ACTAGAGTGAAGCTGAGGATGGGTGTGTTACTCTCAACACTTGTAGAGTATCCA 395
Db 101 SerArgValLysAlaGluAspValGlyValTyLysCysGlnGlnLeuValGluTyPro 120

RESULT 4
KWMS16
Ig kappa chain V region (M511) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C:Accession: A01910
R:Appella, E.
Mol. Immunol. 17, 711-718, 1980
A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine
A:Reference number: A01910; MUID:81052016; PMID:6776396
A:Accession: A01910
A:Molecule type: protein
A:Residues: 1-113 <APP>
```

```
QY 336 ACTAGAGTGAAGCTGAGGATGGGTGTGTTACTCTCAACACTTGTAGAGTATCCA 395
Db 101 SerArgValGluAlaGluAspValGlyValTyLysCysGlnGlnLeuValGluTyPro 120

RESULT 3
KWMS16
Ig kappa chain V region (M167) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
C:Accession: A01908
R:Rudikoff, S.; Potter, M.
Biochemistry 17, 2703-2707, 1978
A:Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma protein
A:Reference number: A01908; MUID:79000273; PMID:99160
A:Accession: A01908
A:Molecule type: protein
A:Residues: 1-112 <RUD>
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la-
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 9,5e-46 Length: 112
Score: 542.00 Matches: 106
Percent Similarity: 97.32% Conservative: 3
Best Local Similarity: 94.64% Mismatches: 3
Query Match: 69.04% Indels: 0
DB: Gaps: 0

US-09-674-716B-2 (1-437) x KWMS16 (1-112)

QY 96 GATATTGTGATACCCAGGATGAACCTCAATCCTGTCTCACTTCTGGAGAAATCAGTTTCC 155
Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20

QY 156 ATCTCTGCAGGCTCTAGTAAAGATCTCTGTATAGATGGGAAGACATACCTGTAATGG 215
Db 21 IleSerCysArgSerSerLysLeuLeuTyLysAspGlyLysThrTyLysLeuAsnTrp 40

QY 216 TTCTCTCAGAGACCCAGACATCTCTCAGCTCCTCATGATGATTTAGTGTCCACCGTGCA 275
Db 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60

QY 276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTCAAGGACAGATTTCCACCTGGAAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle 80

QY 336 ACTAGAGTGAAGCTGAGGATGGGTGTGTTACTCTCAACACTTGTAGAGTATCCA 395
Db 81 SerArgValLysAlaGluAspValGlyValTyLysCysGlnGlnLeuValGluTyPro 100

QY 396 TTCACGTCGCGCTCGGGGACAAAGTTGGAAATAAAA 431
Db 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuLys 112

RESULT 4
KWMS1
Ig kappa chain V region (M511) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C:Accession: A01910
R:Appella, E.
Mol. Immunol. 17, 711-718, 1980
A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine
A:Reference number: A01910; MUID:81052016; PMID:6776396
A:Accession: A01910
A:Molecule type: protein
A:Residues: 1-113 <APP>
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Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 336 AGTAGAGTGAAGCTGAGATGGGTGGTGTATTACTGCAACACTGTGAGAGTATCCA 395  
 Db 101 SerArgValGluAlaGluAspValGlyValTyTyCysMetGlnAlaLeuGlnThrPro 120  
 QY 396 TTCACCTTCGGCTCGGGGCAAGTGGAAATAAAACGTAACG 437  
 Db 121 TrpThrPheGlyGlnGlyThrLysValGluLeuLysArgThr 134

## RESULT 7

S40372  
 Ig kappa chain V-J region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S40372  
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A:Reference number: S40312; MUID:94080891; PMID:8258341  
 A:Accession: S40372  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-131 <KDE>  
 A:Cross-references: EMBL:X72482; NID:g441432; PIDN:CAA51150.1; PID:g441433  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:36-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 8,98e-41 Length: 131  
 Score: 492.00 Matches: 93  
 Percent Similarity: 83.97% Conservative: 17  
 Best Local Similarity: 70.99% Mismatches: 21  
 Query Match: 62.68% Indels: 0  
 Gaps: 0

US-09-674-716B-2 (1-437) X S40372 (1-131)

QY 36 ATGAGGTTCTCTGTTTCAGTTTCGGGGTCTTATGTTCTGATCTCTGAGTCAGTGG 95  
 Db 1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValSerGlySerGly 20  
 QY 96 GATATTGTGATACCCAGAGTGAACCTCCATCTCTGCTCAGTCTGGAGAACTTC 155  
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluSerAlaSer 40  
 QY 156 ATCTCTGATACCCAGAGTGAACCTCCATCTCTGCTCAGTCTGGAGAACTTC 155  
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluSerAlaSer 40  
 QY 156 ATCTCTGATACCCAGAGTGAACCTCCATCTCTGCTCAGTCTGGAGAACTTC 155  
 Db 41 PheSerCysIleThrSerGlnSerLeuLeuHisSerAsnGlyHisAsnTyLeuAspTrp 60  
 QY 216 TTCTCGACAGACAGACAAATCTCTCAGTCTCTGATGTTGATGTTCCACCGTGA 275  
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80  
 QY 276 TCAGGAGTCTCAGACCGGTTTACTGTCAGTGGGTGAGGACAGATTCACCTGGAATC 335  
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 336 AGTAGAGTGAAGCTGAGATGGGTGGTGTATTACTGCAACACTGTGAGAGTATCCA 395  
 Db 101 SerArgValGluAlaGluAspValGlyValTyTyCysMetGlnProLeuGlnThrPro 120  
 QY 396 TTCACCTTCGGCTCGGGGCAAGTGGAAATA 428  
 Db 121 TyrThrPheGlyGlnGlyThrLysValGluLeuLysile 131

## RESULT 8

S26882  
 Ig kappa chain V region (V607) - human  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
 C:Accession: S26882

R:Weichhold, G.M.; Klobbeck, H.G.; Ohnheiser, R.; Combriato, G.; Zachau, H.G.  
 Nature 347, 90-92, 1990  
 A:Title: Megabase inversions in the human genome as physiological events.  
 A:Reference number: S26882; MUID:90370099; PMID:2118596  
 A:Accession: S26882  
 A:Status: preliminary; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-132 <MEI>  
 A:Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367  
 C:Genetics: 17/1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:36-115/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.: 1,79e-40 Length: 132  
 Score: 489.00 Matches: 94  
 Percent Similarity: 82.58% Conservative: 15  
 Best Local Similarity: 71.21% Mismatches: 23  
 Query Match: 62.29% Indels: 0  
 Gaps: 0

US-09-674-716B-2 (1-437) X S26882 (1-132)

QY 36 ATGAGGTTCTCTGTTTCAGTTTCGGGGTCTTATGTTCTGATCTCTGAGTCAGTGG 95  
 Db 1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValSerGlySerGly 20  
 QY 96 GATATTGTGATACCCAGAGTGAACCTCCATCTCTGCTCAGTCTGGAGAACTTC 155  
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40  
 QY 156 ATCTCTGAGTCTAGTAGAGTCTCTGATAGAGTCTCTGATAGAGTGGGAGACATCTGATGG 215  
 Db 41 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyAsnTyLeuAspTrp 60  
 QY 216 TTCTCGACAGACAGACAAATCTCTCAGTCTCTGATGTTGATGTTCCACCGTGA 275  
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80  
 QY 276 TCAGGAGTCTCAGACCGGTTTACTGTCAGTGGGTGAGGACAGATTCACCTGGAATC 335  
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 336 AGTAGAGTGAAGCTGAGATGGGTGGTGTATTACTGCAACACTGTGAGAGTATCCA 395  
 Db 101 SerArgValGluAlaGluAspValGlyValTyTyCysMetGlnAlaLeuGlnThrPro 120  
 QY 396 TTCACCTTCGGCTCGGGGCAAGTGGAAATAAAA 431  
 Db 121 GlnThrPheGlyGlnGlyThrLysValGluLeuLysile 132

## RESULT 9

S23230  
 Ig kappa chain precursor V-J region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S23230  
 R:Kennedy, M.A.  
 J. Exp. Med. 173, 1033-1036, 1991  
 A:Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and light  
 A:Reference number: S23230; MUID:91178498; PMID:1840606  
 A:Accession: S23230  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-133 <KEN>  
 A:Cross-references: EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:g34000  
 C:Genetics: 17/1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:36-115/Domain: immunoglobulin homology <IMM>





A;Reference number: A93588; MUID:86041852; PMID:2997711  
A;Accession: A01890

A;Reference number: S40324; MOJID:94080591; FMIJ:6235351  
A;Accession: S40324

Alignment Scores:	2.48e-39	Length:	130
Pred. No.:	Score:	Matches:	93
	477.50	Conservative:	15
Percent Similarity:	83.08%	Mismatches:	21
Best Local Similarity:	71.54%	Indels:	1
Query Match:	60.83%	Gaps:	1
DB:	2		

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:20:22 ; Search time 9.48126 Seconds  
(without alignments)  
4799.922 Million cell updates/sec

Title: US-09-674-716B-2  
Perfect score: 785  
Sequence: 1 aagttttacagttactacgc.....agttggaaataaaacgtacg 437

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xl  
-Q/cgn2\_1/USPTO\_spool\_p/US09674716/runat\_30092004\_070257\_25855/app\_query.fasta\_1.3164  
-DB=SwissProt\_42 -Qfmt=fastan -SUFFIX=rs -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=EPT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09674716 @CGN 1.1.82 @runat\_30092004\_070257\_25855 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEVO\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	601	76.6	120	1 KV2B_MOUSE	P01627 mus musculu
2	542	69.0	112	1 KV2A_MOUSE	P01626 mus musculu
3	539	68.7	113	1 KV2C_MOUSE	P01628 mus musculu
4	479	61.0	133	1 KV2F_HUMAN	P06310 homo sapien
5	435	55.4	113	1 KV2D_HUMAN	P01617 homo sapien
6	431	54.9	113	1 KV2E_MOUSE	P01630 mus musculu
7	431	54.9	117	1 KV2E_HUMAN	P08309 homo sapien
8	427.5	54.5	115	1 KV2A_HUMAN	P01614 homo sapien
9	427	54.4	113	1 KV2B_MOUSE	P03976 mus musculu
10	422	53.8	113	1 KV2B_HUMAN	P01615 homo sapien
11	417	53.1	112	1 KV2D_MOUSE	P01629 mus musculu
12	400	51.0	113	1 KV2G_MOUSE	P01631 mus musculu
13	398.5	50.8	112	1 KV2C_HUMAN	P01616 homo sapien
14	398.5	50.8	134	1 KV4B_HUMAN	P06313 homo sapien
15	378	48.2	133	1 KV4B_HUMAN	P06313 homo sapien
16	357.5	45.5	114	1 KV4A_HUMAN	P01625 homo sapien
17	353.5	45.0	108	1 KV1_CANFA	P01618 canis famil
18	351	44.7	129	1 KV3L_HUMAN	P18135 homo sapien

19	350	44.6	129	1 KV3M_HUMAN	P18136 homo sapien
20	348.5	44.4	128	1 KV5E_MOUSE	P01637 mus musculu
21	339.5	43.2	128	1 KV3K_HUMAN	P06311 homo sapien
22	337.5	43.0	121	1 KV40_HUMAN	P06312 homo sapien
23	336.5	42.9	129	1 KV1W_HUMAN	P04331 homo sapien
24	336.5	42.9	131	1 KV3I_MOUSE	P01661 mus musculu
25	335.5	42.7	132	1 KV3F_MOUSE	P01658 mus musculu
26	334.5	42.6	111	1 KV3M_MOUSE	P01665 mus musculu
27	333.5	42.5	149	1 KV5A_MOUSE	P01633 mus musculu
28	333	42.4	129	1 KV3H_HUMAN	P04207 homo sapien
29	329.5	42.0	111	1 KV3Q_MOUSE	P01667 mus musculu
30	325.5	41.5	111	1 KV3L_MOUSE	P01664 mus musculu
31	323.5	41.2	111	1 KV3N_MOUSE	P01666 mus musculu
32	322.5	41.1	109	1 KV4D_HUMAN	P83593 homo sapien
33	322.5	41.1	111	1 KV3Q_MOUSE	P01669 mus musculu
34	320.5	40.8	111	1 KV3U_MOUSE	P01673 mus musculu
35	320	40.8	110	1 KV3P_MOUSE	P01668 mus musculu
36	319	40.6	108	1 KV3A_HUMAN	P01619 homo sapien
37	319	40.6	109	1 KV3D_HUMAN	P01622 homo sapien
38	315.5	40.2	111	1 KV3E_MOUSE	P01671 mus musculu
39	315	40.1	136	1 KV5E_MOUSE	P01634 mus musculu
40	313.5	39.9	111	1 KV3R_MOUSE	P01670 mus musculu
41	312	39.7	109	1 KV3B_HUMAN	P01620 homo sapien
42	310	39.5	109	1 KV3E_HUMAN	P01623 homo sapien
43	309	39.4	109	1 KV3G_HUMAN	P04206 homo sapien
44	308.5	39.3	111	1 KV3C_MOUSE	P01656 mus musculu
45	306.5	39.0	111	1 KV3T_MOUSE	P01672 mus musculu

#### ALIGNMENTS

RESULT 1  
KV2B\_MOUSE  
ID KV2B\_MOUSE STANDARD; PRT; 120 AA.  
AC P01627;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region vkappa167 precursor.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82002223; PubMed=6791832;  
RA Selsing E., Storb U;  
RT "Somatic mutation of immunoglobulin light-chain variable-region  
genes.";  
RL Cell 25:47-58(1981).  
CC -----  
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CC -----  
DR EMBL; J00562; AAA39032.1; -;  
DR EMBL; K02415; AAA39051.1; -;  
DR PIR; A01909; KWSG67.  
DR HSP; P80362; IWTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IGLIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 120 IG KAPPA CHAIN V-II REGION VKAPPA167.  
FT DOMAIN 21 43 FRAMEWORK-1.  
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 60 74 FRAMEWORK-2.  
 FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 82 113 FRAMEWORK-3.  
 FT DOMAIN 114 120 COMPLEMENTARITY-DETERMINING-3.  
 FT DISULFID 43 113 BY SIMILARITY.  
 SQ SEQUENCE 120 AA; 13280 MW; 63BB571F084D3E8 CRC64;

Alignment Scores:  
 Pred. No.: 6,95e-57 Length: 120  
 Score: 601.00 Matches: 117  
 Percent Similarity: 99.17% Conservative: 2  
 Best Local Similarity: 97.50% Mismatches: 1  
 Query Match: 76.56% Indels: 0  
 DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2B\_MOUSE (1-120)

QY 36 ATGAGTCTCTGTTTCAGTTCTGGGGTCTTATGTTCTGATCTCTGGAGTCAGTGGG 95  
 DB 1 MetArgCysSerLeuGlnPheLeuGlyValLeuMetPheTrpIleSerGlyValSerGly 20  
 QY 96 GATATTGTGATACCCAGGATGAACTCTCCATCTCTGCTCAGTCTGGAGATCAGTTTCC 155  
 DB 21 AspIleValIleThrGlnAspGluSerAsnProValThrSerGlyGluSerValSer 40  
 QY 156 ATCTCTCGAGGCTAGTAAAGAGTCTCTGTTATAGGATGGGAAGACATACCTGAATTGG 215  
 DB 41 IleSerCysArgSerSerLysSerLeuValLysAspGlyValThrTyrLeuAsnTrp 60  
 QY 216 TTTCTCAGAGACAGGACAACTCTCAGCTCTGATGATTTGATGTCACCCGTGCA 275  
 DB 61 PheLeuGlnArgProGlnSerProGlnLeuLeuIleTyrLeuMetSerThrArgala 80  
 QY 276 TCAGGAGTCTCAGCCGTTTACTGTCAGTGGTGGGACAGATTCACCTGGAAATC 335  
 DB 81 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLe 100  
 QY 336 AGTAGAGTGAAGCTCAGGATGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395  
 DB 101 SerArgValLysAlaGluAspValGlyValTyrCysGlnGlnLeuValGluTyrPro 120

## RESULT 2

KV2A\_MOUSE STANDARD; PRT; 112 AA.  
 ID KV2A\_MOUSE  
 AC P01626;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region MOPC 167.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RN SEQUENCE  
 RP MEDLINE=79000273; PubMed=99160;  
 RX Rudikoff S., Potter M.;  
 RA "kappa Chain variable region from M167, a phosphorylcholine binding  
 RT myeloma protein.";  
 RL Biochemistry 17:2703-2707(1978).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY  
 CC CHAIN HAS ALSO BEEN DETERMINED.  
 DR PIR; A01908; KWS16.  
 DR HSSP; P80362; IWTLL.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 DR Immunoglobulin v region.  
 KW DOMAIN 1 23  
 FT DOMAIN 24 39 FRAMEWORK-1.  
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 40 54 FRAMEWORK-2.  
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 62 93 FRAMEWORK-3.  
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.  
 FT DISULFID 103 112 BY SIMILARITY.  
 FT NON TER 112 112  
 SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;

Alignment Scores:  
 Pred. No.: 1.63e-50 Length: 112  
 Score: 542.00 Matches: 106  
 Percent Similarity: 97.32% Conservative: 3  
 Best Local Similarity: 94.64% Mismatches: 3  
 Query Match: 69.04% Indels: 0  
 DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2A\_MOUSE (1-112)

QY 96 GATATTGTGATACCCAGGATGAACTCTCCATCTCTGCTCAGTCTGGAGATCAGTTTCC 155  
 DB 1 AspIleValIleThrGlnAspGluSerAsnProValThrSerGlyGluSerValSer 20  
 QY 156 ATCTCTCGAGGCTAGTAAAGAGTCTCTGTTATAGGATGGGAAGACATACCTGAATTGG 215  
 DB 21 IleSerCysArgSerSerLysSerLeuValLysAspGlyValThrTyrLeuAsnTrp 40  
 QY 216 TTTCTCAGAGACAGGACAACTCTCAGCTCTGATGATTTGATGTCACCCGTGCA 275  
 DB 41 PheLeuGlnArgProGlnSerProGlnLeuLeuIleTyrLeuMetSerThrArgala 60  
 QY 276 TCAGGAGTCTCAGCCGTTTACTGTCAGTGGTGGGACAGATTCACCTGGAAATC 335  
 DB 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLe 80  
 QY 336 AGTAGAGTGAAGCTCAGGATGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395  
 DB 81 SerArgValLysAlaGluAspValGlyValTyrCysGlnGlnLeuValGluTyrPro 100  
 QY 396 TTCACGTCGCGCTCGGGGACAAAGTTGGAAATAAAA 431  
 DB 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuLys 112

## RESULT 3

KV2C\_MOUSE STANDARD; PRT; 113 AA.  
 ID KV2C\_MOUSE  
 AC P01628;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region MOPC 511.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RN SEQUENCE  
 RP MEDLINE=81052016; PubMed=6776396;  
 RX Appella E.;  
 RA "Amino acid sequence of the light chain variable region of M511, a  
 RT phosphorylcholine-binding murine myeloma protein.";  
 RL Mol. Immunol. 17:711-718(1980).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS PHOSPHORYLCHOLINE.  
 DR PIR; A01910; KWS11.  
 DR HSSP; P80362; IWTLL.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 DR Immunoglobulin v region.  
 KW DOMAIN 1 23  
 FT DOMAIN 24 23 FRAMEWORK-1.

```

FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Alignment Scores:
Pred. No.: 3 45e-50 Length: 113
Score: 539.00 Matches: 105
Percent Similarity: 96.48% Conservative: 4
Best Local Similarity: 92.92% Mismatches: 0
Query Match: 68.66% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2C_MOUSE (1-113)
QY 96 GATATTGTGATAACCCAGAGTAACTCTCCATCTCTGACCTCTGAGATCAGTTTCC 155
Db 1 AspIleValIleThrGlnAspGluSerLysProValThrSerGlyGluSerValSer 20
QY 156 ATCTCTCGAGTCTAGTAAGAGTCTCTGTATAGGATGGACACATCTTGAATTGG 215
Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrllysAspGlyLysThrTyrllysAsnTrp 40
QY 216 TTCTCTGCAGAGACCAAGCAATCTCTCAGCTCTCTGATGTTGATTCACCCCGTGCA 275
Db 41 PheLeuGlnGlyProGlnGlnSerProArgLeuLeuLeuTyrllysMetSerThrArgala 60
QY 276 TCAGAGTCTCAGACCGGTTAGTGGCAGTGGTCAGCAGACAGATTTCCACCTGGAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLeu 80
QY 336 AGTAGAGTCAAGGCTCAGAGTCTGGTGTGTATTACTGTCAACACTTGTAGAGTATCCA 395
Db 81 SerA-gValLysAlaGluAspValGlyValTyrllysGlnGlnLeuValGluTyrlPro 100
QY 396 TTCACGTTCCGTCGGGACAAAGTGGAAATAAAACGT 434
Db 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuTyrllysArg 113

RESULT 4
KV2F_HUMAN
ID KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2957711;
RA Klobeck H.G., Weindl A., Combrato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and III."
RL Nucleic Acids Res. 13:6499-6513(1985).
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DR PIR; A01890; K0HURP.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT CHAIN 21 133 FRAMEWORK-1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 59 FRAMEWORK-2.
FT DOMAIN 60 74 FRAMEWORK-3.
FT DOMAIN 75 81 FRAMEWORK-4.
FT DOMAIN 82 113 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Alignment Scores:
Pred. No.: 1 09e-43 Length: 133
Score: 479.00 Matches: 91
Percent Similarity: 79.70% Conservative: 15
Best Local Similarity: 68.42% Mismatches: 27
Query Match: 61.02% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2F_HUMAN (1-133)
QY 36 ATAGGTTCTCTCTTCTGATTTCTGGGTCCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
Db 1 MetArgLeuProAlaGlnLeuLeuMetLeuTrpValProGlySerSerGly 20
QY 96 GATATTCTGATAACCCAGGATGAATCTCCAACTCTGCTCACTCTCGAGAAATCAGTTTCC 155
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 40
QY 156 ATCTCTCGAGTCTAGTAAGAGTCTCTGATGTTGATTCACCCCGTGCA 215
Db 41 IleSerCysArgSerSerGlnSerLeuValTyrllysAspGlyAsnThrTyrlLeuAsnTrp 60
QY 216 TTCTCTGCAGAGACCAAGCAATCTCTCAGCTCTCTGATGTTGATTCACCCCGTGCA 275
Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuLeuLeuTyrllysValSerAsnArgAsp 80
QY 276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGTCAGGCACAGATTTCCACCTGGAATC 335
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
QY 336 AGTAGAGTCAAGGCTCAGAGTCTGGTGTGTATTACTGTCAACACTTGTAGAGTATCCA 395
Db 101 SerArgValGluAlaGluAspValGlyValTyrllysCysMetGlnGlyThrHisTrpSer 120
QY 396 TTCACGTTCCGTCGGGACAAAGTGGAAATAAAACGT 434
Db 121 TrpThrPheGlyGlnGlyThrLysValGluLeuLysArg 133

RESULT 5
KV2D_HUMAN
ID KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE (BENCE-JONES PROTEIN TEW).  
RX MEDLINE=74148480; PubMed=4596149;  
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;  
RT "Amino acid sequence of a kappa Bence Jones protein from a case of  
RT primary amyloidosis".  
RL Biochemistry 12:3763-3780(1973).  
RN [2]  
RN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).  
RP MEDLINE=7316638; PubMed=4700495;  
RX Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,  
RA Glenner G.G.;  
RT "Structural identity of Bence Jones and amyloid fibril proteins in a  
RT patient with plasma cell dyscrasia and amyloidosis.";  
RL J. Clin. Invest. 52:1276-1281(1973).  
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL  
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.  
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A  
CC PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
CC MARKER.  
DR PIR; A90370; K2HUTW.  
DR HSP; P01607; IREI.  
DR GO; G0:0005576; C:extracellular; NAS.  
DR GO; G0:0003823; F:antigen binding; NAS.  
DR GO; G0:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
DR Immunoglobulin V region; Bence-Jones protein; Amyloid.  
KW DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 55 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DOMAIN 23 93  
FT DISULFID 23 93  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;  
  
Alignment Scores:  
Pred. No.: 6,02e-39 Length: 113  
Score: 435.00 Matches: 82  
Percent Similarity: 84.96% Conservative: 14  
Best Local Similarity: 72.57% Mismatches: 17  
Query Match: 55.41% Indels: 0  
DB: 1 Gaps: 0  
  
US-09-674-716B-2 (1-437) x KV2D\_HUMAN (1-113)  
  
QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTGTCTCACTCTCGGAGATCAGTTTCC 155  
Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20  
  
QY 156 ATCTCTCGAGGCTCTAGTAAGAGTCTCTGTATAAGGATGGGAGACATACCTGGAATTGG 215  
Db 21 IleSerCysArgSerGlnSerLeuLeuHisSerAspGlyPheAspTyrLeuAsnTrp 40  
  
QY 216 TTCTCTCAGACAGCAGACATCTCTCAGCTGATGATTTATGATGATCCACCGTGCA 275  
Db 41 TyrLeuGlnArgProGlyGlnSerPro\*\*\*LeuLeuIleTyrAlaLeuSerAsnArgAla 60  
  
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTCCACCTGGAATC 335  
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLeuSile 80  
  
QY 336 AGTAGAGTGAAGCTGAGATGTGGGTGTGTTACTGTCAACAACCTGTAGAGTATCCA 395  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMet\*\*\*AlaLeuGlnAlaPro 100

QY 396 TTCAGTTCGGCTCGGGGACAAAGTTGGAAATAAAACGT 434  
Db 101 IleThrPheGlyGlnGlyThrArgLeuGluIleLysArg 113  
  
RESULT 6  
KV2F\_MOUSE  
ID\_KV2F\_MOUSE STANDARD; PRT; 113 AA.  
AC P01630;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region 7834.1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83256427; PubMed=6409088;  
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;  
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-  
RT light chains from a mouse hybridoma-derived anti-(streptococcal group  
RT A polysaccharide) antibody containing an additional cysteine residue.  
RT Application of the dimethylaminoazobenzene isothiocyanate technique  
RT for the isolation of peptides.";  
RL Biochem. J. 211:173-180(1983).  
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL  
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.  
DR PIR; A01913; KVM57S.  
DR HSP; P80362; IWTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
DR Immunoglobulin V region; Monoclonal antibody; Hybridoma.  
KW DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 55 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;  
  
Alignment Scores:  
Pred. No.: 1.63e-38 Length: 113  
Score: 431.00 Matches: 87  
Percent Similarity: 82.30% Conservative: 6  
Best Local Similarity: 76.99% Mismatches: 20  
Query Match: 54.90% Indels: 0  
DB: 1 Gaps: 0  
  
US-09-674-716B-2 (1-437) x KV2F\_MOUSE (1-113)

QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTGTCTCACTCTCGGAGATCAGTTTCC 155  
Db 1 AspIleValMetThrGlnThrAlaProSerAlaLeuValThrProGlyGluSerValSer 20  
  
QY 156 ATCTCTCGAGGCTCTAGTAAGAGTCTCTGTATAAGGATGGGAGACATACCTGGAATTGG 215  
Db 21 IleSerCysArgSerGlySerLeuLeuHisSerAsnGlyAsnThrTyrLeuTyrTrp 40  
  
QY 216 TTCTCTCAGACAGCAGACATCTCTCAGCTGATGATTTATGATGATCCACCGTGCA 275  
Db 41 PheLeuGlnArgProGlyGlnCysProGlnLeuLeuIleTyrArgMetSerAsnLeuAla 60  
  
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTCCACCTGGAATC 335  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAlaPheThrLeuArgIle 80



QY 336 AGTAGAGTGAAGCTGAGGATGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 395  
 Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlnArgGluTyrPro 100  
 QY 336 TTCAGTTCGGCTCGGACAAAGTTGGAATAAACCT 434  
 Db 101 TyrThrPheGlyGlyThrLysLeuGluLeuLysArg 113

RESULT 7  
 KV2E\_HUMAN STANDARD; PRT; 117 AA.  
 AC P06309;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region GM607 precursor (Fragment).  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84191506; PubMed=6325927;  
 RA Kloeck H.G., Solomon A., Zachau H.G.;  
 RT "Contribution of human V kappa II germ-line genes to light-chain  
 RT diversity."; <http://www.isb-sib.ch/announce/>  
 RL Nature 309:73-76(1984).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; Z00009; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A01889; K2HUGM.  
 DR HSSP; P80382; LWTU.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 4  
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.  
 FT DOMAIN 5 27 FRAMEWORK-1.  
 FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 44 58 FRAMEWORK-2.  
 FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 66 97 FRAMEWORK-3.  
 FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 107 116 FRAMEWORK-4.  
 FT DISULFID 27 117 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12664 MW; 92057DC719E558B1 CRC64;

Alignment Scores:  
 Pred. No.: 1,64e-38 Length: 117  
 Score: 431.00 Matches: 85  
 Percent Similarity: 83.76% Conservative: 13  
 Best Local Similarity: 72.65% Mismatches: 19  
 Query Match: 54.90% Indels: 0  
 DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2E\_HUMAN (1-117)

QY 84 GGAGTCAGTGGGATATTGTGATTAACCCAGGATGAATCTCCAAATCCTGTCACTTCTGGA 143  
 Db 1 GlySerSerGlyAspIleValMetThrGlnSerProLeuSerLeuProValThrProGly 20  
 QY 144 GAATCAGTTTCCATCTCCAGCTCTAGTAAGAGTCTCTGTATATAAGATGGGAAGACA 203  
 Db 21 GluProAlaSerIleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsn 40  
 QY 204 TACTGAATTGGTTTCTGAGAGACCAGGACAAATCTCCTCAGCTCCTGTATTTGATG 263  
 Db 41 TyrLeuAspTyrLeuGlnLysProGlnGlnSerProGlnLeuLeuIleTyrLeuGly 60  
 QY 264 TCCACCGCTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCCAGCAGATTTTC 323  
 Db 61 SerAsnArgAlaSerGlyValProAspArgPheSerGlySerGlyThrAspPhe 80  
 QY 324 ACCCTGGAATCAGTAGAGTGAAGGCTGAGGATGTCGGTGTGTATTACTGTCAACAATT 383  
 Db 81 ThrLeuLysIleSerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnGly 100  
 QY 384 GTAGATATCCATTCAGTTCGGCTCGGACAAAGTTGGAATAAAACGT 434  
 Db 101 LeuGlnThrProGlnThrPheGlyGlnGlyThrLysValGluLeuLysArg 117

RESULT 8  
 KV2A\_HUMAN STANDARD; PRT; 115 AA.  
 AC P01614;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region Cum.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=68242259; PubMed=5586923;  
 RA Hilschmann N.;  
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-  
 RT type).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
 RN [2]  
 RP REVISIONS TO 50; 52; 96 AND 97.  
 RX MEDLINE=70063440; PubMed=4188189;  
 RA Hilschmann N.;  
 RT "Molecular basis of antibody formation."  
 RL Naturwissenschaften 56:195-205(1969).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PIR; B91639; K2HUCM.  
 DR HSSP; P01607; 1REI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DISULFID 24 95 BY SIMILARITY.  
 FT NON\_TER 115 115  
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Alignment Scores:  
 Pred. No.: 3.9e-38 Length: 115  
 Score: 427.50 Matches: 85  
 Percent Similarity: 84.21% Conservative: 11  
 Best Local Similarity: 74.56% Mismatches: 17  
 Query Match: 54.46% Indels: 1  
 DB: 1 Gaps: 1

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US-09-674-716B-2 (1-437) x KV2A_HUMAN (1-115)
QY 96 GATATTGTGATACCCAGGAGTAACCTCTCAATCTCTGTCAGTCTCTGGAGAAATCAGTTTCC 155
DB 2 AspIleValMetThrGlnThrProLeuSerLeuProValThrProGlyLeuProAlaSer 21
QY 156 ATCTCTGAGGCTAGTAAAGTCTCTGTATAAG--GATGGGAGACATCTGAT 212
DB 22 ILeSerCysArgSerGlnSerLeuAspSerGlyAspGlyAsnThrTyrLeuAsn 41
QY 213 TGGTTTCTGAGAGACAGGACAAATCTCTCAGCTCTCTGATGATTGATGTCACCCCGT 272
DB 42 TriTy-LeuGlnLysAlaGlyGlnSerProGlnLeuLeuIleTyrThrLeuSerTyrArg 61
QY 273 GCATCAGGAGTCTCAGACCGGTTTAGTCAGTGGTTCAGGACAGATTTCCACCTGGAA 332
DB 62 AlaSerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLys 81
QY 333 ATCAGTAGAGTGAAGCTCAGAGTGGGTGTATTACTGTCAACAACCTGTAGAGTAT 392
DB 82 ILeSerArgValGlnAlaGluAspValGlyValTyrTyrCysMetGlnArgLeuGluLeu 101
QY 393 CATTACAGTTCGGCTCGGGGACAAAGTTGGAAATAAAACGT 434
DB 102 ProTyrThrPheGlyGlnGlyThrLysLeuGluIleArg 115

RESULT 9
KV2E_MOUSE STANDARD; PRT; 113 AA.
ID KV2E_MOUSE AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DE "Murine v kappa 25 and v kappa 27 amino-acid sequences of C57Bl/6
DE Ig kappa chain V-II region 17S29.1."
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP TISSUE=Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA Abersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine v kappa 25 and v kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide."
RL Hoppe-Sevler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR: A01912; KWS17.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin v region; Hybridoma.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 123 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Alignment Scores:
Pred. No.: 4,41e-38 Length: 113
Score: 427.00 Matches: 84
Percent Similarity: 82.30% Conservatives: 9
Best Local Similarity: 74.34% Mismatches: 20

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Query Match: 54.39% Indels: 0
DB: 1 Gaps: 0
US-09-674-716B-2 (1-437) x KV2E_MOUSE (1-113)
QY 96 GATATTGTGATACCCAGGAGTAACCTCTCAATCTCTGTCAGTCTCTGGAGAAATCAGTTTCC 155
DB 1 AspIleValMetThrGlnAlaValPheSerAsnProValThrLeuGlyThrSerAlaSer 20
QY 156 ATCTCTGAGGCTAGTAAAGTCTCTGTATAAGATCGGAGACATCTGTAATTGG 215
DB 21 ILeSerCysArgSerSerLysSerLeuLeuHisSerAsnGlyIleThrTyrLeuTyrTrp 40
QY 216 TTCTCTGAGAGACAGGACAAATCTCTCAGCTCTCTGATGATTGATGTCACCCCGTGA 275
DB 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrGlnMetSerAsnLeuAla 60
QY 276 TCAGGAGTCTCAGACCGGTTTAGTCAGTGGTTCAGGACAGATTTCCACCTGGAAATC 335
DB 61 SerGlyValProAspArgPheSerSerGlySerGlyThrAspPheThrLeuArgIle 80
QY 336 AGTAGAGTGAAGCTCAGGAGTGGGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395
DB 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysAlaHisAsnLeuGluLeuPro 100
QY 396 TTCAGTTCGGCTCGGGGACAAAGTTGGAAATAAAACGT 434
DB 101 TyrThrPheGlyGlyThrLysLeuGluIleLysArg 113

RESULT 10
KV2B_HUMAN STANDARD; PRT; 113 AA.
ID KV2B_HUMAN AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DE "Variable region sequence of the light chain from a Waldenstroms IgM
DE with specificity for phosphorylcholine."
RT Biochemistry 15:3829-3833(1976).
RL Biochemistry 15:3829-3833(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR: A01886; K2HUF.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin v region.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 123 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Alignment Scores:

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Pred. No.: 1,53e-37 Length: 113  
 Score: 422.00 Matches: 77  
 Percent Similarity: 83.19% Conservatives: 17  
 Best Local Similarity: 68.14% Mismatches: 19  
 Query Match: 53.76% Indels: 0  
 DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2B\_HUMAN (1-113)

QY 96 GATATTGTGATAACCCAGGATGAACCTCTCCAACTCTGTCCTCTGAGAAATCAGTTTCC 155  
 Db 1 AspValValMetThrGlnSerProLeuPheLeuProValThrLeuGlyGluProAlaSer 20  
 QY 156 ATCTCTCCAGGCTCTAGTAAGAGCTCTCTGTATAGGATGGAGACATACCTTGAATTGG 215  
 Db 21 IleGlnCysArgSerGlnSerLeuValTyrArg\*\*\*Gly\*\*\*ThrTyrLeu\*\*\*Tyr 40  
 QY 216 TTTCTGCAGACACAGGACAACTCTCTCAGCTCTGATGATTTGATGATCCACCGGTGCA 275  
 Db 41 TyrLeuGlnLysProGlyGlnSerProGluLeuLeuTyrLeuSerSerTyrArgAsp 60  
 QY 276 TCAGAGCTCAGACCGGCTTAGTGGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 335  
 Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlySerGlySerGlySerGlySer 80  
 QY 336 AGTAGAGTCAAGGCTCAGGATGCGGTGTGTATTAATCTCAACACTTGTAGAGTATCCA 395  
 Db 81 ThrArgValGlnAlaGluAspValGlyValTyrTyrCysMetGlnAlaThr\*\*\*SerPro 100  
 QY 396 TTCAGGTTCCGGCTCGGGACAAAGTTGGAATAAAGCT 434  
 Db 101 TyrThrPheGlyGlnGlyThrLysLeu\*\*\*IleLysArg 113

RESULT 11

KV2D MOUSE  
 ID KV2D\_MOUSE STANDARD; PRT; 112 AA.  
 AC P01629;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region 2S1.3.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83055101; PubMed=7141411;  
 RA Herbat H., Chang J.Y., Abersold R., Braun D.G.;  
 RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for  
 the group A streptococcal polysaccharide";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).  
 CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL  
 ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.  
 DR PIR; A01911; KVMSS1.  
 DR HSSP; P01607; IREI.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Monoclonal antibody.  
 FT DOMAIN 1 23 FRAMEWORK-1  
 FT DOMAIN 24 39 FRAMEWORK-2  
 FT DOMAIN 40 54 FRAMEWORK-2  
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 62 93 FRAMEWORK-3  
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 103 112 FRAMEWORK-4  
 FT DISULFID 123 93 BY SIMILARITY.  
 FT NON\_TER 112 112  
 SQ SEQUENCE 112 AA; 12221 MW; BD5EF5B6D789FBEC CRC64;

Alignment Scores: 5.3e-37 Length: 112  
 Pred. No.: 417.00 Matches: 83  
 Score: 79.46% Conservatives: 6  
 Best Local Similarity: 74.11% Mismatches: 23  
 Query Match: 53.12% Indels: 0  
 DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2D\_MOUSE (1-112)

QY 96 GATATTGTGATAACCCAGGATGAACCTCTCCAACTCTGTCCTCTGAGAAATCAGTTTCC 155  
 Db 1 AspValValMetThrGlnSerProLeuPheLeuProValThrLeuGlyThrSerAlaSer 20  
 QY 156 ATCTCTCCAGGCTCTAGTAAGAGCTCTCTGTATAGGATGGAGACATACCTTGAATTGG 215  
 Db 21 PheSerCysArgSerSerLysSerLeuGlnSerLysGlyIleThrTyrLeuTyrTyr 40  
 QY 216 TTTCTGCAGACACAGGACAACTCTCTCAGCTCTGATGATTTGATGATCCACCGGTGCA 275  
 Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrGlnMetSerAsnLeuAla 60  
 QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 335  
 Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlySerGlySerGlySerGlySer 80  
 QY 336 AGTAGAGTCAAGGCTCAGGATGCGGTGTGTATTAATCTCAACACTTGTAGAGTATCCA 395  
 Db 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysAlaAsnLeuGlnLeuPro 100  
 QY 396 TTCAGGTTCCGGCTCGGGACAAAGTTGGAATAAAGCT 431  
 Db 101 TyrThrPheGlyGlyThrLysLeuGluLeuLys 112

RESULT 12

KV2G MOUSE  
 ID KV2G\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01631;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region 26-10.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX STRAIN=A/J;  
 RX MEDLINE=83178921; PubMed=6404298;  
 RA Novotny J., Margolies M.N.;  
 RT "Amino acid sequence of the light chain variable region from a mouse  
 anti-digoxin hybridoma antibody";  
 RL Biochemistry 22:1153-1158(1983).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA  
 PROTEIN THAT BINDS DIGOXIN.  
 DR PIR; A01914; KVMSS26.  
 DR HSSP; P80362; 1WTL.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.  
 FT DOMAIN 1 23 FRAMEWORK-1  
 FT DOMAIN 24 39 FRAMEWORK-2  
 FT DOMAIN 40 54 FRAMEWORK-2  
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 62 93 FRAMEWORK-3  
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 103 112 FRAMEWORK-4  
 FT DISULFID 123 93 BY SIMILARITY.  
 FT NON\_TER 113 113

SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Alignment Scores:  
 Pred. No.: 3,65e-35 Length: 113  
 Score: 400.00 Matches: 75  
 Percent Similarity: 82.30% Conservatives: 18  
 Best Local Similarity: 66.37% Mismatches: 20  
 Query Match: 50.96% Indels: 0  
 DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2C\_MOUSE (1-113)

QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTCTGCTACTTCTGGAGAAATCAGTTTCC 155  
 Db 1 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20  
 QY 156 ATCTCTGTCAGGCTCTAGTAAGATCTCTGTATAAGGATGGGAGACATCTTGAATTGG 215  
 Db 21 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAsnThrTyrLeuAsnTrp 40  
 QY 216 TTCTGTCAGAGACACAGCAATCTCTCAGCTCTCTGATGATTTGATGTCACCCGTCGA 275  
 Db 41 TyrLeuGlnIysAlaGlyGlnSerProLysLeuLeuIleTyrLysValSerAsnArgPhe 60  
 QY 276 TCAGGAGTCTCAGACCGGTTTAGTCAGTGGGTGAGGACACAGATTTCACCCCTGGAAATC 335  
 Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 80  
 QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTGTTACTGTCACAACTTGTAGAGTATCCA 395  
 Db 81 SerArgValGluAlaGluAspLeuGlyIleTyrPheCysSerGlnThrThrHisValPro 100  
 QY 396 TTCACGTTGGCTCGGGGCAAGATTGGAATAAAGCT 434  
 Db 101 ProThrPheGlyGlyThrLysLeuGluIleLysArg 113

#### RESULT 13

KV2C\_HUMAN STANDARD; PRT; 112 AA.  
 ID KV2C\_HUMAN  
 AC P01616;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region MIL.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA Dreyer W.J., Gray W.R., Hood L.E.;  
 RT "The genetic, molecular, and cellular basis of antibody formation:  
 RT some facts and a unifying hypothesis";  
 RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).  
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01887; K2HML.  
 DR HSSP; P80362; 1WTL.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 112 112

SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Alignment Scores:  
 Pred. No.: 5,29e-35 Length: 112  
 Score: 398.50 Matches: 74  
 Percent Similarity: 83.19% Conservatives: 20  
 Best Local Similarity: 65.49% Mismatches: 18  
 Query Match: 50.76% Indels: 1  
 DB: 1 Gaps: 1

US-09-674-716B-2 (1-437) x KV2C\_HUMAN (1-112)

QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTCTGCTACTTCTGGAGAAATCAGTTTCC 155  
 Db 1 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20  
 QY 156 ATCTCTGTCAGGCTCTAGTAAGATCTCTGTATAAGGATGGGAGACATCTTGAATTGG 215  
 Db 21 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAsnThrTyrLeuAsnTrp 39  
 QY 216 TTCTGTCAGAGACACAGCAATCTCTCAGCTCTCTGATGATTTGATGTCACCCGTCGA 275  
 Db 40 TyrLeuGlnIysAlaGlyGlnSerProLysLeuLeuIleTyrLysValSerAsnArgPhe 59  
 QY 276 TCAGGAGTCTCAGACCGGTTTAGTCAGTGGGTGAGGACACAGATTTCACCCCTGGAAATC 335  
 Db 60 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 79  
 QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTGTTACTGTCACAACTTGTAGAGTATCCA 395  
 Db 80 SerArgVal\*\*\*Ala\*\*\*\*\*ValGlyValTyrTyrCysMetGlnAlaLeuGlnThrPro 99  
 QY 396 TTCACGTTGGCTCGGGGCAAGATTGGAATAAAGCT 434  
 Db 100 LeuThrPheGlyGlyThrAsnValGluIleLysArg 112

#### RESULT 14

KV4C\_HUMAN STANDARD; PRT; 134 AA.  
 ID KV4C\_HUMAN  
 AC P06314;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-IV region B17 precursor.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86041854; PubMed=2997713;  
 RA Marsh P., Mills P., Gould H.;  
 RT "Detection of a unique human V kappa IV germline gene by a cloned  
 RT cDNA probe";  
 RL Nucleic Acids Res. 13:6531-6544 (1985).  
 CC [2]  
 RN REVISION TO 76.  
 RA Marsh P.;  
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL; X02990; CAA26733.1; -.  
 DR HSSP; P80362; 1WTL.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.

```
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00407; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULFID 143 134 BY SIMILARITY.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Alignment Scores:
Pred. No.: 5,48e-35 Length: 134
Score: 398.50 Matches: 78
Percent Similarity: 75.8% Conservative: 16
Best Local Similarity: 62.90% Mismatches: 29
Query Match: 50.76% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-2 (1-437) x KV4B_HUMAN (1-134)
QY 66 CTTATGTTCTGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAACCTCTCC 125
Dy 11 LeuLeuLeuTrpIleSerGlyAlaTyrGlyAspIleValMetThrGlnSerProAspSer 30
QY 126 AATCCTGTCACCTCTGGAGAACAGTTCCTCCATCTCTCGAGTCTAGTAAGAGTCTCTCG 185
Dy 31 LeuAlaValSerLeuGlyGluArgAlaThrIleAsnCysLysSerSerGlnSerIleLeu 50
QY 186 TAT---AAGATGGGAAGACATACCTTGAATGGTTTCTGCAGACACAGGACATCTCTCT 242
Dy 51 TyrSerSerAspAsnLysAsnTyrLeuAlaTyrTyrGlnGlnLysProGlyGlnProPro 70
QY 243 CAGCTCCTGATCTATTTGATGTCACCCGTCATCAGGAGTCTCAGACCGGTTTAGTGGC 302
Dy 71 LysLeuLeuIleTyrTrpAlaSerThrArgLysGlyValProAspArgPheSerGly 90
QY 303 AGTGGGTGAGGACAGATTTCCACCTCGAATACAGTAGAGTGAAGCTGAGGATGGGT 362
Dy 91 SerGlySerGlyThrAspPheThrIleSerSerLeuGlnAlaGluAspValAla 110
QY 363 GTGTATTACTGTCAACAACTTGTAGATATCCATTACGTTTCGGCTCGGGGACAAAGTTG 422
Dy 111 ValTyrTyrCysGlnGlnTyrTyrAsnLeuProTrpThrPheGlyGlnGlyThrLysVal 130
QY 423 GAAATAAAACGT 434
Dy 131 GluIleLysArg 134

RESULT 15
KV4B_HUMAN
ID KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-IV region JI precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlenz H.D.,
```

```
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RL Nucleic Acids Res. 13:6515-6529 (1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00022; CAA77317.1; -.
DR PIR; A01904; K4HUIJ.
DR HSP; P80362; IWTJ.
DR GO; GO:0005576; Extracellular; NAS.
DR GO; GO:0003823; Antigen binding; NAS.
DR GO; GO:0006955; P:Immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00407; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 133 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AP4 CRC64;

Alignment Scores:
Pred. No.: 8,59e-33 Length: 133
Score: 378.00 Matches: 77
Percent Similarity: 75.00% Conservative: 16
Best Local Similarity: 62.10% Mismatches: 29
Query Match: 48.15% Indels: 2
DB: 1 Gaps: 2

US-09-674-716B-2 (1-437) x KV4B_HUMAN (1-133)
QY 66 CTTATGTTCTGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAACCTCTCC 125
Dy 11 LeuLeuLeuTrpIleSerGlyAlaTyrGlyAspIleValMetThrGlnSerProAspSer 30
QY 126 AATCCTGTCACCTCTGGAGAACAGTTCCTCCATCTCTCGAGTCTAGTAAGAGTCTCTCG 185
Dy 31 LeuAlaValSerLeuGlyGluArgAlaThrIleAsnCysLysSerSerGlnSerValLeu 50
QY 186 TAT---AAGATGGGAAGACATACCTTGAATGGTTTCTGCAGACACAGGACATCTCTCT 242
Dy 51 TyrSerSerAsnLysAsnTyrLeuAlaTyrTyrGlnGlnLysProGlyGlnProPro 70
QY 243 CAGCTCCTGATCTATTTGATGTCACCCGTCATCAGGAGTCTCAGACCGGTTTAGTGGC 302
Dy 71 LysLeuLeuIleTyrTrpAlaSerThrArgLysGlyValProAspArgPheSerGly 90
QY 303 AGTGGGTGAGGACAGATTTCCACCTCGAATACAGTAGAGTGAAGCTGAGGATGGGT 362
Dy 91 SerGlySerGlyThrAspPheThrIleSerSerLeuGlnAlaGluAspValAla 110
QY 363 GTGTATTACTGTCAACAACTTGTAGATATCCATTACGTTTCGGCTCGGGGACAAAGTTG 422
Dy 111 ValTyrTyrCysGlnGlnTyrAspThrIlePro---ThrPheGlyGlyThrLysVal 129
QY 423 GAAATAAAACGT 434
```

Thu Sep 30 13:18:44 2004

us-09-674-716b-2.rsp

Page 10

Db 130 GluileLysArg 133  
|||||

Search completed: September 30, 2004, 08:42:45  
Job time : 11.4813 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: September 30, 2004, 08:27:18 ; Search time 55.3361 Seconds  
(without alignments)  
4983.418 Million cell updates/sec

Title: US-09-674-716B-2  
Perfect score: 785  
Sequence: 1 aagtttcaagttactcagc.....agttggaataaaaacgtacg 437

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_scool\_p/US09674716/runat\_30092004\_070258\_25867/app\_query.fasta\_1.3164  
-DB=SPREMBL\_25 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09674716 @CNCN 1.1 499 @runat\_30092004\_070258\_25867 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_prodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	497	63.3	239	4 Q8NEK0	Q8nek0 homo sapien

2	482	61.4	239	4 Q8TCD0	Q8tcd0 homo sapien
3	447.5	57.0	238	11 Q9NM37	Q9nm37 mus musculu
4	442.5	56.4	238	11 Q8VC16	Q8vc16 mus musculu
5	433	55.2	239	11 Q8VC55	Q8vc55 mus musculu
6	418	53.2	239	11 Q8K0F8	Q8k0f8 mus musculu
7	400.5	51.0	114	4 Q9UL80	Q9ul80 homo sapien
8	400	51.0	148	11 Q8K122	Q8k122 mus musculu
9	383	48.8	104	11 Q9JL82	Q9jl82 mus musculu
10	352.5	44.9	234	4 Q7Z473	Q7z473 homo sapien
11	339.5	43.2	236	11 Q7TS98	Q7ts98 mus musculu
12	332.5	42.4	236	4 Q7Z3Y4	Q7z3y4 homo sapien
13	330.5	42.1	236	11 Q7TMK3	Q7tmk3 mus musculu
14	326.5	41.6	237	13 Q7S236	Q7s236 xenopus lae
15	322.5	41.1	234	11 Q8R062	Q8r062 mus musculu
16	322	41.0	109	4 Q9UL78	Q9ul78 homo sapien
17	320	40.8	86	4 Q7Z3V5	Q7z3v5 homo sapien
18	319.5	40.7	111	11 Q9Z0E9	Q9z0e9 mus musculu
19	315.5	40.2	234	11 Q8VCP0	Q8vcp0 mus musculu
20	310.5	39.6	111	11 Q811U6	Q811u6 mus musculu
21	309.5	39.4	234	11 Q91WF8	Q91wf8 mus musculu
22	308	39.2	112	11 Q8K1F2	Q8k1f2 mus musculu
23	307.5	39.2	107	11 Q9ERZ9	Q9erz9 mus musculu
24	306.5	39.0	108	4 Q9UL83	Q9ul83 homo sapien
25	305.5	38.9	108	4 Q9UL79	Q9ul79 homo sapien
26	303	38.6	109	4 Q9UL86	Q9ul86 homo sapien
27	301.5	38.4	214	11 Q9RIAS	Q9rias mus musculu
28	300	38.2	106	5 Q9U410	Q9u410 schistosoma
29	298.5	38.0	108	4 Q9UL77	Q9ul77 homo sapien
30	297.5	37.9	108	11 Q8VIJ0	Q8vij0 mus musculu
31	296	37.7	112	11 Q8K1F3	Q8k1f3 mus musculu
32	295	37.6	134	11 Q8VDD0	Q8vdd0 mus musculu
33	294	37.5	114	11 Q8K1F1	Q8k1f1 mus musculu
34	292	37.2	235	11 Q7TMK0	Q7tmk0 mus musculu
35	290	36.9	107	4 Q96SA9	Q96sa9 homo sapien
36	288.5	36.8	298	11 Q9QVFO	Q9qvfo mus musculu
37	287.5	36.6	108	4 Q9UL70	Q9ul70 homo sapien
38	286	36.4	109	4 Q9UL85	Q9ul85 homo sapien
39	285	36.3	107	4 Q9UL81	Q9ul81 homo sapien
40	283.5	36.1	109	11 Q9Z0E6	Q9z0e6 mus musculu
41	280.5	35.7	131	11 Q811C3	Q811c3 mus musculu
42	279.5	35.6	233	11 Q91WS9	Q91ws9 mus musculu
43	276.5	35.2	99	11 Q9JL74	Q9jl74 mus musculu
44	274.5	35.0	103	11 Q9JL80	Q9jl80 mus musculu
45	270	34.4	235	11 Q91W12	Q91w12 mus musculu

## ALIGNMENTS

RESULT 1					
Q8NEK0	PRELIMINARY;	PRT;	239	AA.	
ID Q8NEK0					
AC Q8NEK0;					
DT 01-OCT-2002 (TReMBLrel. 22, Created)					
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)					
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)					
DE Hypothetical protein.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
OX NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Prostate;					
RA Strauberg R.;					
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.					
DR EMBL; BC030814; AAH30814.1; -					
DR PIR; S23638; S23638.					
DR PIR; S34091; S34091.					
DR PIR; S40357; S40357.					
DR InterPro; IPR007110; IG-like.					
DR InterPro; IPR003597; IG cl.					
DR InterPro; IPR003006; IG_MHC.					
DR InterPro; IPR003596; IG_v.					

DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00407; IG1; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Alignment Scores:  
 Pred. No.: 1.35e-48 Length: 239  
 Score: 497.00 Matches: 95  
 Percent Similarity: 82.84% Conservative: 16  
 Best Local Similarity: 70.90% Mismatches: 23  
 Query Match: 63.31% Indels: 0  
 DB: 4 Gaps: 0

US-09-674-716B-2 (1-437) x Q8NEK0 (1-239)

QY 36 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95  
 Db 1 MetArgLeuProAlaGlnLeuLeuMetLeuTrpValSerGlySerGly 20  
 QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTCTGTCAGTCTGGAGATCAGTTTCC 155  
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40  
 QY 156 ATCTCTGAGGTCCTAGTAAAGATCTCTCTGATAGGATGGGAGACATACCTGGAATTGG 215  
 Db 41 IleSerCysArgSerGlnSerLeuLeuHisSerAspGlyTyrAsnTyrLeuAspTrp 60  
 QY 216 TTCTCTGAGACGACGAGCAATCTCTCAGCTCCTGATGTTATGTTGATCTCCACCGGTGCA 275  
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 80  
 QY 276 TCAGGAGTCTCAGACCGGTTTATGTCAGTGGGTGAGGACAGATTCACCTCGAAATC 335  
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCAACAACTGTAGAGTATCCA 395  
 Db 101 SerLysValGluAlaGluAspValGlyIleTyrTyrCysMetGlnGlyLeuGlnThrPro 120  
 QY 396 TTCACGTTCCGGTCGGGGCAAAAGTTGGAAATAAAACGTACG 437  
 Db 121 GlnThrPheGlyGlnGlyThrLysValGluIleLysArgThr 134

## RESULT 2

Q8TCD0 PRELIMINARY; PRT; 239 AA.  
 ID Q8TCD0  
 AC Q8TCD0  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC022362; AAH2362.1; -.  
 DR PIR; S34095; S34095.  
 DR PIR; S42267; S42267.  
 DR PIR; S42268; S42268.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 2.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.

DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Alignment Scores:  
 Pred. No.: 7.48e-47 Length: 239  
 Score: 482.00 Matches: 91  
 Percent Similarity: 79.85% Conservative: 16  
 Best Local Similarity: 67.91% Mismatches: 27  
 Query Match: 61.40% Indels: 0  
 DB: 4 Gaps: 0

US-09-674-716B-2 (1-437) x Q8TCD0 (1-239)

QY 36 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95  
 Db 1 MetArgLeuProAlaGlnLeuLeuMetLeuTrpValSerGlySerGly 20  
 QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTCTGTCAGTCTGGAGATCAGTTTCC 155  
 Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40  
 QY 156 ATCTCTGAGGTCCTAGTAAAGATCTCTCTGATAGGATGGGAGACATACCTGGAATTGG 215  
 Db 41 IleSerCysArgSerThrGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60  
 QY 216 TTCTCTGAGACGACGAGCAATCTCTCAGCTCCTGATGTTATGTTGATCTCCACCGGTGCA 275  
 Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 80  
 QY 276 TCAGGAGTCTCAGACCGGTTTATGTCAGTGGGTGAGGACAGATTCACCTCGAAATC 335  
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCAACAACTGTAGAGTATCCA 395  
 Db 101 ThrArgValGluAlaGluAspValGlyValTyrPheCysMetGlnGlyThrHisTrpPro 120  
 QY 396 TTCACGTTCCGGTCGGGGCAAAAGTTGGAAATAAAACGTACG 437  
 Db 121 SerThrPheGlyGlnGlyThrLysLeuGluIleLysArgThr 134

## RESULT 3

Q99M37 PRELIMINARY; PRT; 238 AA.  
 ID Q99M37  
 AC Q99M37  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002035; AAH02035.1; -.  
 DR PIR; A31807; A31807.  
 DR PIR; A32248; A32248.  
 DR PIR; B32248; B32248.  
 DR PIR; C32248; C32248.  
 DR PIR; F32530; F32530.  
 DR PIR; PH1042; PH1042.  
 DR PIR; PH1043; PH1043.  
 DR PIR; PH1044; PH1044.  
 DR PIR; S07455; S07455.  
 DR PIR; S16112; S16112.  
 DR PIR; S24500; S24500.  
 DR PIR; S24501; S24501.  
 DR PIR; S24503; S24503.  
 DR PIR; S24504; S24504.



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DR PIR; S24529; S24529.
DR PIR; S24532; S24532.
DR PIR; S24533; S24533.
DR PIR; S24535; S24535.
DR PIR; S24536; S24536.
DR PIR; S24538; S24538.
DR PDB; 1I9I; 25-DEC-02.
DR PDB; 1LO2; 31-JUL-02.
DR PDB; 1LO4; 31-JUL-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB206A08B01330A CRC64;

Alignment Scores:
Pred. No.: 7,628-43 Length: 238
Score: 447.50 Matches: 87
Percent Similarity: 80.45% Conservativity: 20
Best Local Similarity: 65.41% Mismatches: 25
Query Match: 57.01% Indels: 1
DB: 11 Gaps: 1

US-09-674-716B-2 (1-437) x Q99M37 (1-238)
QY 36 ATGAGTCTCTGTTTCAGTTCTGGGGTGTATGTTCTGATCTCTGGAGTCAGTGGG 95
DB 1 MetLysLeuProValArgLeuLeu---ValLeuMetPheTrpIleProAlaSerSerSer 19
QY 96 GATATTGTGATAACCCAGATGAACTCTCCAAATCCTGCTCACTCTCTGGAGATCAGTTCC 155
DB 20 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 39
QY 156 ATCTCTGAGTCTAGTAAAGTGTCTCTGATGATGATGATGATGATGATGATGATGATG 215
DB 40 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAsnThrTyLeuHisTrp 59
QY 216 TTTCTGACAGACAGGACAACTCTCTCAGTCTCTGATGATGATGATGATGATGATGATG 275
DB 60 TyrLeuGlnLysProGlyGlnSerProLysLeuLeuLeuTyLysValSerAsnArgPhe 79
QY 276 TCAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTCAGGCACAGATTTACCTCGAATC 335
DB 80 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 99
QY 336 AGTAGAGTGAAGGTGAGGATGTTGGTGTGATGATGATGATGATGATGATGATGATGAT 395
DB 100 SerArgValGluAlaGluAspLeuGlyValTyLysPheCysSerGlnSerThrHisValPro 119

RESULT 4
Q8VC16 PRELIMINARY; PRT; 238 AA.
ID Q8VC16
AC Q8VC16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SQ SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;

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Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

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RL EMBL; BC019760; AAH19760.1; -.
DR PIR; A27887; A27887.
DR PIR; A32248; A32248.
DR PIR; A33933; A33933.
DR PIR; B27887; B27887.
DR PIR; B30577; B30577.
DR PIR; B31485; B31485.
DR PIR; B32248; B32248.
DR PIR; B41940; B41940.
DR PIR; C27887; C27887.
DR PIR; C32248; C32248.
DR PIR; C34904; C34904.
DR PIR; D27887; D27887.
DR PIR; D29380; D29380.
DR PIR; E28833; E28833.
DR PIR; F32530; F32530.
DR PIR; H31485; H31485.
DR PIR; PH0106; PH0106.
DR PIR; PH1030; PH1030.
DR PIR; PH1031; PH1031.
DR PIR; PH1034; PH1034.
DR PIR; PL0257; PL0257.
DR PIR; PT0359; PT0359.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S26334; S26334.
DR PIR; S53750; S53750.
DR PIR; S60066; S60066.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Alignment Scores:
Pred. No.: 2,98-42 Length: 238
Score: 442.50 Matches: 86
Percent Similarity: 79.70% Conservativity: 20
Best Local Similarity: 64.66% Mismatches: 26
Query Match: 56.37% Indels: 1
DB: 11 Gaps: 1

US-09-674-716B-2 (1-437) x Q8VC16 (1-238)
QY 36 ATGAGTCTCTGTTTCAGTTCTGGGGTGTATGTTCTGATCTCTGGAGTCAGTGGG 95
DB 1 MetLysLeuProValArgLeuLeu---ValLeuMetPheTrpIleProAlaSerSerSer 19
QY 96 GATATTGTGATAACCCAGATGAACTCTCCAAATCCTGCTCACTCTCTGGAGATCAGTTCC 155
DB 20 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 39
QY 156 ATCTCTGAGTCTAGTAAAGTGTCTCTGATGATGATGATGATGATGATGATGATGATG 215
DB 40 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAsnThrTyLeuHisTrp 59
QY 216 TTTCTGACAGACAGGACAACTCTCTCAGTCTCTGATGATGATGATGATGATGATGATG 275
DB 60 TyrLeuGlnLysProGlyGlnSerProLysLeuLeuLeuTyLysValSerAsnArgPhe 79
QY 276 TCAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTCAGGCACAGATTTACCTCGAATC 335
DB 80 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 99
QY 336 AGTAGAGTGAAGGTGAGGATGTTGGTGTGATGATGATGATGATGATGATGATGATGAT 395
DB 100 SerArgValGluAlaGluAspLeuGlyValTyLysPheCysSerGlnSerThrHisValPro 119

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QY 396 TTCAGGTTCTGGCTCGGGACAAAGTTGGAATAAAGCT 434  
 Db 120 ProThrPheGlyGlyThrLysLeuGluLeuLysArg 132

## RESULT 5

Q8VC55  
 ID Q8VC55 PRELIMINARY; PRT; 239 AA.  
 AC Q8VC55;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC021781; AAH21781.1; -  
 DR PIR; A33933; A33933.  
 DR PDB; 1KCS; 24-JUL-02.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0015070; F:toxin activity; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR004214; Conotoxin.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF02950; Conotoxin; 1.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Alignment Scores:  
 Pred. No.: 3,69e-41 Length: 239  
 Score: 433.00 Matches: 85  
 Percent Similarity: 77.44% Conservative: 18  
 Best Local Similarity: 63.91% Mismatches: 30  
 Query Match: 55.16% Indels: 0  
 DB: 11 Gaps: 0  
 US-09-674-716B-2 (1-437) x Q8VC55 (1-239)

QY 36 ATGAGGTTCTCTGTTCTGAGTTCTGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95  
 Db 1 MetLeuProValLeuLeuValLeuLeuPheLeuLeuPheThrSerProAlaSerSer 20  
 QY 96 GATATTGTGATACCCAGGATGAATCTCCAAATCTCTGTCACATCTCTGGAGAATCAGTTTCC 155  
 Db 21 AspValValLeuThrGlnThrProLeuSerLeuProValLeuLeuLeuGlyAspGlnAlaSer 40  
 QY 156 ATCTCTGAGGTCAGTATAGAGTCTCTGATATAGGATGGGAGACATATCTGAAATGG 215  
 Db 41 IleSerCysLysSerThrLysSerLeuLeuAsnSerAspGlyPheThrTyrLeuAspTrp 60  
 QY 216 TTCTCTGACAGACCCAGGAAATCTCTCAGCTCCCTGATGTTGATCTCCACCGTGCA 275  
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuIleTyrLeuValSerAsnArgPhe 80  
 QY 276 TCAGAGTCTGACACGGTTTGTAGTGGCGTGGGTGAGGATGAGGATGAGGATGAGGATG 335  
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 336 AGTAGAGTGAAGCGTGGAGTGTGGTGTGTTACTGTCAACACTTTGTAGATATCCA 395  
 Db 101 SerArgValGluAlaGluAspLeuGlyValTyrTyrCysPheGlnSerAsnHisLeuPro 120

QY 396 TTCAGGTTCTGGCTCGGGACAAAGTTGGAATAAAGCT 434  
 Db 121 TyrThrPheGlyGlyThrLysLeuGluLeuLysArg 133

## RESULT 6

Q8KOF8  
 ID Q8KOF8 PRELIMINARY; PRT; 239 AA.  
 AC Q8KOF8;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Breast tumor;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC031498; AAH31498.1; -  
 DR PIR; A33933; A33933.  
 DR PDB; 1KN2; 13-MAR-02.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002198; ADH\_short.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;

Alignment Scores:  
 Pred. No.: 2,04e-39 Length: 239  
 Score: 418.00 Matches: 82  
 Percent Similarity: 76.69% Conservative: 20  
 Best Local Similarity: 61.65% Mismatches: 31  
 Query Match: 53.25% Indels: 0  
 DB: 11 Gaps: 0  
 US-09-674-716B-2 (1-437) x Q8KOF8 (1-239)

QY 36 ATGAGGTTCTCTGTTCTGAGTTCTGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95  
 Db 1 MetMetSerProAlaGlnPheLeuPheLeuLeuValLeuSerIleGlnGluLeuGly 20  
 QY 96 GATATTGTGATACCCAGGATGAATCTCCAAATCTCTGTCACATCTCTGAGGAAATCAGTTTCC 155  
 Db 21 AspValValMetThrGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSer 40  
 QY 156 ATCTCTGAGGTCAGTATAGAGTCTCTGATATAGGATGGGAGACATATCTGAAATGG 215  
 Db 41 IleSerCysLysSerThrLysSerLeuLeuLeuIleTyrLeuValSerAsnArgPhe 60  
 QY 216 TTCTCTGACAGACCCAGGAAATCTCTCAGCTCCCTGATGTTGATGTTGATGTTGATGTTG 275  
 Db 61 LeuLeuGlnArgProGlyGlnSerProLysArgLeuLeuSerLeuValSerLysLeuAsp 80  
 QY 276 TCAGGAGTCTGACACGGTTTGTAGTGGCGTGGGTGAGGATGAGGATGAGGATGAGGATG 335  
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 336 AGTAGAGTGAAGCGTGGAGTGTGGTGTGTTACTGTCAACAACTTTGTAGATATCCA 395

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Db      101 SerArgValGluAlaGluAspLeuGlyValTyrTyrCysLeuGlnSerThrHisPhePro 120
Qy      396 TTCAGCTTCGGCTCGGGGACAAAGTTGGAATAAAACGT 434
Db      121 TyrThrPheGlyGlyThrLysLeuGluLeuLysArg 133

RESULT 7
Q9UL80
ID      Q9UL80      PRELIMINARY;      PRT;      114 AA.
AC      Q9UL80;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Myosin-reactive immunoglobulin light chain variable region
DE      (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RX      SEQUENCE FROM N.A.
RP      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR      ENBL; AF035034; AAD56270.1; -
DR      PIR; B49002; B49002
DR      PIR; S23638; S23638.
DR      PIR; S34094; S34094.
DR      PIR; S34095; S34095.
DR      HSP; P80362; IWLTL.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PSS0835; IG_LIKE; 1.
FT      NON_TER      1
FT      NON_TER      114
SQ      SEQUENCE      114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Alignment Scores:
Pred. No.:      1,81e-37      Length:      114
Score:      400.50      Matches:      79
Percent Similarity:      80.70%      Conservative:      13
Best Local Similarity:      69.30%      Mismatches:      21
Query Match:      51.02%      Indels:      1
DB:      4      Gaps:      1

US-09-674-716B-2 (1-437) x Q9UL80 (1-114)

Qy      96 GATATTGTGATACCCAGGATGAATCTCCAACTCTGTCACTTCGGAGATCAGTTTCC 155
Db      1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuArgGlnProAlaSer 20
Qy      156 ATCTCTCGCAGGCTAGTAAAGAGTCTCTGTATAGGATGGGAGACATACCTGAATTGG 215
Db      21 ILSerCyArgSerSerGlnSerProValTyrSerAspGlyAsnThrTyrLeuAsnTyr 40
Qy      216 TTCTCTCAGACGACCAGGACAAATCTCTCTCAGTCTCTGATGATTTGATGTCCACCGTGCA 275
Db      41 PheGlnGlnArgProGlyGlnSerProArgLeuLeuTyrLysValSerAsnArgAsp 60
Qy      276 TCAGGAGTCTCACACCGGTTTAGTGGCAGTGGTCCAGGCACAGATTTCCACCTGGAATC 335
Db      61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
Qy      336 AGTAGAGTGAAGCTCAGGATGTGGTGTGTTACTTACTCTCAACAACCTGTAGAGTAT--- 392
Db      81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpPro 100

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Qy	393	CAATTCAGTTTCGGTCGGGACAAAGTTGGAAATAAAACGT	434
Db	101	ProtrpThrPheGlyGlnGlyThrLysValGluLeuLysArg	114
RESULT 8			
Q8K122		PRELIMINARY;	PRT; 148 AA.
AC	Q8K122;		
DT	01-OCT-2002 (TRENBLrel. 22, Created)		
DT	01-OCT-2002 (TRENBLrel. 22, Last sequence update)		
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)		
DE	Hypothetical protein.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
NCBI_TaxID=10090;			
EN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Salivary gland;		
RA	Strausberg R.;		
EL	Submitted (May-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC028925; AAH28925.1; -.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF00047; IG. 1.		
DR	SMART; SM00409; IG; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS050935; IG_LIKE; 1.		
DR	Hypothetical protein.		
SW	HYPOTHECAL PROTEIN.		
KQ	SEQUENCE 148 AA; 16345 MW; 183920BDD9F3B521 CRC64;		
Alignment Scores:			
Pred. No.:	2,22e-37	Length:	148
Score:	400.00	Matches:	80
Percent Similarity:	75.78%	Conservative:	17
Best Local Similarity:	62.50%	Mismatches:	30
Query Match:	50.96%	Indels:	1
DB:	11	Gaps:	0
US-09-674-716B-2 (1-437) x Q8K122 (1-148)			
Qy	51	CAGTTTCGGGGTGCTTATGTCTGGATCTCTGGAGTCAGTGGGATATTGTGAT	
Db	5	GlnPheLeuPheLeuLeuValLeuTrpIleArgGluThrAsnGlyAspValValMet	
Qy	111	CAGGATGAACCTCCAACTCTGTCTCAGTCTGGAGAAATCAGTTTCCATCTCTCGACGAG	
Db	25	GlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSerIleSerCysIys	
Qy	171	AGTAAGAGTCTCTGTATATAGGATGGGAAGACATCTGAATTTGGTTTCTCGACAGAG	
Db	45	SerGlnSerLeuLeuAspSerAspGlyLysThrTyLeuAsnTrpLeuLeuGlnArg	
Qy	231	GGACATCTCTCAGCTCCTGTATTTGATGTCTCCACCGTCATCAGGAGTCTCTC	
Db	65	GlyGlnSerProLysArgLeuIleTyLeuValSerLysLeuAspSerGlyValPro	
Qy	291	CGGTTTACTGGCAGTGGGTCCAGCACAGATTTCCACCTGGAAATCAGTAGAGTGA	
Db	85	ArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIleSerArgValGly	
Qy	351	GAGGATGGGGTGCTATTACTGTCAACACTTGTAGAGTATCCATTACCGTTCGG	
Db	105	GluAspLeuGlyValTyTyCysTrpGlnGlyThrHisPhePro-GlyArgSerVal	
Qy	411	GGGACAAAGTTGGAAATAAAAC	432
Db	124	uAlaProSerTrpLysSerAsn	131
RESULT 9			
ID	Q9JL82	PRELIMINARY;	PRT; 104 AA.
ID	Q9JL82		

RESULT 9  
Q9JL82  
ID Q9J



```
Db 116 TrpThrPheGlyGlnGlyThrLysValGluIleLysArgThr 129
RESULT 11
Q7TS98 PRELIMINARY; PRT; 236 AA.
AC Q7TS98;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA MEDLINE=9338497; PubMed=8372513;
RA Tonge D.W., Hennan J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 116NS19.9 heavy and light chain
RT cDNAs and expression of antibody fragments in Escherichia coli.";
RL Year Immunol. 7:56-62(1993).
DR EMBL; S65921; AAB28160.1; -.
SQ SEQUENCE 236 AA; 26454 MW; 2C586BFBF5EA10F4C CRC64;

Alignment Scores:
Pred. No.: 2,686-30 Length: 236
Score: 339.50 Matches: 66
Percent Similarity: 67.41% Conservative: 25
Best Local Similarity: 48.89% Mismatches: 39
Query Match: 43.25% Indels: 5
DB: 11 Gaps: 1

US-09-674-716B-2 (1-437) x Q7TS98 (1-236)
QY 30 CTCACATGAGTCTCTCTCTCAGTTCTGGGGGCTTATGTTCTGGATCTCTGGAGTC 89
Db 1 MetAspMetArgThrProIaGlnPheLeuGlyIleLeuLeuLeuTrpPheProGlyMet 20
QY 90 AGTGGGATATTGTGATTAACCCAGATGAATCTCTCAATCTGTCACTCTGGAGATCA 149
Db 21 LysCysAspIleLysMetThrGlnSerProSerMetTyrAlaSerLeuGlyGluArg 40
QY 150 GTTTCATCTCTCGAGCTAGTAAAGTCTCTCTGATAGGATGAGGAGGAGACATCTG 209
Db 41 ValThrIleThrCysLysAlaSer-----GlnAspIleAsnSerTyrLeu 55
QY 210 AATTGTTTCTGCAGACAGACCAATCTCTCAGCTCTGATGATTTGATGTCACC 269
Db 56 SerTrpPheGlnGlnLysProGlyLysSerProLysThrLeuIleTyrArgAlaAsnArg 75
QY 270 CGTGATCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGACAGATTCACCTG 329
Db 76 LeuValAspGlyValProSerArgPheSerGlySerGlySerGlyGlnAspTyrSerLeu 95
QY 330 GAAATCAGTAGAGTGAAGCTGAGGATGGGTGTATTACTGTCAACAACTTGTAGAG 389
Db 96 ThrIleSerSerLeuGluTyrGluAspMetGlyIleTyrTyrCysLeuGlnTyrAspGlu 115
QY 390 TATCCATTACGTTCCGGTCCGGGACAAAGTTGGAAATAAAACGTT 434
Db 116 PheProArgThrPheGlyGlyGlyThrLysLeuGluIleLysArg 130

RESULT 12
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA TISSUE=Skeletal muscle;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA TISSUE=Skeletal muscle;
RA Strausberg R.;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC005332; AA05332.1; -.
RW Hypothetical protein.
DR SEQUENCE 236 AA; 25702 MW; 7BFE4ED23084BC6 CRC64;

Alignment Scores:
Pred. No.: 1,75e-29 Length: 236
Score: 332.50 Matches: 68
Percent Similarity: 64.71% Conservative: 20
Best Local Similarity: 50.00% Mismatches: 43
Query Match: 42.36% Indels: 5
DB: 4 Gaps: 1

US-09-674-716B-2 (1-437) x Q7Z3Y4 (1-236)
QY 30 CTCACATGAGTCTCTCTCTCAGTTCTGGGGGCTTATGTTCTGGATCTCTGGAGTC 89
Db 1 MetAspMetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuLeuLeuLeuLeuLeu 20
QY 90 AGTGGGATATTGTGATAACCCAGATGAATCTCTCAATCTGTCACTCTGGAGATCA 149
Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspThr 40
QY 150 GTTTCATCTCTCGAGTCTAGTAAAGTCTCTCTGATAGGATGAGGAGGAGACATCTG 209
Db 41 ValThrIleThrCysArgAlaSer-----GlnAspIleSerAsnTyrLeu 55
QY 210 AATTGTTTCTGCAGACAGACCAATCTCTCAGCTCTGATGATTTGATGTCACC 269
Db 56 AlaTrpPheGlnGlnLysProGlyLysAlaProLysSerLeuIleTyrGlyAlaSerSer 75
QY 270 CGTGATCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGACAGATTCACCTG 329
Db 76 LeuGlnSerGlyValGlnSerLysPheSerGlySerGlySerGlyThrAspPheThrLeu 95
QY 330 GAAATCAGTAGAGTGAAGCTGAGGATGGGTGTATTACTGTCAACAACTTGTAGAG 389
Db 96 ThrIleSerSerLeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrLysSer 115
QY 390 TATCCATTACGTTCCGGTCCGGGACAAAGTTGGAAATAAAACGTTACG 437
Db 116 TyrProValThrPheGlyGlnGlyThrLysLeuGluIleLysArgThr 131

RESULT 13

```

QY 330 GAAATCAGTAGAGTGAAGCTGAGAGTGGTGTGTATTACTGTGCAACAACCTGTAGAG 389  
 ||||| :  
 Db 96 ThrIleSerSerLeuGluSerAspThrAlaThrTyrTyrCysLeuGlnHisGlyGlu 115  
 ||||| :  
 QY 390 TATCCATTACAGTTCGGCTCGGGGACAAAGTTGGAAATAAAACGT 434  
 ||||| :  
 Db 116 SerProTyrThrPheGlySerGlyThrLysLeuGluLeuLysarg 130  
 ||||| :  
 RESULT 14  
 Q7S236 PRELIMINARY; PRT; 237 AA.  
 ID Q7S236  
 AC C7S236;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OC NCBI\_Taxid=8355;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Whole;  
 RC MEDLINE=22341132; PubMed=12454917;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative.";   
 RL Dev. Dyn. 225:384-391(2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Whole;  
 RC MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Whole;  
 RC Klein S., Strausberg R.;  
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, BC054155; AAHS4155.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 237 AA; 26300 MW; 47B8D0D2639CB436 CRC64;  
 Alignment Scores:  
 Pred. No.: 8.7e-29 Length: 237  
 Score: 326.50 Matches: 65  
 Percent Similarity: 70.08% Conservative: 24  
 Best Local Similarity: 51.18% Mismatches: 35  
 Query Match: 41.59% Indels: 3  
 DB: 13 Gaps: 2  
 US-09-674-716B-2 (1-437) x Q7S236 (1-237)



Blank Sheet



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:19:42 ; Search time 52.0607 Seconds  
(without alignments)  
4743.430 Million cell updates/sec

Title: US-09-674-716B-2  
Perfect score: 785  
Sequence: 1 aggtttacagttactcagc.....agttggaaataaaacgacg 437

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame-n2p.model -DEV=xlpl  
-Q=/cgn2.1/USPTO\_spool\_p/US0674716/runat\_30092004\_070257\_25848/app\_query.fasta\_1.3154  
-DB=A\_Geneseq\_29Jan04 -QFWT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US0674716 @CGN 1 1 475 @runat\_30092004\_070257\_25848 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT\_DSBELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_29Jan04: \*  
1: Geneseq1980s: \*  
2: Geneseq1990s: \*  
3: Geneseq2000s: \*  
4: Geneseq2001s: \*  
5: Geneseq2002s: \*  
6: Geneseq2003as: \*  
7: Geneseq2003bs: \*  
8: Geneseq2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	737	93.9	145	3	AAY32261 Mouse ant
2	631	80.4	132	2	AAR12354 Light (ka
3	626	79.7	131	2	AAR12232 Mouse Mab
4	555	70.7	113	2	Aaw39804 Variable
5	549	69.9	113	2	Aaw39882 Light cha
6	547	69.7	113	2	Aaw39803 Variable
7	547	69.7	113	2	Aaw39801 Variable
8	542	69.0	122	3	Aay70790 Murine an
9	541	68.9	113	2	Aaw39802 Variable
10	530	67.5	113	2	Aaw39886 Light cha

11	516	65.7	116	3	AAY32262	Aay32262 Humanised
12	509	64.8	100	4	AAE06989	Aae06989 Mouse ger
13	508	64.7	239	7	ADE28461	Ade28461 Human ant
14	505	64.3	239	3	AAW82617	Aay82617 Human PTH
15	505	64.3	239	3	AAW82615	Aay82615 Human PTH
16	505	64.3	274	2	AAW39899	Aaw39899 Single ch
17	504	64.2	239	3	AAW82611	Aay82611 Human PTH
18	504	64.2	239	3	ABG70338	Abg70338 Human MDD
19	500	63.7	239	7	ADE28405	Ade28405 Human ant
20	499	63.6	239	3	AAW82616	Aay82616 Human PTH
21	499	63.6	239	7	ADE28421	Ade28421 Human ant
22	499	63.6	239	7	ADE28465	Ade28465 Human ant
23	498	63.4	239	7	ADE28397	Ade28397 Human ant
24	497	63.3	142	7	ABR82929	AbR82929 Anti-huma
25	495.5	63.1	170	5	ABP64972	Abp64972 Human pro
26	495	63.1	141	2	AAR30454	Aar30454 C242:11 M
27	495	63.1	141	2	AAR32541	Aar32541 C242 kapp
28	495	63.1	239	3	AAW82614	Aay82614 Human PTH
29	495	63.1	239	3	AAW82610	Aay82610 Human PTH
30	494	62.9	133	2	AAR33951	Aar33951 CTMO1 VL
31	494	62.9	133	3	AAW56874	Aay56874 Mab CT-M-
32	493	62.8	242	6	ABU09337	Abu09337 Feline Ig
33	492	62.7	239	7	ADE28469	Ade28469 Human ant
34	491	62.5	239	7	ADE28521	Ade28521 Human ant
35	491	62.5	239	7	ADE28477	Ade28477 Human ant
36	490	62.4	239	3	AAW82618	Aay82618 Human PTH
37	489	62.3	139	4	AAW99117	Aab99117 Human pro
38	488	62.2	133	7	ADD25800	Add25800 Binding d
39	488	62.2	271	7	ADD25801	Add25801 Binding d
40	488	62.2	505	7	ADD25802	Add25802 Binding d
41	488	62.2	556	7	ADD25803	Add25803 Binding d
42	488	62.2	556	7	ADE86040	Ade86040 Anti-4-1B
43	487	62.0	239	6	ABR48456	Abr48456 Human Cal
44	483	61.5	134	2	AAR09420	Aar09420 B38.1 Lig
45	483	61.5	134	2	AAW06209	Aaw06209 Mab B38-1

#### ALIGNMENTS

RESULT 1  
AAY32261  
ID AAY32261 standard; protein; 145 AA.

XX AC AAY32261;

XX DT 15-FEB-2000 (first entry)

XX DE Mouse anti-CD23 Mab C11 light chain variable region.

XX KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
KW monoclonal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;  
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
KW therapy.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Region 55..70

FT /note= "CDR L1"

FT Region 83..92

FT /note= "CDR L2"

FT Region 125..134

FT /note= "CDR L3"

XX WO9958679-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001434.  
 XX PR 09-MAY-1998; 98GB-00009839.  
 XX PA (GLAX ) GLAXO GROUP LTD.  
 XX PI Bonhefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 XX DR WPI; 2000-053101/04.  
 XX DR N-PSDB; AA234746.  
 XX PT Cell receptor specific antibodies useful for treating e.g. arthritis,  
 XX PT diabetes, multiple sclerosis and psoriasis.  
 XX PS Claim 8; Fig 2; 81pp; English.  
 XX CC This sequence represents the light chain variable region (VL) of murine  
 CC anti-CD23 (PCERII) monoclonal antibody C11. The invention provides  
 CC altered antibodies, such as chimeric or humanised antibodies (see  
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions (see AAY32254-59) to render them capable of binding to the CD23  
 CC type II molecule expressed on haematopoietic cells. The antibodies are  
 CC used to block soluble CD23 formation in human therapy, for the treatment  
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents  
 XX SQ Sequence 145 AA;

Alignment Scores:  
 Pred. No.: 2,76e-72 Length: 145  
 Score: 737.00 Matches: 145  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 93.89% Indels: 0  
 DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x AAY32261 (1-145)

QY 3 GCTTTACGTTACTCAGCACACAGACCTCACCACGAGTTCTCTGTTTCAGTTCTGGG 62  
 Db 1 AlaLeuGlnLeuSerThrGlnAspLeuThrMetArgPheSerValGlnPheLeuGly 20  
 QY 63 GTGCTTATCTTCGAGTCTCTGGAGTCTAGTGGGATATTGTGATAACCCAGGATGAATC 122  
 Db 21 ValLeuMetPheTrpIleSerGlyValSerGlyAspIleValIleThrGlnAspGluLeu 40  
 QY 123 TCCATCTGTCTACTCTCGAATCAGTTCCTCCATCTCTCGAGTCTAGTAAGTCTC 182  
 Db 41 SerAsnProValThrSerGlyGluSerValSerIleSerCysArgSerSerIleSerLeu 60  
 QY 183 CTGTATAAGGATGGGAAGACATCTTGAATGGTTTCTGCAGACACAGGACAACTCTCT 242  
 Db 61 LeuTyrLysAspGlyLysThrThrLeuAsnTrpPheLeuGlnArgProGlyGlnSerPro 80  
 QY 243 CAGCTCTCTGATGTTTGTATGTCACCCGTCGATCAGAGTCTCAGACGGTTTAGTGGC 302  
 Db 81 GlnLeuLeuMetTyrLeuMetSerThrArgAlaSerGlyValSerAspArgPheSerGly 100  
 QY 303 AGTGGGTGAGGACAGATTTTACCCTGGAAATCAGTAGTGAAGCTGAGAGTGTGGGT 362  
 Db 101 SerGlySerGlyThrAspPheThrLeuGluIleSerArgValIleAlaGluAspValGly 120  
 QY 363 GTGTATTACTGTCAACAATCTGTAGAGTATCCATTCAGTTCGGCTCGGGGACAAAGTTG 422

Db 121 ValTyrTyrCysGlnGlnLeuValGluTyrProPheThrPheGlySerGlyThrLysLeu 140  
 QY 423 GAAATAAACGTACG 437  
 Db 141 GluIleLysArgThr 145  
 RESULT 2  
 AAR12354  
 ID AAR12354 standard; protein; 132 AA.  
 XX AC AAR12354;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 15-AUG-1991 (first entry)  
 XX DE Light (kappa) chain variable region of murine 2E12 immunoglobulin.  
 XX KW Chimeric antibodies; immunoconjugates; HIV; AIDS.  
 XX OS Mus musculus.  
 XX FN W09107493-A.  
 XX PD 30-MAY-1991.  
 XX PF 13-NOV-1989; 89US-00433730.  
 XX PR 13-NOV-1989; 89US-00433730.  
 XX PA (XOMA ) XOMA CORP.  
 XX PA (GREC ) GREEN CROSS CORP.  
 XX PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;  
 XX DR WPI; 1991-178105/24.  
 XX DR N-PSDB; AAQ12056.  
 XX PT New chimeric mouse-human antibodies - used to detect, kill and remove HIV  
 XX PS -1 antigen from sample.  
 XX SQ Disclosure; Fig 1; 107pp; English.  
 CC This is the light (kappa)- chain variable (V) region of a mouse  
 CC monoclonal antibody (MAB), 2E12, and is specific for an HIV-1 viral  
 CC antigen. It is used in the construction of a chimeric MAB comprising  
 CC heavy and light chains having murine V regions and human C regions. The  
 CC chimeric MABs are more effective than murine MAB 2E12 since they have an  
 CC increased compatibility in humans. The heavy and light chain V-regions  
 CC are joined by manipulating their respective joining (J) regions, to  
 CC generate restriction enzyme recognition sites. The chimeric MABs can be  
 CC used as immuno- conjugates, in association with e.g. toxins for HIV  
 CC treatment. They can also be used in diagnosis of HIV. See also AAQ12057-  
 CC 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003  
 CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)  
 XX SQ Sequence 132 AA;

Alignment Scores:  
 Pred. No.: 1,29e-60 Length: 132  
 Score: 631.00 Matches: 122  
 Percent Similarity: 96.21% Conservative: 5  
 Best Local Similarity: 92.42% Mismatches: 5  
 Query Match: 80.38% Indels: 0  
 DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x AAR12354 (1-132)

QY 36 ATGAGGTTCTCTCTCAGTTCTTGGGGTCTTATCTCTGGATCTCTGGAGTGGG 95  
 Db 1 MetArgCysSerLeuGlnPheLeuGlyValLeuMetPheTrpIleSerGlyValSerGly 20  
 QY 96 GATATTGTGATAAACCCAGGATGAATCTCCATCTCTGTCCTCTGGAGAAATCAGTTTC 155

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Db      21 GluIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 40
QY      156 ATCTCTCAGGCTAGTAAGAGTCTCTGTATTAAGATGGAAGACATATCTGAATGG 215
Db      41 PheSerCysAspSerSerLysSerLeuLeuTyrlYsaaspGlyLysThrTyrlLeuSerTrp 60
QY      216 TTTCTGCAGACAGGACCAATCTCCTCAGCTCCTGTATTTGATGATCTCCACCCGTGCA 275
Db      61 PheLeuGlnAsgProGlyGlnSerProGlnLeuLeuIleTyrlLeuMetSerThrArgVal 80
QY      276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGCAGCAGATTTTACCCCTGGAATC 335
Db      81 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 100
QY      336 AGTAGAGTCAGGCTGAGAGTGGGTGTATTACTGTCAACACTTGTAGAGTATCCA 395
Db      101 SerGlyValLysAlaGluAspValGlyValTyrlCysGlnGlnLeuValGluTyrlPro 120
QY      396 TTCACGTTCCGGTCCGGGACAAAGTTGGAATAFAAAA 431
Db      121 TyrThrPheGlyGlyThrLysLeuGluIleLys 132

RESULT 3
ID      AA012232 standard; protein; 131 AA.
AC      AAR12232;
XX      AAR12232;
DT      25-MAR-2003 (revised)
DT      19-AUG-1991 (first entry)
DE      Mouse MAB 2E12 L chain V region.
KW      HIV-1; chimera.
XX      Mus sp.
OS      WO9107494-A.
PN      30-MAY-1991.
PD      13-NOV-1989; 89US-00433703.
PF      13-NOV-1989; 89US-00433703.
PR      (XOMA ) XOMA CORP.
PA      (GREC ) GREEN CROSS CORP.
PA      (ZOMA-) ZOMA CORP.
XX      Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
PI      WPI; 1991-178106/24.
DR      N-PSDB; AAQ12012.
XX      New chimeric mouse human antibodies - used in treatment, diagnosis and
PT      prophylaxis of HIV infections.
XX      Disclosure; Fig 1; 108pp; English.
XX      The mouse VL gene product may be used to produce chimeric mouse- human
CC      Abs against HIV-1 comprising human Ig constant regions and murine
CC      variable regions. These novel sequence are useful in treatment, diagnosis
CC      and prophylaxis of HIV infections, and may be produced by a bacterial,
CC      yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
CC      PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX      SQ
XX      Sequence 131 AA;

Alignment Scores:
Pred. No.: 4.6e-60 Length: 131
Score: 626.00 Matches: 121
Percent Similarity: 96.18% Conservative: 5
Best Local Similarity: 92.37% Mismatches: 5

```

```

Query Match: 79.75% Indels: 0
DB: Gaps: 0
US-09-674-716B-2 (1-437) x AAR12232 (1-131)
QY      36 ATGAGGTTCTCTGTTCTCAGTTTCTGGGGTGCTTATGTTCTGATCTCTGGAGTCACTGGG 95
Db      1 MetArgCysSerLeuGlnPheLeuGlyValLeuMetPheTrpIleSerGlyValSerGly 20
QY      96 GATATTGTGTAACCCAGGATGNACTCTCAATCCTGTCTCACTCTCTGGAGAATCAGTTTCC 155
Db      21 GluIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 40
QY      156 ATCTCTCAGGCTCTAGTAAGAGTCTCTCTGTATTAAGATGGAAGACATATCTGAATGG 215
Db      41 PheSerCysArgSerSerLysSerLeuLeuTyrlYsaaspGlyLysThrTyrlLeuSerTrp 60
QY      216 TTTCTGCAGACAGCAGACAAATCTCCTCAGCTCCTGTATTTGATGATCTCCACCCGTGCA 275
Db      61 PheLeuGlnAsgProGlyGlnSerProGlnLeuLeuIleTyrlLeuMetSerThrArgVal 80
QY      276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGCAGCAGATTTTACCCCTGGAATC 335
Db      81 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 100
QY      336 AGTAGAGTCAGGCTGAGAGTGGGTGTATTACTGTCAACACTTGTAGAGTATCCA 395
Db      101 SerGlyValLysAlaGluAspValGlyValTyrlCysGlnGlnLeuValGluTyrlPro 120
QY      396 TTCACGTTCCGGTCCGGGACAAAGTTGGAATA 428
Db      121 TyrThrPheGlyGlyThrLysLeuGluIle 131

RESULT 4
AAW39804
ID      AAW39804 standard; protein; 113 AA.
AC      AAW39804;
XX      16-JUN-1998 (first entry)
DT      Variable domain of the Kappa light chain of catalytic antibody 2A10.
DE      Variable domain; lambda light chain; catalytic antibody; degradation;
KW      cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW      phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW      overdose; addiction.
XX      Mus sp.
XX      WO9749800-A1.
XX      31-DEC-1997.
XX      25-JUN-1997; 97WO-US010965.
XX      25-JUN-1996; 96US-00672345.
XX      (UYCO ) UNIV COLUMBIA NEW YORK.
XX      Landry DW;
XX      WPI; 1998-077166/07.
XX      New catalytic antibodies able to decompose cocaine, single-chain
PT      analogues - used to treat cocaine overdose and addiction, required in far
PT      smaller doses than antibodies that antagonise cocaine by simply binding.
XX      Claim 16; Page 73-74; 147pp; English.
XX      AAW39801-05 represent the amino acid sequences of the variable domain of
CC      the Kappa light chain of catalytic antibodies which are able to degrade
CC      cocaine. A series of cocaine transition state analogues (TSAs) were

```

CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809  
 CC represents the heavy chain) was identified using TSA1, which is an  
 CC immunogenic conjugate of a phosphate monoester transition state analogue.  
 CC Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the  
 CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved)

XX Sequence 113 AA;

Alignment Scores:  
 Pred. No.: 2,95e-52 Length: 113  
 Score: 555.00 Matches: 107  
 Percent Similarity: 97.35% Conservative: 3  
 Best Local Similarity: 94.69% Mismatches: 3  
 Query Match: 70.70% Indels: 0  
 DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x AAW39804 (1-113)

QY 96 GATATTGTGATACCCAGGATGAATCTCCAACTCTGCTCACTTCTGGAGATCAGTTTCC 155  
 Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
 QY 156 ATCTCTCGAGGCTCTAGTAAAGCTCTCCTGTATAGGATGGGAGACATCTGAAATTGG 215  
 Db 21 IleSerCysArgSerSerIysSerLeuLeuTyGluAspGlyLeuThrThrLeuAsnTrp 40  
 QY 216 TTTCTCGAGACAGACCAATCTCTCAGCTCCTGATGTTTGTATGTCACCCGTCGA 275  
 Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyLeuMetSerThrArgAla 60  
 QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGTCAAGTGGGTACGACAGATTTCACCTGGAATC 335  
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80  
 QY 336 AGTAGAGTGAAGGCTCAGGATGGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 395  
 Db 81 SerArgValIysAlaGluAspValGlyAlaTyTyCysGlnGlnPheValGluTyPro 100  
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACGT 434  
 Db 101 PheThrPheGlySerGlyThrLysLeuGluIleArgArg 113

RESULT 5

ID AAW39882 standard; protein; 113 AA.

AC AAW39882;

DT 16-JUN-1998 (first entry)

DE Light chain of the catalytic antibody 2A10.

KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX

PI Landry DW;

XX WPI; 1998-077166/07.

DR N-PSDB; AAV09789.

XX New catalytic antibodies able to decompose cocaine, single-chain

PT analogues - used to treat cocaine overdose and addiction, required in far

PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX Disclosure; Fig 21; 147pp; English.

XX The present sequence represents the light chain of a catalytic antibody  
 CC which is capable of degrading cocaine. A series of cocaine transition  
 CC state analogues (TSAs) were prepared and used to immunise mice for  
 CC production of hybridomas. Catalytic antibodies were identified by their  
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The  
 CC antibodies reduce the concentration of cocaine in a subject, and are used  
 CC particularly for the treatment of an overdose. They are also used for  
 CC treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

SQ Sequence 113 AA;

Alignment Scores:  
 Pred. No.: 1,35e-51 Length: 113  
 Score: 549.00 Matches: 105  
 Percent Similarity: 97.35% Conservative: 5  
 Best Local Similarity: 92.92% Mismatches: 3  
 Query Match: 69.94% Indels: 0  
 DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x AAW39882 (1-113)

QY 96 GATATTGTGATACCCAGGATGAATCTCCAACTCTGCTCACTTCTGGAGATCAGTTTCC 155  
 Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
 QY 156 ATCTCTCGAGGCTCTAGTAAAGCTCTCCTGTATAGGATGGGAGACATCTGAAATTGG 215  
 Db 21 IleSerCysArgSerSerIysSerLeuLeuTyGluAspGlyLeuThrThrLeuAsnTrp 40  
 QY 216 TTTCTCGAGACAGACCAATCTCTCAGCTCCTGATGTTTGTATGTCACCCGTCGA 275  
 Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyLeuMetSerThrArgAla 60  
 QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGTCAAGTGGGTACGACAGATTTCACCTGGAATC 335  
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80  
 QY 336 AGTAGAGTGAAGGCTCAGGATGGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 395  
 Db 81 SerArgValIysAlaGluAspValGlyAlaTyTyCysGlnGlnPheValGluTyPro 100  
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACGT 434  
 Db 101 PheThrPheGlySerGlyThrLysLeuGluIleArgArg 113

RESULT 6

AAW39803

ID AAW39803 standard; protein; 113 AA.

AC AAW39803;

XX 16-JUN-1998 (first entry)

XX Variable domain of the Kappa light chain of catalytic antibody 12H1.

KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX Mus sp.

XX	AC	AAW39801;
XX	PN	WO9749800-A1.
XX	PD	31-DEC-1997.
XX	DE	Variable domain of the Kappa light chain of catalytic antibody 3B9.
XX	PF	25-JUN-1997; 97WO-US010965.
XX	PR	25-JUN-1996; 96US-00672345.
XX	PA	(UYCO ) UNIV COLUMBIA NEW YORK.
XX	PI	Landry DW;
XX	OS	Mus sp.
XX	DR	WPI; 1998-077166/07.
XX	DN	P-PSDB; AAV09802.
XX	PD	New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addition, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
XX	PP	Claim 18; Page 73; 147pp; English.
XX	PS	AAW39801-05 represent the amino acid sequences of the variable domain of the kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808 represents the heavy chain) was identified using TSA2, and has a per minute Kcat of 0.016. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)
XX	SQ	Sequence 113 AA;
Alignment Scores:		
Pred. No.:	2,25e-51	Length: 113
Score:	547.00	Matches: 104
Percent Similarity:	98.23%	Conservative: 7
Best Local Similarity:	92.04%	Mismatches: 2
Query Match:	69.68%	Indels: 0
DB:	2	Gaps: 0
US-09-674-716B-2 (1-437) x AAW39803 (1-113)		
Qy	96	GATATTGTGATAACCCAGGATGAATCTCCAATCTGTCACTTCTGGAGATCAGTTTC 155
Dd	1	ASpIleValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
Qy	156	ATCTCTCGAGGTCTAGTAAGAGTCTCTGTATAAGAGTGGGAACATACTTGATGG 215
Dd	21	IleSerCysArgSerSerArgSerLeuTyArGaspGlyLysThrTyLeuAsnTrp 40
Qy	216	TTCCTGCAGAGCACGACAATCTCTCATCTCTAGTCTCTGATGTTTCATCTGCCCGTGCA 275
Dd	41	PheLeuGlnArgProGlyArgSerProGlnLeuLeuLeuTyLeuMetSerThrArgala 60
Qy	276	TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCCCTGGAATC 335
Dd	61	SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluile 80
Qy	336	AGTAGAGTMAGCTCAGAGTGGGTGTATTACTGTTCACACTTGTAGAGTATCCA 395
Dd	81	SerArgValLysalaGluAspValGlyValTyTyTyCysGlnHisPheValAspTyPro 100
Qy	396	TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAACAAGT 434
Dd	101	PheThrPheGlySerGlyThrLysLeuGluileLysArg 113
RESULT 7		
AAW39801		
ID	AAW39801 standard; protein; 113 AA.	

Db 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle 80  
 QY 336 AGTAGAGTGAAGCTGAGGAGTGGGTGTGTTACTGTCAACAACTGTAGAGTATCCA 395  
 Db 81 SerArgValIysAlaGluAspValGlyValTyr-Ty-CysGlnHisPheValAspTyrPro 100  
 QY 396 TTCACGTTCGGCTCGGGACAAAGTTGGAATFAAACGT 434  
 Db 101 PheThrPheGlySerGlyThrIysLeuGluIleLysArg 113

## RESULT 8

AAV70790

ID AAV70790 standard; protein; 122 AA.

XX

AC AAV70790;

XX

31-JUL-2000 (first entry)

XX

Murine anti-PAB-421 IDI-1 mAb light chain variable region.

XX

Murine; p53 protein; PAB-421; monoclonal antibody; mAb; IDI-1;

KW

anti-idiotypic antibody; DNA-binding domain; dermatological;

KW

immunosuppressive; antiinflammatory; autoimmune response; SLE;

KW

systemic lupus erythematosus; diagnosis; treatment; autoantigen;

KW

light chain variable region; VL; complementarity determining region; CDR.

XX

OS Mus sp.

XX

Key Location/Qualifiers

FH Region

FT 27..42

FT /label= CDR

FT /note= "Complementarity determining region"

FT 58..64

FT /label= CDR

FT /note= "Complementarity determining region"

FT 97..105

FT /label= CDR

FT /note= "Complementarity determining region"

XX WO200023082-A1.

XX

XX 27-APR-2000.

XX

PF 19-OCT-1999; 99WO-US024443.

XX

PR 19-OCT-1998; 98US-0104816P.

XX

PA (YEDA ) YEDA RES &amp; DEV CO LTD.

XX

PI Cohen IR, Rotter V, Erez-Alon N, Herkel J;

XX

DR WPI; 2000-339512/29.

XX

PT Treatment of systemic lupus erythematosus by down-regulating the

PT

protein response to the C-terminal DNA-binding domain of the p53

PT

protein by an active compound comprising of antibodies to p53 or

PT

fragments of p53.

XX

PS Claim 78; Fig 9; 87pp; English.

XX

CC The patent discloses a method for the treatment of systemic lupus

CC

erythematosus (SLE) by down-regulating the autoimmune response to the C-

CC

terminal DNA-binding domain of p53 protein by an active compound. The

CC

present sequence is a light chain variable region of IDI-1 an anti-

CC

idiotypic antibody/Ab2 monoclonal antibody (mAb) specific for PAB-421

## Alignment Scores:

Pred. No.: 8,15e-51 Length: 122  
 Score: 542.00 Matches: 104  
 Percent Similarity: 97.35% Conservative: 6  
 Best Local Similarity: 92.04% Mismatches: 3  
 Query Match: 69.04% Indels: 0  
 DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x AAY70790 (1-122)

QY 96 GATATTGTGATAACCCAGGATGAACCTCCCAATCCTGTCTACTTCTGGAGAAATCAGTTTCC 155  
 Db 4 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 23  
 QY 156 ATCTCTGCAGGTCTAGTAAGAGTCTCCTGTATAAGATCGGGAAGACATCTTGAATTGG 215  
 Db 24 IleSerCysArgSerArgGlnSerLeuLeuTyrLysAsnGlyLysThrTyrLeuAsnTrp 43  
 QY 216 TTTCTGCAGAGACAGGACACATCTCCTCAGCTCCTGATGATTTGATGTCCACCCGTGCA 275  
 Db 44 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleTyrLeuMetSerIleArgAla 63  
 QY 276 TCAGGAGTCTCAGACCCGGTTTAGTGGCAGTGGTTCAGGCACAGATTTCCCTGGAAATC 335  
 Db 64 SerGlyValSerAspArgPheSerGlyAsnGlySerGlyThrAspPheThrLeuGluIle 83  
 QY 336 AGTAGAGTGAAGCTGAGGAGTGGGTGTGTTACTGTCAACAACTGTAGAGTATCCA 395  
 Db 84 SerArgValArgAlaGluAspValGlyValTyr-Ty-CysGlnHisPheValAspTyrPro 103  
 QY 396 TTCACGTTCGGCTCGGGACAAAGTTGGAATFAAACGT 434  
 Db 104 TyrThrPheGlyGlyThrIysLeuGluIleLysArg 116

## RESULT 9

AAW39802

ID AAW39802 standard; protein; 113 AA.

XX

AC AAW39802;

XX

DT 16-JUN-1998 (first entry)

XX

DE Variable domain of the Kappa light chain of catalytic antibody 6A12.

XX

KW Variable domain; lambda light chain; catalytic antibody; degradation;

KW

cocaine; cocaine transition state analogue; TSA; benzoic acid;

KW

phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;

KW

overdose; addiction.

XX

OS Mus sp.

XX

FN WO9749800-A1.

XX

PD 31-DEC-1997.

XX

PF 25-JUN-1997; 97WO-US010965.

XX

XX 25-JUN-1996; 96US-00672345.

XX

(UYCO ) UNIV COLUMBIA NEW YORK.

PA

XX Landry DW;

XX

DR WPI; 1998-077166/07.

XX

PT New catalytic antibodies able to decompose cocaine, single-chain

PT

analogues - used to treat cocaine overdose and addiction, required in far

PT

smaller doses than antibodies that antagonise cocaine by simply binding.

XX

PS Claim 14; Page 72; 147pp; English.

XX

CC AAW39801-05 represent the amino acid sequences of the variable domain of



KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
XX therapy.  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
XX Region 1..23 /note= "framework region 1"  
XX Region 24..39 /note= "CDR 1"  
XX Region 40..54 /note= "framework region 2"  
XX Region 55..61 /note= "CDR 2"  
XX Region 62..93 /note= "framework region 3"  
XX Region 94..102 /note= "CDR 3"  
XX Region 103..113 /note= "framework region 4"  
XX WO9958679-A1.  
XX  
XX 18-NOV-1999.  
XX  
XX 07-MAY-1999; 99WO-GB001434.  
XX  
XX 09-MAY-1998; 98GB-00009839.  
XX  
XX (GLAX ) GLAXO GROUP LTD.  
XX  
XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
XX WPI; 2000-053101/04.  
XX N-PSDB; AA234747.  
XX  
XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
XX diabetes, multiple sclerosis and psoriasis.  
XX  
XX Claim 9; Fig 3; 81pp; English.  
XX  
XX This sequence represents the light chain variable region (VL) of  
XX humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human  
XX framework (H5IGKVII) and the light chain complementarity determining  
XX regions (see AY32254-56) of murine antibody C11. The DNA was constructed  
XX by splice overlap PCR. The invention provides altered antibodies, such as  
XX chimeric or humanised antibodies, which comprise sufficient of the amino  
XX acid sequences of the C11 light and heavy chain complementarity  
XX determining regions to render them capable of binding to the CD23 type II  
XX molecule expressed on haematopoietic cells. The antibodies are used to  
XX block soluble CD23 formation in human therapy, for the treatment of  
XX arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
XX sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
XX syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
XX colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
XX intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
XX versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
XX bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
XX malignancies (claimed). They are also useful for studying interactions  
XX between CD23 and various ligands and determining the binding agents  
XX Sequence 116 AA;

Alignment Scores:  
Pred. No.: 5.9e-48 Length: 116  
Score: 516.00 Matches: 99  
Percent Similarity: 92.98% Conservative: 7  
Best Local Similarity: 86.84% Mismatches: 8

Query Match: 65.73% Indels: 0  
Db: 3 Gaps: 0  
US-09-674-716B-2 (1-437) x AAY32262 (1-116)  
QY 96 GATATTCGTGTAACCCAGGATGAACCTCCCAACTCTGTCTCTGAGAGATCAGTTTCC 155  
Db 1 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20  
QY 156 ATCTCTCCAGGCTAGTACAGCTCCCTCTATAGATGGGAGACATCTGATTCG 215  
Db 21 IleSerCysArgSerSerLysSerLeuLeuTyLysAspGlyLysThrTyLysAsnTrp 40  
QY 216 TTTCTGCAGACACGAGCAATCTCTCAGCTCCTGATGATTTGATGTCACCCGTGCA 275  
Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLysLeuMetSerThrArgAla 60  
QY 276 TCAGAGTCTCAGACCGGTTTAGTGGAGTGGTTCAGGACAGATTCACCTGGAAATC 335  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAATTTAGAGTATCCA 395  
Db 81 SerArgValGluAlaGluAspValGlyValTyTyCysGlnGlnLeuValGluTyPro 100  
QY 396 TTCACGTTCCGCTCGGGGCAAAAGTTGGAAATAAAACGTACG 437  
Db 101 PheThrPheGlyGlnGlyThrLysValGluLeuLysArgThr 114  
RESULT 12  
AAE06969  
ID AAE06969 standard; protein; 100 AA.  
XX  
XX AAE06969;  
XX  
XX 16-OCT-2001 (first entry)  
XX  
XX Mouse germline kappa light chain variable (VK) region, 167/24.  
XX  
XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
XX neuroprotective; immunosuppressive; human immunodeficiency virus;  
XX HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
XX inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
XX multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
XX anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
XX fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
XX inflammatory glomerulopathy; vascular intervention;  
XX necrotic hyperplasia; VK; kappa light chain variable region.  
XX  
XX Mus sp.  
XX  
XX WO200157226-A1.  
XX  
XX 09-AUG-2001.  
XX  
XX 02-FEB-2001; 2001WO-US003537.  
XX  
XX 03-FEB-2000; 2000US-00497625.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Larosa GU, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
XX WPI; 2001-488888/53.  
XX  
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
XX disorder in a patient, comprises a binding specificity for CCR2, and a  
XX non-human antigen binding region and human immunoglobulin.  
XX  
XX Disclosure; Page 151; 183pp; English.  
XX  
XX The patent discloses a humanised antibody or its antigen-binding  
XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),





AAY82617  
 ID AAY82617 standard; protein; 239 AA.  
 AC  
 XX  
 DT  
 XX  
 XX  
 DE Human PTHrP monoclonal antibody clone 3G4-3 protein SEQ ID NO:18.  
 XX  
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;  
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
 KW antiarthritic; cytostatic; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 3 /label= Phe, Leu, Ile, Val  
 FT  
 FT Misc-difference 4 /label= Leu, Pro, His, Arg  
 FT  
 FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys  
 FT  
 FT Misc-difference 117 /label= Leu, Ile, Val  
 FT  
 FT  
 XX JP2000080100-A.  
 XX  
 XX 21-MAR-2000.  
 XX  
 XX 12-OCT-1998; 98JP-00304793.  
 XX  
 XX 17-JUN-1998; 98JP-00188196.  
 XX  
 XX 26-JUN-1998; 98JP-00196729.  
 XX  
 XX (NISR) JAPAN TOBACCO INC.  
 XX  
 XX WPI; 2000-286723/25.  
 XX N-PSDB; AAA13927.  
 XX  
 XX A human monoclonal antibody to parathyroid hormone related protein. -  
 XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 XX including metastasis, and pain.  
 XX  
 XX Claim 31; Page 51-52; 88pp; Japanese.  
 XX  
 XX The present invention describes a human monoclonal antibody to  
 XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 XX its fragments, following the stimulation of PTHrP has the following  
 XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 XX the release of calcium from bone; or (c) inhibits elevation of blood  
 XX calcium content. The monoclonal antibody can be used in the treatment of  
 XX hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 XX diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 XX (SIRS), and hypophosphataemia. It has antiarthritic, cytostatic and  
 XX antiinflammatory activities. The present sequence represents a human  
 XX PTHrP monoclonal antibody clone protein sequence from the present  
 XX invention  
 XX  
 XX Sequence 239 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1.15e-46 Length: 239  
 Score: 505.00 Matches: 96  
 Percent Similarity: 82.84% Conservative: 15  
 Best Local Similarity: 71.64% Mismatches: 23  
 Query Match: 64.33% Indels: 0  
 DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x AAY82617 (1-239)

QY 36 ATGAGGTTCTCTGTTCAAGTTTCTGGGGTGGCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95  
 |||||  
 Db 1 MetArg\*\*\*\*\*AlaGlnLeuLeuGlyLeuLeuMetPheTrpValSerGlySerSerGly 20  
 |||||  
 QY 96 GATATTGTGATACCCAGGATGAACCTCTCCAACTCTCTCACTCTCTGGAGAAATCAGTTTCC 155  
 |||||  
 Db 21 AspIleValMetThrGln\*\*\*ProLeuSerLeuProValThrProGlyGluProAlaSer 40  
 |||||  
 QY 156 ATCTCTCGAGTCTAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTGAATTGG 215  
 |||||  
 Db 41 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyAsnAsnTyrLeuAspTrp 60  
 |||||  
 QY 216 TTTCTGAGAGACAGGACAAATCTCTCAGCTCTCTGATGTTGATTTGATCCACCCGTGCA 275  
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 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnPheLeuIleTyrLeuGlySerAsnArgAla 80  
 |||||  
 QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTCAGTGGGTGAGGACAGATTCACCCCTGGAATC 335  
 |||||  
 Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 100  
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 QY 336 AGTAGAGTGAAGGCTGAGGATGTTGGTGTGTTATTCTGTCAACAACCTGTAGAGATCCA 395  
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 Db 101 SerArgValGluAlaGluAspValGlyValTyr-TyrCysMetGlnAla\*\*\*GlnThrPro 120  
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 QY 396 TTCAGGTCGGCTCGGGGACAAAGTTGGAAATAAAGCTACG 437  
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 Db 121 PheThrPheGlyProGlyThrLysValAspIleLysArgThr 134  
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 RESULT 15  
 AAY82615  
 ID AAY82615 standard; protein; 239 AA.  
 AC AAY82615;  
 XX  
 DT 02-AUG-2000 (first entry)  
 XX  
 DE Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.  
 XX  
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;  
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
 KW antiarthritic; cytostatic; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 155 /note= "possible Ala"  
 FT  
 FT  
 XX JP2000080100-A.  
 XX  
 XX 21-MAR-2000.  
 XX  
 XX 12-OCT-1998; 98JP-00304793.  
 XX  
 XX 17-JUN-1998; 98JP-00188196.  
 XX  
 XX 26-JUN-1998; 98JP-00196729.  
 XX  
 XX (NISR) JAPAN TOBACCO INC.  
 XX  
 XX WPI; 2000-286723/25.  
 XX N-PSDB; AAA13925.  
 XX  
 XX A human monoclonal antibody to parathyroid hormone related protein. -  
 XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 XX including metastasis, and pain.  
 XX  
 XX Claim 31; Page 45-46; 88pp; Japanese.  
 XX  
 XX The present invention describes a human monoclonal antibody to  
 XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 XX its fragments, following the stimulation of PTHrP has the following  
 XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 XX the release of calcium from bone; or (c) inhibits elevation of blood  
 XX calcium content. The monoclonal antibody can be used in the treatment of  
 XX hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 XX diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 XX (SIRS), and hypophosphataemia. It has antiarthritic, cytostatic and  
 XX antiinflammatory activities. The present sequence represents a human  
 XX PTHrP monoclonal antibody clone protein sequence from the present  
 XX invention  
 XX  
 XX Sequence 239 AA;  
 SQ

CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment of  
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a human  
 CC PTHrP monoclonal antibody clone protein sequence from the present  
 CC invention  
 XX  
 SQ Sequence 239 AA;

Alignment Scores:  
 Pred. No.: 1.15e-46 Length: 239  
 Score: 505.00 Matches: 95  
 Percent Similarity: 83.58% Conservative: 17  
 Best Local Similarity: 70.90% Mismatches: 22  
 Query Match: 64.33% Indels: 0  
 DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x AAY82615 (1-239)

QY	36	ATGAGGTTCTCTGTTTCAGTTCTGGGGTGTCTTATGTTCTGGATCTGGAGTCAGTGGG	95
DB	1	MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValSerGlySerGly	20
QY	96	GATATTGTGATAACCCAGATGAATCTCCATCTCTGTCACCTCTGGAGATCAGTTCC	155
DB	21	AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer	40
QY	156	ATCTCTCTGAGGTCGTAGTAAGAGTCTCTGTATAGGATGGAGACATCTTGAATTGG	215
DB	41	IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyAsnAsnTyrLeuAspTrp	60
QY	216	TTTCTGCAGAGACCGGACAAATCTCTCAGCTCTCTGATGATTTGATGTCACCCGTCCA	275
DB	61	TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla	80
QY	276	TCAGGAGTCTCAGACCGGTTTGTAGTGGGTGAGTGGGACAGATTCACCCCTGGAAATC	335
DB	81	SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle	100
QY	336	AGTAGAGTCAAGGCTGAGGATGTGGTGTATTACTGTCAACAACCTGTAGAGTATCCA	395
DB	101	SerArgValGluAlaGluAspValGlyIleTyrTyrCysMetGlnAlaLeuGlnThrPro	120
QY	396	TTACAGTTCGGCTCGGGCAAGTTGGAATAAAGCTACG	437
DB	121	PheThrPheGlyProGlyThrLysValAspIleLysArgThr	134

Search completed: September 30, 2004, 08:40:53

Job time : 55.0607 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: September 30, 2004, 08:41:28 ; Search time 10.688 Seconds  
(without alignments)  
4221.672 Million cell updates/sec

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Perfect score: 785  
Sequence: 1 aagtttaccagttactcagc.....agttggaaataaaacgtacg 437

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues  
Total number of hits satisfying chosen parameters: 778828  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2\_1/USPTO.spool\_p/US09674716/runat\_30092004.070259.25901/app.query.fasta.1.3164  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:  
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4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pcp:\*  
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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	555	70.7	113	2	US-08-672-345C-98
3	555	70.7	113	3	US-09-214-095D-8
4	549	69.9	113	3	US-09-214-095D-108
5	547	69.7	113	2	US-08-672-345C-5
6	547	69.7	113	2	US-08-672-345C-7
7	547	69.7	113	2	US-08-672-345C-95
8	547	69.7	113	2	US-08-672-345C-97
9	547	69.7	113	3	US-09-214-095D-5
10	547	69.7	113	3	US-09-214-095D-7
11	547	69.7	113	3	US-09-214-095D-100
12	547	69.7	113	3	US-09-214-095D-112

13	547	69.7	280	3	US-09-214-095D-119
14	541	68.9	113	2	US-08-672-345C-6
15	541	68.9	113	2	US-08-672-345C-96
16	541	68.9	113	3	US-09-214-095D-6
17	530	67.5	113	3	US-09-214-095D-104
18	495	63.1	141	1	US-08-438-123-7
19	494	62.9	133	1	US-08-253-877C-10
20	494	62.9	133	1	US-08-452-164A-10
21	494	62.9	133	3	US-08-603-024-4
22	493	62.8	242	4	US-09-479-614-20
23	481	61.3	132	1	US-08-392-419-4
24	477	60.8	135	1	US-08-259-372A-12
25	477	60.8	135	1	US-08-468-671-12
26	455	57.0	113	4	US-09-406-532-14
27	447.5	57.0	131	1	US-08-129-930B-95
28	447.5	57.0	131	3	US-08-134-346A-50
29	447.5	57.0	131	4	US-08-976-288A-95
30	447	56.9	112	3	US-08-483-749A-4
31	447	56.9	132	1	US-08-477-877B-91
32	447	56.9	132	2	US-08-472-281A-91
33	447	56.9	132	3	US-08-477-989B-91
34	439.5	56.0	131	3	US-08-589-939-7
35	438.5	55.9	149	4	US-09-192-838B-2
36	438.5	55.9	149	4	US-09-324-191-2
37	437	55.7	113	4	US-09-025-769B-15
38	436.5	55.6	149	2	US-08-752-844-2
39	436.5	55.6	149	2	US-08-591-196-2
40	436.5	55.6	149	4	US-09-293-533-2
41	436.5	55.6	238	3	US-09-192-545-4
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43	434.5	55.4	113	1	US-08-264-093-10
44	434	55.3	112	1	US-08-053-171-16
45	434	55.3	131	4	US-09-647-468-163

ALIGNMENTS

RESULT 1  
US-08-672-345C-8  
; Sequence 8, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/672,345C  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-672-345C-8

Alignment Scores:  
Pred. No.: 1.49e-59 Length: 113  
Score: 555.00 Matches: 107  
Percent Similarity: 97.35% Conservative: 3  
Best Local Similarity: 94.69% Mismatches: 3  
Query Match: 70.70% Indels: 0  
DB: Gaps: 2

US-09-674-716B-2 (1-437) x US-08-672-345C-8 (1-113)

QY 96 GATATTGTGATACCCAGGATGAACCTCCCAATCTCTGTCACCTTCTGGAGAATCAGTTTCC 155  
Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
QY 156 ATCTCTGAGGCTAGTAAGAGTCTCTGTAAGGATGGGAAGACATACCTGAATTGG 215  
Db 21 IleSerCysArgSerSerLySerLeuLeuTyGluAspGlyLeuThrTyrLeuAsnTrp 40  
QY 216 TTCTCTCAGAGACAGGACAAATCTCTCAGCTCCTGATGATTTGATGTCACCCGTCGA 275  
Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyrLeuMetSerThrArgala 60  
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTCAGGCACAGATTTACCTGGAAATC 335  
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80  
QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395  
Db 81 SerArgValIysAlaGluAspValGlyAlaTyrTyrCysGlnGlnPheValGluTyrPro 100  
QY 396 TTCACGTTCCGGTCGGGACAAAGTTGGAAATAAAACGT 434  
Db 101 PheThrPheGlySerGlyThrIysLeuGluIleArgArg 113

## RESULT 2

US-08-672-345C-8

Sequence 96, Application US/08672345C  
Patent No. 5948658  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald, W.  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper and Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,345C  
FILING DATE: 24-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 96:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-672-345C-98

Alignment Scores:  
Pred. No.: 1.49e-59 Length: 113  
Score: 555.00 Matches: 107  
Percent Similarity: 97.35% Conservative: 3  
Best Local Similarity: 94.69% Mismatches: 3  
Query Match: 70.70% Indels: 0  
DB: Gaps: 2

US-09-674-716B-2 (1-437) x US-08-672-345C-98 (1-113)

QY 96 GATATTGTGATACCCAGGATGAACCTCCCAATCTCTGTCACCTTCTGGAGAATCAGTTTCC 155  
Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
QY 156 ATCTCTGAGGCTAGTAAGAGTCTCTGTAAGGATGGGAAGACATACCTGAATTGG 215  
Db 21 IleSerCysArgSerSerLySerLeuLeuTyGluAspGlyLeuThrTyrLeuAsnTrp 40  
QY 216 TTCTCTCAGAGACAGGACAAATCTCTCAGCTCCTGATGATTTGATGTCACCCGTCGA 275  
Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyrLeuMetSerThrArgala 60  
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTCAGGCACAGATTTACCTGGAAATC 335  
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80  
QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395  
Db 81 SerArgValIysAlaGluAspValGlyAlaTyrTyrCysGlnGlnPheValGluTyrPro 100  
QY 396 TTCACGTTCCGGTCGGGACAAAGTTGGAAATAAAACGT 434  
Db 101 PheThrPheGlySerGlyThrIysLeuGluIleArgArg 113

## RESULT 3

US-09-214-095D-8

Sequence 8, Application US/09214095D  
Patent No. 6280987  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 51400-A-PCT-US  
CURRENT APPLICATION NUMBER: US/09/214,095D  
CURRENT FILING DATE: 1999-07-19  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 8  
LENGTH: 113  
TYPE: PRI  
ORGANISM: Murinae gen. sp.

US-09-214-095D-8

Alignment Scores:  
Pred. No.: 1.49e-59 Length: 113  
Score: 555.00 Matches: 107  
Percent Similarity: 97.35% Conservative: 3  
Best Local Similarity: 94.69% Mismatches: 3  
Query Match: 70.70% Indels: 0  
DB: Gaps: 2

US-09-674-716B-2 (1-437) x US-09-214-095D-8 (1-113)

QY 96 GATATTGTGATACCCAGGATGAACCTCCCAATCTCTGTCACCTTCTGGAGAATCAGTTTCC 155  
Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
QY 156 ATCTCTGAGGCTAGTAAGAGTCTCTGTAAGGATGGGAAGACATACCTGAATTGG 215

Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrGluAspGlyLysThrTyrLeuAsnTrp 40  
QY 216 TTTCTGCAGACACAGACAACTCTCCAGCTCCTGATGATTTGATGTCACCCGTGCA 275  
Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyrLeuMetSerThrArgala 60  
QY 276 TCAGGAGTCTCAGACCCGTTTAGTGGCAGTGCGGTGAGGTCAGGCACAGATTTTCACCCCTGGAAATC 335  
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80  
QY 336 AGTAGAGTGAAGCTGAGGATGCTGGGTGTGTATTACTGTCAACAACTTTAGAGTATCCA 395  
Db 81 SerArgValLysAlaGluAspValGlyAlaTyrTyrCysGlnGlnPheValGluTyrPro 100  
QY 396 TTCAGTTTCGGCTCGGGGACAAAGTTGGAATAAAACGT 434  
Db 101 PheThrPheGlySerGlyThrLysLeuGluileArgarg 113

## RESULT 4

US-09-214-095D-108

; Sequence 108, Application US/09214095D

; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214,095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 108

; LENGTH: 113

; TYPE: PRT

; ORGANISM: Murine

US-09-214-095D-108

## Alignment Scores:

Pred. No.:	8.1e-59	Length:	113
Score:	549.00	Matches:	105
Percent Similarity:	97.95%	Conservative:	5
Best Local Similarity:	92.92%	Mismatches:	3
Query Match:	69.94%	Indels:	0
DB:	3	Gaps:	0

US-09-674-716B-2 (1-437) x US-09-214-095D-108 (1-113)

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QY 156 ATCTCTGCAGGCTCTAGTAAGAGTCTCCTGTATAGGATGGAGACATCTTGAATTGG 215  
Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrGluAspGlyLysThrTyrLeuAsnTrp 40  
QY 216 TTTCTGCAGACACAGGACAACTCTCCTCAGCTCCTGTATTTGATGTCCACCCGTGCA 275  
Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyrLeuMetSerThrArgala 60  
QY 276 TCAGGAGTCTCAGACCCGTTTAGTGGCAGTGCGGTGAGGTCAGGCACAGATTTTCACCCCTGGAAATC 335  
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## RESULT 5

US-08-672-345C-5

; Sequence 5, Application US/08672345C

; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM: Floppy disk  
; MEDIUM TYPE: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-351-0525  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-672-345C-5

## Alignment Scores:

Pred. No.:	1.43e-58	Length:	113
Score:	547.00	Matches:	104
Percent Similarity:	98.23%	Conservative:	7
Best Local Similarity:	92.04%	Mismatches:	2
Query Match:	69.68%	Indels:	0
DB:	2	Gaps:	0

US-09-674-716B-2 (1-437) x US-08-672-345C-5 (1-113)

QY 96 GATATTGTGATAACCCAGGATGAATCTCCAACTCTGCTCACTTCTGGAGATCAGTTTC 155  
Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
QY 156 ATCTCTGCAGGCTCTAGTAAGAGTCTCCTGTATAGGATGGAGACATCTTGAATTGG 215  
Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrGluAspGlyLysThrTyrLeuAsnTrp 40  
QY 216 TTTCTGCAGACACAGGACAACTCTCCTCAGCTCCTGTATTTGATGTCCACCCGTGCA 275  
Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyrLeuMetSerThrArgser 60  
QY 276 TCAGGAGTCTCAGACCCGTTTAGTGGCAGTGCGGTGAGGTCAGGCACAGATTTTCACCCCTGGAAATC 335  
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80  
QY 336 AGTAGAGTGAAGCTGAGGATGCTGGGTGTGTATTACTGTCAACAACTTTGAGAGTATCCA 395  
Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro 100  
QY 396 TTCAGTTTCGGCTCGGGGACAAAGTTGGAATAAAACGT 434  
Db 101 PheThrPheGlySerGlyThrLysLeuGluileArgarg 113

## RESULT 6

US-08-672-345C-7

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; Sequence 7, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-7

```

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Alignment Scores:
Pred. No.: 1.43e-58 Length: 113
Score: 547.00 Matches: 104
Percent Similarity: 98.23% Conservative: 7
Best Local Similarity: 92.04% Mismatches: 2
Query Match: 69.68% Indels: 0
DB: 2 Gaps: 0

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US-09-674-716B-2 (1-437) x US-08-672-345C-7 (1-113)

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QY 96 GATATTGTGATAACCCAGGATGAATCTCCAAATCCTGTCACTCTCTGGAGAATCAGTTTCC 155
Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY 156 ATCTCTGAGCTCTAGTAAGAGTCTCCTGTATAGGATGGAGACATCTGTAATGG 215
Db 21 IleSerCysArgSerSerArgSerLeuLeuTyrArgAspGlyLysThrThrLeuAsnTrp 40
QY 216 TTCTCTCAGAGACCCAGGACAAATCTCCTCAGCTCTCTGATGTTTGTATGTCACCCGTCGA 275
Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuLeuTyrLeuMetSerThrArgAla 60
QY 276 TCAGAGATCTCAGCCGGTTTATGTCAGTGGGTGAGGACAGATTCACCTCGGAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLeu 80
QY 336 ACTAGAGTCAAGCGTCAGGATGTGGTGTGTATTACTGTCAACAACTGTGTAGATATCCA 395
Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro 100
QY 396 TTCACGTTCCGGTCGGGACAAAGTTGGAATAAAACGT 434
Db 101 PheThrPheGlySerGlyThrLysLeuGluLeuLysArg 113

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RESULT 7

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US-08-672-345C-95
; Sequence 95, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-95

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Alignment Scores:
Pred. No.: 1.43e-58 Length: 113
Score: 547.00 Matches: 104
Percent Similarity: 98.23% Conservative: 7
Best Local Similarity: 92.04% Mismatches: 2
Query Match: 69.68% Indels: 0
DB: 2 Gaps: 0

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US-09-674-716B-2 (1-437) x US-08-672-345C-95 (1-113)

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QY 96 GATATTGTGATAACCCAGGATGAATCTCCAAATCCTGTCACTCTCTGGAGAATCAGTTTCC 155
Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY 156 ATCTCTGAGCTCTAGTAAGAGTCTCCTGTATAGGATGGAGACATCTGTAATGG 215
Db 21 IleSerCysArgSerSerArgSerLeuLeuTyrArgAspGlyLysThrThrLeuAsnTrp 40
QY 216 TTCTCTCAGAGACCCAGGACAAATCTCCTCAGCTCTCTGATGTTTGTATGTCACCCGTCGA 275
Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuLeuTyrLeuMetSerThrArgSer 60
QY 276 TCAGAGATCTCAGCCGGTTTATGTCAGTGGGTGAGGACAGATTCACCTCGGAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLeu 80
QY 336 ACTAGAGTCAAGCGTCAGGATGTGGTGTGTATTACTGTCAACAACTGTGTAGATATCCA 395
Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro 100
QY 396 TTCACGTTCCGGTCGGGACAAAGTTGGAATAAAACGT 434
Db 101 PheThrPheGlySerGlyThrLysLeuGluLeuLysArg 113

```





Score: 547.00 Matches: 104  
 Percent Similarity: 98.23% Conservative: 7  
 Best Local Similarity: 92.04% Mismatches: 2  
 Query Match: 69.68% Indels: 0  
 DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-214-095D-7 (1-113)

QY 96 GATATTGTGATACCCAGGATGAATCTCCAACTCCTGTGACATCTCGGAGATCAATTTCC 155  
 DB 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
 QY 156 ATCTCTCGAGTCTAGTAAGAGTCTCTCTGTATAGGATGGGAGACATACCTTGAATTGG 215  
 DB 21 IleSerCysArgSerArgSerLeuLeuTyrArgAspGlyLysThrTyrLeuAsnTrp 40  
 QY 216 TTTCTGCAGAGCAGGACAAATCTCTCAGCTCCTGATGATGATTTGATGTCCACCCGTGCA 275  
 DB 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuTyrLeuMetSerThrArgala 60  
 QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTCCACCTGGAAATC 335  
 DB 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80  
 QY 336 AGTAGAGTGAAGCTGAGGATGTGGTGTGATTTACTGTCAACAACCTTGTAGAGTATCCA 395  
 DB 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro 100  
 QY 396 TTCACGTTCCGGTTCGGGGACAAAGTTGGAATAAAACGT 434  
 DB 101 PheThrPheGlySerGlyThrLysLeuGluileLysArg 113

## RESULT 11

US-09-214-095D-100  
 ; Sequence 100, Application US/09214095D  
 ; Patent No. 6280987  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 51400-A-PCT-US  
 ; CURRENT APPLICATION NUMBER: US/09/214,095D  
 ; CURRENT FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 100  
 ; LENGTH: 113  
 ; TYPE: PRT  
 ; ORGANISM: Murine  
 US-09-214-095D-100

Alignment Scores:  
 Pred. No.: 1,438-58 Length: 113  
 Score: 547.00 Matches: 104  
 Percent Similarity: 98.23% Conservative: 7  
 Best Local Similarity: 92.04% Mismatches: 2  
 Query Match: 69.68% Indels: 0  
 DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-214-095D-100 (1-113)

QY 96 GATATTGTGATACCCAGGATGAATCTCCAACTCCTGTGACATCTCGGAGATCAATTTCC 155  
 DB 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
 QY 156 ATCTCTCGAGTCTAGTAAGAGTCTCTCTGTATAGGATGGGAGACATACCTTGAATTGG 215  
 DB 21 IleSerCysArgSerArgSerLeuLeuTyrArgAspGlyLysThrTyrLeuAsnTrp 40  
 QY 216 TTTCTGCAGAGCAGGACAAATCTCTCAGCTCCTGATGATGATTTGATGTCCACCCGTGCA 275  
 DB 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuTyrLeuMetSerThrArgSer 60  
 QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTCCACCTGGAAATC 335

Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80  
 QY 336 AGTAGAGTGAAGCTGAGGATGTGGTGTGATTTACTGTCAACAACCTTGTAGAGTATCCA 395  
 Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro 100  
 QY 396 TTCACGTTCCGGTTCGGGGACAAAGTTGGAATAAAACGT 434  
 Db 101 PheThrPheGlySerGlyThrLysLeuGluileLysArg 113

## RESULT 12

US-09-214-095D-112  
 ; Sequence 112, Application US/09214095D  
 ; Patent No. 6280987  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 51400-A-PCT-US  
 ; CURRENT APPLICATION NUMBER: US/09/214,095D  
 ; CURRENT FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 112  
 ; LENGTH: 113  
 ; TYPE: PRT  
 ; ORGANISM: Murine  
 US-09-214-095D-112

Alignment Scores:  
 Pred. No.: 1,438-58 Length: 113  
 Score: 547.00 Matches: 104  
 Percent Similarity: 98.23% Conservative: 7  
 Best Local Similarity: 92.04% Mismatches: 2  
 Query Match: 69.68% Indels: 0  
 DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-214-095D-112 (1-113)

QY 96 GATATTGTGATACCCAGGATGAATCTCCAACTCCTGTGACATCTCGGAGATCAATTTCC 155  
 Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
 QY 156 ATCTCTCGAGTCTAGTAAGAGTCTCTCTGTATAGGATGGGAGACATACCTTGAATTGG 215  
 Db 21 IleSerCysArgSerArgSerLeuLeuTyrArgAspGlyLysThrTyrLeuAsnTrp 40  
 QY 216 TTTCTGCAGAGCAGGACAAATCTCTCAGCTCCTGATGATGATTTGATGTCCACCCGTGCA 275  
 Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuTyrLeuMetSerThrArgala 60  
 QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTCCACCTGGAAATC 335  
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80  
 QY 336 AGTAGAGTGAAGCTGAGGATGTGGTGTGATTTACTGTCAACAACCTTGTAGAGTATCCA 395  
 Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro 100  
 QY 396 TTCACGTTCCGGTTCGGGGACAAAGTTGGAATAAAACGT 434  
 Db 101 PheThrPheGlySerGlyThrLysLeuGluileLysArg 113

## RESULT 13

US-09-214-095D-119  
 ; Sequence 119, Application US/09214095D  
 ; Patent No. 6280987  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 51400-A-PCT-US  
 ; CURRENT APPLICATION NUMBER: US/09/214,095D  
 ; CURRENT FILING DATE: 1999-07-19

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; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 119
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-119

Alignment Scores:
Pred. No.: 2,1e-58 Length: 280
Score: 547.00 Matches: 105
Percent Similarity: 95.76% Conservatives: 8
Best Local Similarity: 88.98% Mismatches: 5
Query Match: 69.68% Indels: 0
DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-214-095D-119 (1-280)
QY 81 TCTGAGTCAGTGGGATATCTGTGATACCCAGGATGAACCTCTCAATCTCTGTCACCTTCT 140
Db 132 SerGlyGlyAlaMetAspIleValMetThrGlnAspGluLeuSerAsnProValThrSer 151
QY 141 GGAGAAATCAGTTCCATCTCTGAGGCTCTAGTAAGAGTCTCTGTATAAGGATGGGAAG 200
Db 152 GlyGluSerValSerIleSerCysArgSerSerArgSerLeuLeuTyrArgAspGlyLys 171
QY 201 ACATCTTGAATGGTTCTTCTGAGAGACAGACAACTCTCTAGCTCTCTGATGATTTTG 260
Db 172 ThrTyrLeuAsnTrpPheLeuGlnArgProGlyArgProGlnLeuLeuIleTyrLeu 191
QY 261 ATGTCCACCCGTCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGACGACAGAT 320
Db 192 MetSerThrArgSerSerGlyValSerAspArgPheSerGlySerGlySerGlyThrAsp 211
QY 321 TTCACCTCGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAA 380
Db 212 PheThrLeuGluIleSerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHis 231
QY 381 CTGTAGAGTATCCATTACGTTCCGCTCGGGACAAAGTTGGAAATAAAGCT 434
Db 232 PheValAspTyrProPheThrPheGlySerGlyThrLysLeuGluIleLysArg 249

RESULT 14
US-08-672-345C-6
; Sequence 6, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-6

Alignment Scores:
Pred. No.: 7,76e-58 Length: 113
Score: 541.00 Matches: 103
Percent Similarity: 97.35% Conservatives: 7
Best Local Similarity: 91.15% Mismatches: 3
Query Match: 68.92% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x US-08-672-345C-6 (1-113)
QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTCTGTCACCTCTCGAGAAATCAGTTTCC 155
Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY 156 ATCTCTCTGAGGCTCTAGTAAGAGTCTCTCTGTATAAGGATGGGAAGACATACCTTGAATTGG 215
Db 21 IleSerCysArgSerSerArgSerLeuLeuTyrArgAspGlyLysThrTyrLeuAsnTrp 40
QY 216 TTCTCGAGAGACAGACAACTCTCTAGCTCTCTGATGATTTGATGTCACCCCTGCA 275
Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyrLeuMetSerThrArgAla 60
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGACGACAGATTTCCCTGGAAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80
QY 336 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395
Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheGluAspTyrPro 100
QY 396 TTCAGTTCGGCTCGGGACAAAGTTGGAAATAAAGCT 434
Db 101 PheThrPheGlySerGlyThrLysLeuGluIleLysArg 113

RESULT 15
US-08-672-345C-96
; Sequence 96, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
```

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; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 113 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-672-345C-96

Alignment Scores:
Pred. No.:      7.76e-58      Length:      113
Score:          541.00        Matches:    103
Percent Similarity: 97.35%    Conservative: 7
Best Local Similarity: 91.15% Mismatches:    3
Query Match:     68.92%      Indels:      0
DB:              2          Gaps:          0

US-09-674-716B-2 (1-437) x US-08-672-345C-96 (1-113)

QY   96 GATATTGTGATACCCAGGATCAACTCTCCAATCCTGTCACTTCGAGAAATCAGTTTCC 155
Db   1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20

QY   156 AICTCTCTGAGGTCTAGTAAGAGTCTCCTGTATAGGATGGGAAGACATACCTGAATTGG 215
Db   21 IleSerCysArgSerSerArgSerLeuLeuTyArgAspGlyLysThrTyLeuAsnTrp 40

QY   216 TTTCTGCAGAGACGACGACAACTCTCTCAGCTCCTGATGTTATTTGATGTCACCGTGCA 275
Db   41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyLeuMetSerThrArgala 60

QY   276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTGAGGCACAGATTTCACCTGGAATC 335
Db   61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluile 80

QY   336 AGTAGAGTGAAGCTCAGGATGCTGGTGATGTTACTGTCAACAACCTTGTAGAGTATCCA 395
Db   81 SerArgValLysAlaGluAspValGlyValTyTyCysGlnHisPheGluAspIyrPro 100

QY   396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAATACGT 434
Db   101 PheThrPheGlySerGlyThrLysLeuGluIleLysArg 113
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Search completed: September 30, 2004, 09:31:35  
Job time : 12.688 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:54:09 ; Search time 57.3185 Seconds  
(without alignments)  
4906.833 Million cell updates/sec

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Perfect score: 785  
Sequence: 1 aagctttacagttactcagc.....agttggaataaaacgtacg 437

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1351062 seqs, 321799191 residues

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Minimum DB seq length: 0  
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Maximum Match 100%  
Listing first 45 summaries

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-TRANS=human40 cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
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-MAXLEN=200000000 -USER=US09674716@cgn 1.1.496 @runat\_30092004\_070302\_26027  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 4: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 12: /cgn2\_6/ptodata/1/pubpaa/US09E\_PUBCOMB.pep.\*
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- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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RESULT 1  
US-09-940-727B-8  
; Sequence 8, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-8

ALIGNMENTS

1	555	70.7	113	10	US-09-940-727B-8	Sequence 8, Appli
2	549	69.9	113	10	US-09-940-727B-108	Sequence 108, App
3	547	69.7	113	10	US-09-940-727B-5	Sequence 5, Appli
4	547	69.7	113	10	US-09-940-727B-7	Sequence 7, Appli
5	547	69.7	113	10	US-09-940-727B-100	Sequence 100, App
6	547	69.7	113	10	US-09-940-727B-112	Sequence 112, App
7	547	69.7	280	10	US-09-940-727B-119	Sequence 119, App
8	541	68.9	113	10	US-09-940-727B-6	Sequence 6, Appli
9	530	67.5	113	10	US-09-940-727B-104	Sequence 104, App
10	509	64.8	100	9	US-09-840-458-32	Sequence 32, Appl
11	509	64.8	100	16	US-10-766-773-32	Sequence 32, Appl
12	509	64.8	100	16	US-10-766-610-32	Sequence 32, Appl
13	509	64.8	100	16	US-10-733-563-32	Sequence 40, Appl
14	508	64.7	239	12	US-10-292-088-40	Sequence 41, Appl
15	506	64.5	239	12	US-10-404-724-41	Sequence 45, Appl
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17	505	64.3	239	12	US-10-404-724-39	Sequence 39, Appl
18	505	64.3	239	12	US-10-404-724-39	Sequence 39, Appl
19	504	64.2	247	12	US-10-466-164-69	Sequence 69, Appl
20	501	63.8	239	12	US-10-404-724-49	Sequence 49, Appl
21	500	63.7	239	12	US-10-292-088-16	Sequence 16, Appl
22	500	63.7	239	12	US-10-404-724-43	Sequence 43, Appl
23	500	63.7	239	12	US-10-404-724-47	Sequence 47, Appl
24	499	63.6	239	12	US-10-292-088-32	Sequence 32, Appl
25	499	63.6	239	12	US-10-292-088-56	Sequence 56, Appl
26	498	63.4	239	12	US-10-292-088-8	Sequence 1, Appli
27	497	63.3	142	15	US-10-372-719-1	Sequence 8, Appli
28	493	62.8	242	10	US-09-479-614-20	Sequence 20, Appl
29	493	62.8	242	15	US-10-409-772-20	Sequence 20, Appl
30	492	62.7	239	12	US-10-292-088-64	Sequence 64, Appl
31	492	62.7	239	12	US-10-404-724-12	Sequence 12, Appl
32	491	62.5	239	12	US-10-292-088-80	Sequence 80, Appl
33	491	62.5	239	12	US-10-292-088-102	Sequence 102, App
34	488	62.2	133	14	US-10-207-655-361	Sequence 361, App
35	488	62.2	271	14	US-10-207-655-362	Sequence 362, App
36	488	62.2	505	14	US-10-207-655-363	Sequence 363, App
37	488	62.2	556	12	US-10-107-991B-4	Sequence 364, App
38	488	62.2	556	14	US-10-207-655-364	Sequence 364, App
39	487	62.0	239	10	US-09-992-600A-8	Sequence 8, Appli
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41	487	62.0	239	10	US-09-992-095B-8	Sequence 8, Appli
42	487	62.0	239	10	US-09-999-570-8	Sequence 8, Appli
43	487	62.0	239	14	US-10-000-489-8	Sequence 8, Appli
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Alignment Scores:
Pred. No.: 6.08e-49 Length: 113
Score: 555.00 Matches: 107
Percent Similarity: 97.35% Conservative: 3
Best Local Similarity: 94.69% Mismatches: 3
Query Match: 70.70% Indels: 0
DB: 10 Gaps: 0

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QY 156 ATCTCTCGAGGCTTAGTAAGAGTCTCCTGTATAGAGTGGGAAGACATCTGAAATGG 215
Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrgluAspGlyLysThrThrLeuAsnTrp 40
QY 216 TTCTCTCAGACAGCAGGATCCTCCTCAGCTCCTGATGTTGATGTCACCCGTCGA 275
Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyLeuMetSerThrArgala 60
QY 276 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAGATTTCACCTGGAAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80
QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTCTATCTGTCACCAACTTGTAGAGTATCCA 395
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RESULT 3
US-09-940-727B-5
; Sequence 5, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940, 727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-5
Alignment Scores:
Pred. No.: 4.13e-48 Length: 113
Score: 547.00 Matches: 104
Percent Similarity: 98.23% Conservative: 7
Best Local Similarity: 92.04% Mismatches: 2
Query Match: 69.68% Indels: 0
DB: 10 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-940-727B-5 (1-113)
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QY 156 ATCTCTCGAGGCTTAGTAAGAGTCTCCTGTATAGAGTGGGAAGACATCTGAAATGG 215
Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrgluAspGlyLysThrThrLeuAsnTrp 40
QY 216 TTCTCTCAGACAGCAGGATCCTCCTCAGCTCCTGATGTTGATGTCACCCGTCGA 275
Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyLeuMetSerThrArgSer 60
QY 276 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAGATTTCACCTGGAAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80
QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTCTATCTGTCACCAACTTGTAGAGTATCCA 395
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US-09-940-727B-108
; Sequence 108, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940, 727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR FILING DATE: 09/214, 095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-108
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Pred. No.: 2.56e-48 Length: 113
Score: 549.00 Matches: 105
Percent Similarity: 97.35% Conservative: 5
Best Local Similarity: 92.92% Mismatches: 3
Query Match: 69.94% Indels: 0
DB: 10 Gaps: 0

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QY 396 TTCAGTTCGGCTCGGGACAAAGTTGGAATAAAACGT 434  
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Db 101 PheThrPheGlySerGlyThrLysLeuGluLeuLysArg 113

## RESULT 4

US-09-940-727B-7  
; Sequence 7, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-7

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Score: 547.00 Matches: 104  
Percent Similarity: 98.23% Conservative: 7  
Best Local Similarity: 92.04% Mismatches: 2  
Query Match: 69.68% Indels: 0  
DB: 10 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-940-727B-7 (1-113)

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QY 216 TTTCTGCAGACACGAGCAATCTCTCAGCTCCTGATGATTTATGATTCACCCGTGCA 275  
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Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuLeuTyLeuMetSerThrArgala 60  
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QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTATTAATCTGTCAACAACTTGAGAGTATCCA 395  
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QY 396 TTCACGTTCCGCTCGGGACAAAGTTGGAATAAAACGT 434  
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Db 101 PheThrPheGlySerGlyThrLysLeuGluLeuLysArg 113

## RESULT 5

US-09-940-727B-100  
; Sequence 100, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095

; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 100  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-100

Alignment Scores:  
Pred. No.: 4,13e-48 Length: 113  
Score: 547.00 Matches: 104  
Percent Similarity: 98.23% Conservative: 7  
Best Local Similarity: 92.04% Mismatches: 2  
Query Match: 69.68% Indels: 0  
DB: 10 Gaps: 0

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Db 21 IleSerCysArgSerSerArgSerLeuLeuTyraGspGlyLysThrTyLeuAsnTrp 40  
QY 216 TTTCTGCAGACACGAGCAATCTCTCAGCTCCTGATGATTTATGATTCACCCGTGCA 275  
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Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuLeuTyLeuMetSerThrArgSer 60  
QY 276 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGGTGAGTTCACCCGTGAAATC 335  
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Db 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluLe 80  
QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTATTAATCTGTCAACAACTTGAGAGTATCCA 395  
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Db 81 SerArgValLysAlaGluAspValGlyValTyTyrcysGlnHisPheValAspTyPro 100  
QY 396 TTCACGTTCCGCTCGGGACAAAGTTGGAATAAAACGT 434  
|||||  
Db 101 PheThrPheGlySerGlyThrLysLeuGluLeuLysArg 113

## RESULT 6

US-09-940-727B-112  
; Sequence 112, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 112  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-112

Alignment Scores:  
Pred. No.: 4,13e-48 Length: 113

Score: 547.00 Matches: 104  
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 Best Local Similarity: 92.04% Mismatches: 2  
 Query Match: 69.68% Indels: 0  
 DB: 10 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-940-727B-112 (1-113)

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 QY 156 ATCTCTGCAGGCTCTAGTAAGATCTCTCTGATPAGGATGGGAAGACATCTGAAATGG 215  
 Db 21 IleSerCysArgSerArgSerLeuLeuTyArgAspGlyLysThrTyLeuAsnTrp 40  
 QY 216 TTCTCTGAGAGACAGGACAACTCTCTCAGCTCCTGATGATTTGATGTCACCCCGTGA 275  
 Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyLeuMetSerThrArgAla 60  
 QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCCAGGCACAGATTTCCACCTGGAAATC 335  
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80  
 QY 336 AGTAGAGTGAAGCTGAGGATGCGGTGTGTTACTTACTGCAACAACCTGTAGAGTATCCA 395  
 Db 81 SerArgValLysAlaGluAspValGlyValTyTyCysGlnHisPheValAspTyPro 100  
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACGT 434  
 Db 101 PheThrPheGlySerGlyThrLysLeuGluIleLysArg 113

## RESULT 7

US-09-940-727B-119  
 ; Sequence 119, Application US/09940727B  
 ; Publication No. US2003007793A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald W  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 0575/51400-B  
 ; CURRENT APPLICATION NUMBER: US/09/940,727B  
 ; CURRENT FILING DATE: 2002-09-04  
 ; PRIOR FILING DATE: 1998-12-28  
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965  
 ; PRIOR FILING DATE: 1997-06-25  
 ; PRIOR APPLICATION NUMBER: 08/672,345  
 ; PRIOR FILING DATE: 1996-06-25  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 119  
 ; LENGTH: 280  
 ; TYPE: PRT  
 ; ORGANISM: mouse  
 US-09-940-727B-119.

Alignment Scores:  
 Pred. No.: 4,88e-48 Length: 280  
 Score: 547.00 Matches: 105  
 Percent Similarity: 95.76% Conservative: 8  
 Best Local Similarity: 88.98% Mismatches: 5  
 Query Match: 69.68% Indels: 0  
 DB: 10 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-940-727B-119 (1-280)

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 Db 132 SerGlyGlyAlaMetAspIleValMetThrGlnAspGluLeuSerAsnProValThrSer 151  
 QY 141 GGAGATCAGTTTCCATCTCTCGCAGGCTCTAGTAAGATCTCTGTATAGCATGGGAAG 200  
 Db 152 GlyGluSerValSerIleSerCysArgSerArgSerLeuLeuTyArgAspGlyLys 171

QY 201 ACATACTGATTTGGTTCTCTCAGAGACAGGACAAATCTCTCAGCTCCTGATGATTTG 260  
 Db 172 ThrTyLeuAsnTrpPheLeuGlnArgProGlyArgProGlnLeuLeuIleTyLeu 191  
 QY 261 ATGTCACCCCGTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCCAGGCACAGAT 320  
 Db 192 MetSerThrArgSerSerGlyValSerAspArgPheSerGlySerGlyThrAsp 211  
 QY 321 TTACCCCTGGAAATCAGTAGAGTGAAGCTCAGGATGTGGTGTGTTACTGTGCAACA 380  
 Db 212 PheThrLeuGluIleSerArgValLysAlaGluAspValGlyValTyTyCysGlnHis 231  
 QY 381 CTTCAGAGTATCATTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACGT 434  
 Db 232 PheValAspTyProPheThrPheGlySerGlyThrLysLeuGluIleLysArg 249

## RESULT 8

US-09-940-727B-6  
 ; Sequence 6, Application US/09940727B  
 ; Publication No. US2003007793A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald W  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 0575/51400-B  
 ; CURRENT APPLICATION NUMBER: US/09/940,727B  
 ; CURRENT FILING DATE: 2002-09-04  
 ; PRIOR FILING DATE: 1998-12-28  
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965  
 ; PRIOR FILING DATE: 1997-06-25  
 ; PRIOR APPLICATION NUMBER: 08/672,345  
 ; PRIOR FILING DATE: 1996-06-25  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 113  
 ; TYPE: PRT  
 ; ORGANISM: mouse  
 US-09-940-727B-6

Alignment Scores:  
 Pred. No.: 1,74e-47 Length: 113  
 Score: 541.00 Matches: 103  
 Percent Similarity: 97.35% Conservative: 7  
 Best Local Similarity: 91.15% Mismatches: 3  
 Query Match: 68.92% Indels: 0  
 DB: 10 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-940-727B-6 (1-113)

QY 96 GATATTGTGATACCCAGGATGAACCTCCAAATCCTGTGACTCTCGAGAAATCAGTTTCC 155  
 Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
 QY 156 ATCTCTGCAGGCTCTAGTAAGATCTCTCTGATPAGGATGGGAAGACATCTGAAATGG 215  
 Db 21 IleSerCysArgSerArgSerLeuLeuTyArgAspGlyLysThrTyLeuAsnTrp 40  
 QY 216 TTCTCTGAGAGACAGGACAAATCTCTCAGCTCCTGATGATTTGATGTCACCCCGTGA 275  
 Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyLeuMetSerThrArgAla 60  
 QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCCAGGCACAGATTTCCACCTGGAAATC 335  
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80  
 QY 336 AGTAGAGTGAAGCTGAGGATGCGGTGTGTTACTTACTGCAACAACCTGTAGAGTATCCA 395  
 Db 81 SerArgValLysAlaGluAspValGlyValTyTyCysGlnHisPheGluAspTyPro 100  
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACGT 434



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Db      101 PhetrPheGlySerGlyThrLysLeuGluIleLysArg 113
RESULT 9
US-09-940-727B-104
; Sequence 104, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 104
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-104

Alignment Scores:
Pred. No.:      2,43e-46      Length:      113
Score:          530.00      Matches:      102
Percent Similarity: 96.4%      Conservative: 7
Best Local Similarity: 90.2%      Mismatches: 4
Query Match:    67.52%      Indels:      0
DB:             10      Gaps:        0

US-09-674-716B-2 (1-437) x US-09-940-727B-104 (1-113)
QY      96 GATATTGTGATACCCAGGATGAACTCTCCAAATCTGTCACTTCTGGAGATCAGTTTCC 155
Db      1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY      156 ATCTCTCGCAGGTCTAGTAAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 215
Db      21 IleSerCysArgSerSerGlyLeuLeuTyArgpGlyLysThrTyrLeuAsnTrp 40
QY      216 TTCTTCGACAGACAGGACAACTCTCTCAGTCCTGTATTTGATGTCCACCCGTGCA 275
Db      41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyrLeuMetSerThrArgala 60
QY      276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTCCACCCGAAATC 335
Db      61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80
QY      336 AGTAGAGTGAAGGTGAGGATGTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395
Db      81 SerArgValLysAlaGluAspValGlyValTyrCysGlnLeuValGluTyrPro 100

RESULT 10
US-09-840-459-32
; Sequence 32, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0

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; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-32

Alignment Scores:
Pred. No.:      3.63e-44      Length:      100
Score:          509.00      Matches:      99
Percent Similarity: 100.00%      Conservative: 1
Best Local Similarity: 99.00%      Mismatches: 0
Query Match:    64.84%      Indels:      0
DB:             9      Gaps:        0

US-09-674-716B-2 (1-437) x US-09-840-459-32 (1-100)
QY      96 GATATTGTGATACCCAGGATGAACTCTCCAAATCTGTCACTTCTGGAGATCAGTTTCC 155
Db      1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY      156 ATCTCTCGCAGGTCTAGTAAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 215
Db      21 IleSerCysArgSerSerLysSerLeuLeuTyLysAspGlyLysThrTyrLeuAsnTrp 40
QY      216 TTCTTCGACAGACAGGACAACTCTCTCAGTCCTGTATTTGATGTCCACCCGTGCA 275
Db      41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleTyrLeuMetSerThrArgala 60
QY      276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTCCACCCGAAATC 335
Db      61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80
QY      336 AGTAGAGTGAAGGTGAGGATGTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395
Db      81 SerArgValLysAlaGluAspValGlyValTyrCysGlnLeuValGluTyrPro 100

RESULT 11
US-10-766-773-32
; Sequence 32, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0

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SEQ ID NO 32  
 ; LENGTH: 100  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-766-773-32

## Alignment Scores:

Pred. No.: 3,63e-44 Length: 100  
 Score: 509.00 Matches: 99  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 99.00%  
 DB: 64.84%  
 Indels: 0  
 Gaps: 0

US-09-674-716B-2 (1-437) x US-10-766-773-32 (1-100)

QY 96 GATATTGTGATACCCAGGATGAACCTCCCAATCCTGTCTGAGAGATCAGTTTCC 155  
 Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
 QY 156 ATCTCTGCAGGCTCTAGTAAGAGTCTCTCTGATAGGATGGGAGACATACCTTGAATTGG 215  
 Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrLysAspGlyLysThrTyrLeuAsnTrp 40  
 QY 216 TTCTCTGAGAGACAGACAACTCTCTCAGCTCCTGATGATTTGATGTCACCCCTGGAATC 275  
 Db 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleTyrLysAspGlyLysThrTyrLeuAsnTrp 60  
 QY 276 TCAGGAGTCTCAGACCGGTTTAGTGCGAGTGGGTGAGGACAGATTCACCCCTGGAATC 335  
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLeu 80  
 QY 336 AGTAGAGTGAAGCTGAGAGTGGGTGTGTATTACTGTCAACAACACTTGTAGAGTATCCA 395  
 Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnGlnLeuValGluTyrPro 100

## RESULT 12

US-10-766-610-32  
 ; Sequence 32, Application US/10766610  
 ; Publication No. US20040132980A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Larosa, Gregory J.  
 ; APPLICANT: Horvath, Christopher  
 ; APPLICANT: Newman, Walter  
 ; APPLICANT: Jones, S. Tartan  
 ; APPLICANT: O'Brien, Siobhan H.  
 ; APPLICANT: O'Keefe, Theresa  
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
 ; TITLE OF INVENTION: METHODS OF USE THEREFOR  
 ; FILE REFERENCE: 1855,1052-029  
 ; CURRENT APPLICATION NUMBER: US/10766,610  
 ; PRIOR FILING DATE: 2004-01-27  
 ; PRIOR APPLICATION NUMBER: 09/840,459  
 ; PRIOR FILING DATE: 2001-04-23  
 ; PRIOR APPLICATION NUMBER: PCT/US01/03537  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: 09/497,625  
 ; PRIOR FILING DATE: 2000-02-03  
 ; PRIOR APPLICATION NUMBER: 09/359,193  
 ; PRIOR FILING DATE: 1999-07-22  
 ; PRIOR APPLICATION NUMBER: 09/121,781  
 ; PRIOR FILING DATE: 1998-07-23  
 ; NUMBER OF SEQ ID NOS: 107  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 32  
 ; LENGTH: 100  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-766-610-32

## Alignment Scores:

Pred. No.: 3,63e-44 Length: 100  
 Score: 509.00 Matches: 99

Percent Similarity: 100.00%  
 Best Local Similarity: 99.00%  
 Query Match: 99.00%  
 DB: 64.84%  
 Indels: 0  
 Gaps: 0

US-09-674-716B-2 (1-437) x US-10-766-610-32 (1-100)

QY 96 GATATTGTGATACCCAGGATGAACCTCCCAATCCTGTCTGAGAGATCAGTTTCC 155  
 Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
 QY 156 ATCTCTGCAGGCTCTAGTAAGAGTCTCTCTGATAGGATGGGAGACATACCTTGAATTGG 215  
 Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrLysAspGlyLysThrTyrLeuAsnTrp 40  
 QY 216 TTCTCTGAGAGACAGACAACTCTCTCAGCTCCTGATGATTTGATGTCACCCCTGGAATC 275  
 Db 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleTyrLysAspGlyLysThrTyrLeuAsnTrp 60  
 QY 276 TCAGGAGTCTCAGACCGGTTTAGTGCGAGTGGGTGAGGACAGATTCACCCCTGGAATC 335  
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLeu 80  
 QY 336 AGTAGAGTGAAGCTGAGAGTGGGTGTGTATTACTGTCAACAACACTTGTAGAGTATCCA 395  
 Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnGlnLeuValGluTyrPro 100

## RESULT 13

US-10-733-563-32  
 ; Sequence 32, Application US/10733563  
 ; Publication No. US20040151721A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: O'Keefe, Theresa  
 ; APPLICANT: Ponath, Paul  
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
 ; TITLE OF INVENTION: METHODS OF USE THEREOF  
 ; FILE REFERENCE: 10448-213001  
 ; CURRENT APPLICATION NUMBER: US/10733,563  
 ; CURRENT FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: US 10/272,899  
 ; PRIOR FILING DATE: 2002-10-17  
 ; PRIOR APPLICATION NUMBER: US 60/392,364  
 ; PRIOR FILING DATE: 2002-06-26  
 ; PRIOR APPLICATION NUMBER: US 60/350,166  
 ; PRIOR FILING DATE: 2001-10-19  
 ; NUMBER OF SEQ ID NOS: 122  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 32  
 ; LENGTH: 100  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-733-563-32

## Alignment Scores:

Pred. No.: 3,63e-44 Length: 100  
 Score: 509.00 Matches: 99  
 Percent Similarity: 100.00%  
 Best Local Similarity: 99.00%  
 Query Match: 99.00%  
 DB: 64.84%  
 Indels: 0  
 Gaps: 0

US-09-674-716B-2 (1-437) x US-10-733-563-32 (1-100)

QY 96 GATATTGTGATACCCAGGATGAACCTCCCAATCCTGTCTGAGAGATCAGTTTCC 155  
 Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20  
 QY 156 ATCTCTGCAGGCTCTAGTAAGAGTCTCTCTGATAGGATGGGAGACATACCTTGAATTGG 215  
 Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrLysAspGlyLysThrTyrLeuAsnTrp 40  
 QY 216 TTCTCTGAGAGACAGACAACTCTCTCAGCTCCTGATGATTTGATGTCACCCCTGGAATC 275

Db 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLeuTyrLeuMetSerThrArgAla 60  
QY 276 TCAGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGCAGACAGATTTCAACCTGGAAATC 335  
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80  
QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395  
Db 81 SerArgValValAlaGluAspValGlyValTyrCysGlnGlnLeuValGluTyrPro 100

RESULT 14

US-10-292-088-40  
; Sequence 40, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PP/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-088-40

Alignment Scores:  
Pred. No.: 5,42e-44 Length: 239  
Score: 508.00 Matches: 96  
Percent Similarity: 84.33% Conservative: 17  
Best Local Similarity: 71.64% Mismatches: 21  
Query Match: 64.71% Indels: 0  
DB: 12 Gaps: 0

US-09-674-716B-2 (1-437) x US-10-292-088-40 (1-239)

QY 36 ATGAGGTTCTCTGTTCAAGTTTCGGGGTGTATTGTTCTGGATCTCTGGAGTCAGTGGG 95  
Db 1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValSerGlySerGly 20  
QY 96 GATATTGTGATACCCAGGATGACTCTCCATCTCTGTCACCTCTGGAGAACAGTTCCTCC 155  
Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40  
QY 156 ATCTCTGTCAGGTCTAGTAAAGATCTCTCTGTATAGGATGGGAGACATATCTGAATTGG 215  
Db 41 IleSerCysArgSerSerGlnSerValLeuTyrSerAsnGlyTyrAsnTyrLeuAspTrp 60  
QY 216 TTTCTGCAGACACGACCAATCTCTCAGCTCTGATGTTGATGTTGATGTTGATGTTGATGTTG 275  
Db 41 IleSerCysArgSerSerGlnSerValLeuTyrSerAsnGlyTyrAsnTyrLeuAspTrp 60  
QY 276 TTTCTGCAGACACGACCAATCTCTCAGCTCTGATGTTGATGTTGATGTTGATGTTGATGTTG 275  
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrCysAlaGlnAsnLeuLeuPro 120  
QY 276 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGACAGATTTCAACCTGGAAATC 335  
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100  
QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395  
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnValLeuGlnThrPro 120  
QY 396 TTCACGTTCCGCTCGGGACAAAGTTGGAATAAAACGTACG 437  
Db 121 PheThrPheGlyProGlyThrLysValAspIleLysArgThr 134

RESULT 15

US-10-404-724-41  
; Sequence 41, Application US/10404724  
; Publication No. US20030203447A1  
; GENERAL INFORMATION:  
; APPLICANT: Horwitz, Arnold H.  
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant  
; FILE REFERENCE: Polypeptides  
; FILE REFERENCE: 13698US01  
; CURRENT APPLICATION NUMBER: US/10/404,724  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/368,530  
; PRIOR FILING DATE: 2002-03-29  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 41  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-404-724-41

Alignment Scores:  
Pred. No.: 8,74e-44 Length: 239  
Score: 506.00 Matches: 99  
Percent Similarity: 83.58% Conservative: 13  
Best Local Similarity: 73.88% Mismatches: 22  
Query Match: 64.46% Indels: 0  
DB: 12 Gaps: 0

US-09-674-716B-2 (1-437) x US-10-404-724-41 (1-239)

QY 36 ATGAGGTTCTCTGTTCAAGTTTCGGGGTGTATTGTTCTGGATCTCTGGAGTCAGTGGG 95  
Db 1 MetArgPheSerAlaGlnLeuLeuGlyLeuLeuValLeuTrpIleProGlySerThrAla 20  
QY 96 GATATTGTGATACCCAGGATGAACTCTCCAATCTCTGTCACCTCTCTGGAGAACAGTTCCTCC 155  
Db 21 AspIleValMetThrGlnSerAlaLeuSerAsnProValThrProGlyGluSerGlySer 40  
QY 156 ATCTCTGTCAGGTCTAGTAAAGATCTCTGTATAGGATGGGAGACATATCTGAATTGG 215  
Db 41 IleSerCysArgSerSerLysSerLeuLeuHisSerAsnGlyIleThrTyrLeuTyrTrp 60  
QY 216 TTTCTGCAGACACGACCAATCTCTCAGCTCTCTGATGTTGATGTTGATGTTGATGTTGATGTTG 275  
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrGlnMetSerAsnArgAla 80  
QY 276 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGACAGATTTCAACCTGGAAATC 335  
Db 81 SerGlyValProAspArgPheSerSerSerGlySerGlyThrAspPheThrLeuLysIle 100  
QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395  
Db 101 SerArgValGluAlaGluAspValGlyValTyrTyrCysAlaGlnAsnLeuLeuPro 120  
QY 396 TTCACGTTCCGCTCGGGACAAAGTTGGAATAAAACGTACG 437  
Db 121 ArgThrPheGlyGlnGlyThrLysLeuGluMetLysArgThr 134

Search completed: September 30, 2004, 09:48:30  
Job time : 59.3185 secs

Blank sheet

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 17.3559 Seconds  
(without alignments)  
88.677 Million cell updates/sec

Title: US-09-674-716B-3

Perfect score: 81  
Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	112	1 KVM516	Ig kappa chain V r
2	81	100.0	113	1 KVM551	Ig kappa chain V r
3	81	100.0	120	1 KVM567	Ig kappa chain pre
4	81	100.0	120	2 A23775	Ig kappa chain pre
5	81	100.0	120	2 B23775	Ig kappa chain pre
6	66	81.5	112	2 PLO273	Ig kappa chain V r
7	65	80.2	133	2 S40324	Ig kappa chain V r
8	64	79.0	83	2 S34095	Ig kappa chain V r
9	64	79.0	111	2 S20709	Ig kappa chain V r
10	64	79.0	120	2 S42267	Ig kappa chain V r
11	64	79.0	120	2 S42268	Ig kappa chain V r
12	64	79.0	133	1 K2HURP	Ig kappa chain pre
13	63	77.8	114	2 S49572	Ig kappa chain pre
14	61	75.3	101	2 PH1057	Ig light chain V r
15	61	75.3	113	1 K2HUFH	Ig kappa chain V-I
16	61	75.3	122	2 S40338	Ig kappa chain - h
17	60	74.1	112	2 PLO275	Ig kappa chain V r
18	60	74.1	133	2 S42611	HUNVK protein prec
19	60	74.1	249	2 S41374	single chain Fv an
20	59	72.8	87	2 S34094	Ig kappa chain V r
21	59	72.8	91	2 S42186	Ig kappa chain V r
22	59	72.8	101	2 A33730	Ig kappa chain V r
23	59	72.8	103	2 PH1055	Ig light chain V r
24	59	72.8	103	2 PH1056	Ig light chain V r
25	59	72.8	112	2 S42659	Ig kappa chain V r
26	59	72.8	113	2 F30560	Ig kappa chain V r
27	59	72.8	132	2 S32513	Ig kappa chain pre
28	59	72.8	133	2 S23230	Ig kappa chain pre
29	59	72.8	140	2 S23658	Ig kappa chain pre

## ALIGNMENTS

## RESULT 1

KVM516  
Ig kappa chain V region (M167) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 16-Aug-1996  
C:Accession: A01908  
R:Rudikoff, S.; Potter, M.  
Biochemistry 17, 2703-2707, 1978  
A:Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prote  
A:Reference number: A01908; MUID:79000273; PMID:99160  
A:Accession: A01908  
A:Molecule type: protein  
A:Residues: 1-112 <RUD>  
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine. 1  
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kapp  
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer  
F:16-95/Domain: immunoglobulin homology <IMM>  
F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 81; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
DB 24 RSSKSLLYKDGKTYLN 39

## RESULT 2

KVM551  
Ig kappa chain V region (M511) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000  
R:Appella, E.  
Mol. Immunol. 17, 711-718, 1980  
A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcho  
A:Reference number: A01910; MUID:81052016; PMID:6776396  
A:Accession: A01910  
A:Molecule type: protein  
A:Residues: 1-113 <APP>  
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.  
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kapp  
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer  
F:16-95/Domain: immunoglobulin homology <IMM>  
F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 81; DB 1; Length 113;

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Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
    |||||
Db 24 RSSKSLLYKDGKTYLN 39

RESULT 3
KWS67
Ig kappa chain precursor V region (VK167) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000
C:Accession: A01909
R:Seising, E.; Scorb, U.
Cell 25, 47-58, 1981
A:Title: Somatic mutation of immunoglobulin light-chain variable-region genes.
A:Reference number: A01909; MUID:82002223; PMID:6791832
A:Accession: A01909
A:Molecule type: DNA
A:Residues: 1-120 <SEL>
A:Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted

Query Match 100.0%; Score 81; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
    |||||
Db 44 RSSKSLLYKDGKTYLN 59

RESULT 4
A29775
Ig kappa chain precursor V region (mouse 24.2) - shrew mouse
C:Species: Mus pahari
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C:Accession: A29775
R:Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A:Title: Evolution of a V-kappa gene family.
A:Reference number: A91751; MUID:87006895; PMID:3093373
A:Accession: A29775
A:Molecule type: DNA
A:Residues: 1-120 <YOU>
A:Cross-references: GB:M1552; NID:gl97468; PIDN:AAA39036.1; PID:gl97469
A:Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region 24.2 #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
    |||||
Db 44 RSSKSLLYKDGKTYLN 59

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RESULT 5
B29775
Ig kappa chain precursor V region (mouse 24.1) - shrew mouse
C:Species: Mus pahari
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C:Accession: B29775
R:Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A:Title: Evolution of a V-kappa gene family.
A:Reference number: A91751; MUID:87006895; PMID:3093373
A:Accession: B29775
A:Molecule type: DNA
A:Residues: 1-120 <YOU>
A:Cross-references: GB:M1553; NID:gl97470; PIDN:AAA39037.1; PID:gl97471
A:Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region 24.1 #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
    |||||
Db 44 RSSKSLLYKDGKTYLN 59

RESULT 6
PL0273
Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0273
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0273
A:Molecule type: mRNA
A:Residues: 1-112 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-95/Domain: immunoglobulin homology <IMM>
F:24-39/Region: complementarity-determining 1
F:40-54/Region: framework 2
F:55-61/Region: complementarity-determining 2
F:62-93/Region: framework 3
F:94-102/Region: complementarity-determining 3
F:103-112/Region: framework 4

Query Match 81.5%; Score 66; DB 2; Length 112;
Best Local Similarity 75.0%; Pred. No. 0.00037;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
    |||||
Db 24 RSSKSLLYKDGKTYLN 39

RESULT 7
S40324
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40324
R:Klein, R.; Jaenichen, R.; Zachau, H.G.

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Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:9408091; PMID:8258341
A:Accession: S40324
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-133 <KLE>
A:Cross-references: EMBL:X72434
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-112/Domain: immunoglobulin homology <IMM>

Query Match      80.2%; Score 65; DB 2; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.0017;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
DB 41 RSDQSLVYSDGNTYLN 56

RESULT 8
IG kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34095
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34095
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <WAG>
C:Cross-references: EMBL:X67179
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-80/Domain: immunoglobulin homology <IMM>

Query Match      79.0%; Score 64; DB 2; Length 83;
Best Local Similarity 75.0%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
DB 9 RSDQSLVYSDGNTYLN 24

RESULT 9
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20709
R:Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Ost
submitted to the EMBL Data Library, April 1992
A:Description: Binding specificity and variable region sequences of two monoclonal antib
A:Reference number: S20706
A:Accession: S20709
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <BRE>
A:Cross-references: EMBL:Z11917; NID:G52655; PIDN:CAA77975.1; PID:G52656
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      79.0%; Score 64; DB 2; Length 111;
Best Local Similarity 75.0%; Pred. No. 0.0021;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16

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DB 24 KSSQSLHSDGKTYLN 39

RESULT 10
IG kappa chain V region (A1) - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S42267
R:Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zoc
Eur. J. Immunol. 22, 1023-1029, 1992
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated A regic
A:Reference number: A49043; MUID:92201291; PMID:1551402
A:Accession: S42267
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <LAU>
A:Cross-references: EMBL:X63402
C:Genetics:
A:Introns: 17/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match      79.0%; Score 64; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
DB 44 RSSQSLVYSDGNTYLN 59

RESULT 11
IG kappa chain V region (A17) - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000
C:Accession: S42268
R:Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zoc
Eur. J. Immunol. 22, 1023-1029, 1992
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated A regic
A:Reference number: A49043; MUID:92201291; PMID:1551402
A:Accession: S42268
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <LAU>
A:Cross-references: EMBL:X63403
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match      79.0%; Score 64; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
DB 44 RSSQSLVYSDGNTYLN 59

RESULT 12
K2HURP
IG kappa chain precursor V-II region (RPM1) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997
C:Accession: A01890
R:Klobeck, H.G.; Meindl, A.; Combrato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A:Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A:Reference number: A93588; MUID:86041852; PMID:2997711
A:Accession: A01890

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A:Molecule type: DNA
A:Residues: 1-133 <KLO>
A>Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPM1) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-115/Domain: immunoglobulin homology <IMM>
F:44-59/Region: complementarity-determining 1
F:60-74/Region: framework 2
F:75-81/Region: complementarity-determining 2
F:82-113/Region: framework 3
F:114-122/Region: complementarity-determining 3
F:123-133/Region: framework 4
F:43-113/Disulfide bonds: #status predicted

Query Match 79.0%; Score 64; DB 1; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.0025;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 44 RSSQSLVYDGNLYN 59

RESULT 13
S49572
IG kappa chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C:Accession: S49572
R:Giachino, C.; Padovan, E.; Lanzavecchia, A.
submitted to the EMBL Data Library, November 1994
A:Description: K-1+ dual receptor B cells are present in the human peripheral repertoire
A:Reference number: S49571
A:Accession: S49572
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <GIA>
A:Cross-references: EMBL:246626; NID:g575261; PIDN:CAA6596.1; PID:g575262
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 63; DB 2; Length 114;
Best Local Similarity 75.0%; Pred. No. 0.0031;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSQSLVYDGNLYN 39

RESULT 14
PH1057
IG light chain V region (clone 17s.145) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1057
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell clones
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1057
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA

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A:Residues: 1-101 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 61; DB 2; Length 101;
Best Local Similarity 80.0%; Pred. No. 0.0059;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 15
Db 24 RSSQSLVYDGNLYN 38

RESULT 15
K2HUPR
IG kappa chain V-II region (Fr) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A01886
R:Rieser, W.F.; Jaton, J.C.
Biochemistry 15, 3829-3833, 1976
A:Title: Variable region sequence of the light chain from a Waldenstrom's IgM with specific disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology
C:Superfamily: heterotetramer
C:Keywords: heterotetramer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match 75.3%; Score 61; DB 1; Length 113;
Best Local Similarity 62.5%; Pred. No. 0.0066;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSQSLVYRGGTYLB 39

Search completed: September 30, 2004, 06:00:31
Job time : 18.3559 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 52.339 Seconds  
(without alignments)  
96.454 Million cell updates/sec

Title: US-09-674-716B-3

Perfect score: 81  
Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: sp archaea.\*
- 2: sp bacteria.\*
- 3: sp fungi.\*
- 4: sp human.\*
- 5: sp invertebrate.\*
- 6: sp mammal.\*
- 7: sp mhc.\*
- 8: sp organelle.\*
- 9: sp phage.\*
- 10: sp plant.\*
- 11: sp rodent.\*
- 12: sp virus.\*
- 13: sp vertebrate.\*
- 14: sp unclassified.\*
- 15: sp rvirus.\*
- 16: sp bacteriap.\*
- 17: sp archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	79.0	86	Q723Y5	Q723Y5 homo sapien
2	61	75.3	239	Q8TCD0	Q8TCD0 homo sapien
3	59	72.8	148	Q8K122	Q8K122 mus musculu
4	57	70.4	114	Q9UL80	Q9UL80 homo sapien
5	50	61.7	239	Q8NEK0	Q8NEK0 homo sapien
6	50	61.7	758	Q9C9E8	Q9C9E8 arabidopsis
7	49	60.5	238	Q8VCI6	Q8VCI6 mus musculu
8	48	59.3	104	Q9JL82	Q9JL82 mus musculu
9	48	59.3	239	Q8K0F8	Q8K0F8 mus musculu
10	48	59.3	239	Q8VC55	Q8VC55 mus musculu
11	48	59.3	1561	Q26451	Q26451 methanobact
12	46	56.8	238	Q99M37	Q99M37 mus musculu
13	46	56.8	506	P91035	P91035 streptomyce
14	46	56.8	573	P97179	P97179 streptomyce
15	46	56.8	574	Q86876	Q86876 streptomyce
16	44	54.3	419	Q9CG26	Q9CG26 lactococcus

17	43	53.1	437	3	Q12007	Q12007 saccharomyc
18	43	53.1	481	3	Q9PD03	Q9PD03 sordaria ma
19	43	53.1	487	3	Q8X096	Q8X096 neurospora
20	43	53.1	489	3	Q9P8F3	Q9P8F3 gibberella
21	43	53.1	712	16	Q8EF46	Q8EF46 shewanella
22	43	53.1	822	16	Q56939	Q56939 versinia pe
23	43	53.1	843	16	Q8D0D4	Q8D0D4 versinia pe
24	43	53.1	953	5	Q96602	Q96602 trypanosoma
25	42	51.9	239	16	Q9CMU7	Q9CMU7 pasteurella
26	42	51.9	245	16	Q67538	Q67538 aquifex aeo
27	42	51.9	337	16	Q8PRF6	Q8PRF6 xanthomonas
28	42	51.9	398	16	Q8PEG9	Q8PEG9 xanthomonas
29	42	51.9	434	5	Q23217	Q23217 caenorhabdi
30	42	51.9	755	17	Q97VH4	Q97VH4 sulfolobus
31	42	51.9	786	5	Q77209	Q77209 trypanosoma
32	42	51.9	982	16	Q837Q7	Q837Q7 enterococcu
33	41	50.6	89	16	Q7VKH9	Q7VKH9 haemophilus
34	41	50.6	226	10	Q8LK97	Q8LK97 cucumis mel
35	41	50.6	418	16	Q9XDT5	Q9XDT5 clostridium
36	41	50.6	452	16	Q8EVX1	Q8EVX1 mycoplasma
37	41	50.6	555	16	Q8RIQ5	Q8RIQ5 fuscobacteri
38	41	50.6	574	5	Q8IKC2	Q8IKC2 plasmodium
39	41	50.6	635	2	Q45820	Q45820 clostridium
40	41	50.6	651	16	Q9WYL6	Q9WYL6 thermotoga
41	41	50.6	700	2	Q24781	Q24781 bacillus sp
42	41	50.6	748	16	Q7UE11	Q7UE11 rhodospirell
43	41	50.6	1136	5	Q8IJD8	Q8IJD8 plasmodium
44	40.5	50.0	241	12	Q9YKQ6	Q9YKQ6 banna virus
45	40.5	50.0	249	12	Q9YKQ2	Q9YKQ2 banna virus

## ALIGNMENTS

### RESULT 1

Q723Y5	PRELIMINARY;	PRT;	86 AA.
ID	Q723Y5		
AC	Q723Y5;		
DT	01-OCT-2003 (TrEMBLrel. 25, Created)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Rearranged VKA17 V gene segment (Fragment).		
GN	VKA17.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	Tissue-Hodgkin lymphoma;		
RA	Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,		
RA	Hansmann M.L., Brauning A.;		
RT	"Analysis of a clonally related mantle cell and Hodgkin lymphoma		
RT	indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg		
RT	cell precursor in a germinal center.";		
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ564426; CAD92033.1; -.		
FT	NON TER		
FT	NON TER		
SQ	SEQUENCE 86 AA; 9764 MW; D198FC04FE0C78FD CRC64;		

Query March Similarity 79.0%; Score 64; DB 4; Length 86;

Best Local Similarity 75.0%; Pred. No. 0.0042;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16

Db 3 RSSQSLVYSDGNTYLN 18

### RESULT 2

Q8TCD0	PRELIMINARY;	PRT;	239 AA.
ID	Q8TCD0		

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AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RC Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC022362; AAH22362.1; -
DR PIR: S34095; S34095.
DR PIR: S42267; S42267.
DR PIR: S42268; S42268.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 75.3%; Score 61; DB 4; Length 239;
Best Local Similarity 68.8%; Pred. No. 0.041;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
|||:|:|:|:|:|:|
DB 44 RSTQSLVSDGNTYLN 59

RESULT 3
Q8K122 PRELIMINARY; PRT; 148 AA.
AC Q8K122;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Salivary gland;
RC Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC028925; AAH28925.1; -
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 148 AA; 16345 MW; 183920BBD9F3B521 CRC64;

Query Match 72.8%; Score 59; DB 11; Length 148;
Best Local Similarity 75.0%; Pred. No. 0.052;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
|||:|:|:|:|:|:|
DB 43 KSSQSLSDSGKTYLN 58

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RESULT 4
Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035034; AAD56270.1; -
DR PIR: B49002; B49002.
DR PIR: S23638; S23638.
DR PIR: S34094; S34094.
DR PIR: S34095; S34095.
DR HSSP; P80362; 1WTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070B31E210D1CB01 CRC64;

Query Match 70.4%; Score 57; DB 4; Length 114;
Best Local Similarity 68.8%; Pred. No. 0.085;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
|||:|:|:|:|:|:|
DB 24 RSSQSPVSDGNTYLN 39

RESULT 5
Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Prostate;
RC Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC030814; AAH30814.1; -
DR PIR: S23638; S23638.
DR PIR: S34091; S34091.
DR PIR: S40357; S40357.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART; SM00407; IGcl; 1.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 61.7%; Score 50; DB 4; Length 239;
Best Local Similarity 62.5%; Pred. No. 2.8;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RSSKSLLYKDGKTYLN 16
DB 44 RSSQSLHSDGNYLD 59

RESULT 6
OQC9E8 PRELIMINARY; PRT; 758 AA.
AC OQC9E8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE T10D10.3.
GN Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=sv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen K., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Feng B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Krennsetkaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana."
RL Nature 408:816-820(2000).
DR EMBL; AC016529; AAG52586.1; -.
DR FIC; C96749; C96749.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
DR GO; GO:0006306; P:DNA methylation; IEA.
DR InterPro; IPR002052; N6_Mtase.
DR InterPro; IPR002035; VWFA.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00092; N6_MTASE; 1.
DR PROSITE; PS0234; VWFA; 1.
KW Hypothetical protein.
SQ SEQUENCE 758 AA; 84789 MW; 8434F219D227036B CRC64;

Query Match 61.7%; Score 50; DB 10; Length 758;
Best Local Similarity 64.3%; Pred. No. 10;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 SKSLYKDGKTYLN 16
DB 194 SQSLYKDGKTYLN 207

RESULT 8
OQJL82 PRELIMINARY; PRT; 104 AA.
AC OQJL82;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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RESULT 7
O8VC16 PRELIMINARY; PRT; 238 AA.
AC O8VC16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC019760; AAH19760.1; -.
DR PIR; A27887; A27887.
DR PIR; A32248; A32248.
DR PIR; A33333; A33333.
DR PIR; B27887; B27887.
DR PIR; B30577; B30577.
DR PIR; B31485; B31485.
DR PIR; B32248; B32248.
DR PIR; B41340; B41340.
DR PIR; C27887; C27887.
DR PIR; C32248; C32248.
DR PIR; C34904; C34904.
DR PIR; D27887; D27887.
DR PIR; D29380; D29380.
DR PIR; E28833; E28833.
DR PIR; F32530; F32530.
DR PIR; H31485; H31485.
DR PIR; PH0106; PH0106.
DR PIR; PH1030; PH1030.
DR PIR; PH1031; PH1031.
DR PIR; PH1034; PH1034.
DR PIR; PL0257; PL0257.
DR PIR; PT0359; PT0359.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S26334; S26334.
DR PIR; S53750; S53750.
DR PIR; S60066; S60066.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 60.5%; Score 49; DB 11; Length 238;
Best Local Similarity 56.2%; Pred. No. 4.2;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 RSSKSLLYKDGKTYLN 16
DB 43 RSSQSLVHNSNGTYLN 58

RESULT 8
OQJL82 PRELIMINARY; PRT; 104 AA.
AC OQJL82;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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DE Anti-myosin immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=20448942; PubMed=10992488;  
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "T-Cell-dependent antibody response to the dominant epitope of  
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
 RT with cardiac myosin";  
 RL Infect. Immun. 68:5803-5808 (2000).  
 DR EMBL; AF206024; AAF69322.1; -;  
 DR PIR; S26334; S26334.  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 FT NON TER 1  
 FT NON TER 104 104  
 SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFDF5FOAIAE CRC64;

Query Match 59.3%; Score 48; DB 11; Length 104;  
 Best Local Similarity 56.2%; Pred. No. 2.5;  
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
 |||:|:|:|:|:  
 DB 16 RSSQSLVHTNGNTYLH 31

RESULT 9  
 Q8KOF8 PRELIMINARY; PRT; 239 AA.  
 AC Q8KOF8;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Breast tumor;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC031498; AAH31498.1; -;  
 DR PIR; A33933; A33933.  
 DR PDB; 1KN2; 13-MAR-02.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0008152; F:metabolism; IEA.  
 DR InterPro; IPR002198; ADH\_short.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;

Query Match 59.3%; Score 48; DB 11; Length 239;  
 Best Local Similarity 56.2%; Pred. No. 6.1;  
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 RSSKSLLYKDGKTYLN 16  
 |||:|:|:|:|:  
 DB 44 KSSQSLFYNGKYYLS 59  
 RESULT 10  
 Q8VC55 PRELIMINARY; PRT; 239 AA.  
 AC Q8VC55;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC021781; AAR21781.1; -;  
 DR PIR; A33933; A33933.  
 DR PDB; 1KC5; 24-JUL-02.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0015070; F:toxin activity; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR004214; Conotoxin.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF02950; Conotoxin; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 59.3%; Score 48; DB 11; Length 239;  
 Best Local Similarity 62.5%; Pred. No. 6.1;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 RSSKSLLYKDGKTYLN 16  
 |||:|:|:|:|:  
 DB 44 KSTKSLNSDGFYLD 59  
 RESULT 11  
 O26451 PRELIMINARY; PRT; 1561 AA.  
 ID O26451  
 AC O26451;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Magnesium chelataase subunit.  
 GN MR351.  
 OS Methanobacterium thermoautotrophicum.  
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
 OC Methanobacteriaceae; Methanothermobacter.  
 OX NCBI\_TaxID=187420;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Delta H;  
 RX MEDLINE=98037514; PubMed=9371463;  
 RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,  
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,  
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,  
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,  
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.,  
RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
RT delCah: functional analysis and comparative genomics.";  
RL J. bacteriol. 179:7135-7155 (1997).  
DR EMBL; AF000820; AAB84857.1; -.  
DR FIR; C69145; C69145.  
DR GO; GO:0003779; F:actin binding; IEA.  
DR GO; GO:0009058; P:biosynthesis; IEA.  
DR InterPro; IPR001589; Actbind.actnin.  
DR InterPro; IPR003672; CoBN/Mg\_chitase.  
DR Pfam; PF02514; coBN-Mg\_chel; 1.  
DR PROSITE; PS00019; ACTININ\_1; 1.  
KW Complete proteome.  
SQ SEQUENCE 1561 AA; 170574 MW; 764561FA31D719CE CRC64;

Query Match 59.3%; Score 48; DB 17; Length 1561;  
Best Local Similarity 64.3%; Pred.No. 47;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0

QY 3 SKSLYKDGKTYLN 16  
| : ||||| |  
Db 224 SRELYRDGKLYDN 237

RESULT 12  
ID# 09W37 PRELIMINARY; PRF; 238 AA.  
QC AC Q9W37; 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus [Mouse].  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC02035; AAH02035.1; -.  
DR PIR; A31807; A31807.  
DR PIR; A32248; A32248.  
DR PIR; B32248; B32248.  
DR PIR; C32248; C32248.  
DR PIR; F32530; F32530.  
DR PIR; PH042; PH1042.  
DR PIR; PH043; PH1043.  
DR PIR; PH044; PH1044.  
DR PIR; S07455; S07455.  
DR PIR; S16112; S16112.  
DR PIR; S24500; S24500.  
DR PIR; S24501; S24501.  
DR PIR; S24503; S24503.  
DR PIR; S24504; S24504.  
DR PIR; S24529; S24529.  
DR PIR; S24532; S24532.  
DR PIR; S24533; S24533.  
DR PIR; S24535; S24535.  
DR PIR; S24536; S24536.  
DR PIR; S24538; S24538.  
DR PDB; 1IG1; 25-DEC-02.  
DR PDB; 1LO2; 31-JUL-02.  
DR PDB; 1LO4; 31-JUL-02.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IgV; 1.

DR Pfam; PF02806; alpha-amylase\_C; 1.  
 DR Pfam; PF00686; CBM\_20; 1.  
 DR PRINTS; PR00110; ALPHAAMYLASE.  
 DR PRODOM; PD001568; CBD\_4; 1.  
 DR SMART; SMO0642; Amy; 1.  
 DR SMART; SMO0632; Amy\_C; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 506 AA; 53868 MW; FCC92A3BED9D2DAE CRC64;

Query Match 56.8%; Score 46; DB 16; Length 506;  
 Best Local Similarity 57.1%; Pred. No. 30;  
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTY 14  
 | : : : : :  
 Db 306 RNGETLTYKDGATY 319

RESULT 14  
 ID P97179 PRELIMINARY; PRT; 573 AA.  
 AC P97179;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Alpha-amylase.  
 GN AMLB.  
 OS Streptomyces lividans.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1916;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yin X.H., Gagnat J., Gerbaud C., Guerinneau M., Virolle M.J.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z85949; CAB06622.1; -.  
 DR EMBL; Z86113; CAB06815.1; -.  
 DR HSSP; P29957; IAQM.  
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.  
 DR GO; GO:0003824; F:catalytic activity; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR006048; Alpha-amyl\_C.  
 DR InterPro; IPR006047; Alpha-amyl\_cat.  
 DR InterPro; IPR006589; Alp\_amyl\_cat\_sub.  
 DR InterPro; IPR002044; CBD\_4.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR Pfam; PF02806; alpha-amylase\_C; 1.  
 DR PRODOM; PD001568; CBD\_4; 1.  
 DR PRINTS; PR00110; ALPHAAMYLASE.  
 DR PRODOM; PD001568; CBD\_4; 1.  
 DR SMART; SMO0642; Amy; 1.  
 DR SMART; SMO0632; Amy\_C; 1.  
 SQ SEQUENCE 573 AA; 61214 MW; E474019661C9D6A2 CRC64;

Query Match 56.8%; Score 46; DB 2; Length 573;  
 Best Local Similarity 57.1%; Pred. No. 34;  
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTY 14  
 | : : : : :  
 Db 306 RNGETLTYKDGATY 319

RESULT 15  
 ID O86876 PRELIMINARY; PRT; 574 AA.  
 AC O86876;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Alpha-amylase.  
 GN AML.

OS Streptomyces lividans.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1916;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TK21;  
 RA Isiegas C., Parro V., Mellado R.P.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y13601; CAA73926.1; -.  
 DR HSSP; P29957; IAQM.  
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.  
 DR GO; GO:0003824; F:catalytic activity; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR006048; Alpha-amyl\_C.  
 DR InterPro; IPR006047; Alpha-amyl\_cat.  
 DR InterPro; IPR006589; Alp\_amyl\_cat\_sub.  
 DR InterPro; IPR002044; CBD\_4.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR Pfam; PF02806; alpha-amylase\_C; 1.  
 DR PRINTS; PR00110; ALPHAAMYLASE.  
 DR PRODOM; PD001568; CBD\_4; 1.  
 DR SMART; SMO0642; Amy; 1.  
 DR SMART; SMO0632; Amy\_C; 1.  
 SQ SEQUENCE 574 AA; 61758 MW; A040AA1092C22270 CRC64;

Query Match 56.8%; Score 46; DB 2; Length 574;  
 Best Local Similarity 57.1%; Pred. No. 35;  
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTY 14  
 | : : : : :  
 Db 306 RNGETLTYKDGATY 319

Search completed: September 30, 2004, 05:59:22  
 Job time : 57.5056 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 9.76271 Seconds  
(without alignments)  
85.337 Million cell updates/sec

Title: US-09-674-716B-3

Perfect score: 81

Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	112	1	KV2A MOUSE
2	81	100.0	113	1	KV2C MOUSE
3	81	100.0	120	1	KV2B MOUSE
4	64	79.0	130	1	KV2F HUMAN
5	61	75.3	113	1	KV2E HUMAN
6	55	67.9	113	1	KV2F MOUSE
7	54	66.7	113	1	KV2G MOUSE
8	53	65.4	113	1	KV2D HUMAN
9	52	64.2	113	1	KV2E MOUSE
10	46.5	57.4	115	1	KV2A HUMAN
11	45	55.6	117	1	KV2E HUMAN
12	43	53.1	437	1	ERR1 YEAST
13	42	51.9	343	1	Y535 METJA
14	41	50.6	86	1	R31B VIBPA
15	41	50.6	89	1	R31B HAEDU
16	41	50.6	112	1	KV2D MOUSE
17	41	50.6	891	1	ACON LEGPN
18	40	49.4	87	1	R31B RALSO
19	40	49.4	478	1	AMV STRHY
20	40	49.4	481	1	6PGD DROME
21	40	49.4	489	1	TRPE SCHPO
22	40	49.4	521	1	SYM UREPA
23	40	49.4	713	1	ETP2 YABAM
24	39.5	48.8	134	1	KV4C HUMAN
25	39	48.1	213	1	ZN80 CERAE
26	39	48.1	214	1	LBD7 ARATH
27	39	48.1	293	1	ZN80 MACMU
28	39	48.1	473	1	SACB BACSU
29	39	48.1	478	1	NIFE METTH
30	39	48.1	561	1	YBUL ECOLI
31	39	48.1	561	1	YBUL SALT1
32	39	48.1	561	1	YBUL SALT2
33	39	48.1	562	1	YD26 YERPE

34	39	48.1	580	1	GGT ECOLI	P18956 escherichia
35	39	48.1	853	1	YDZF SCHPO	Q997e9 schizosacch
36	38	46.9	135	1	Y549 RICPR	Q9zd01 rickettsia
37	38	46.9	213	1	YTXB BACSU	P06568 bacillus su
38	38	46.9	216	1	YDCM WETS1	P43388 methylophil
39	38	46.9	262	1	LPXA SALT1	Q829a2 salmonella
40	38	46.9	262	1	LPXA SALT2	P32200 salmonella
41	38	46.9	262	1	LPXA YERPE	Q82H56 yersinia pe
42	38	46.9	273	1	ZN80 GORGO	P51503 gorilla gor
43	38	46.9	273	1	ZN80 HUMAN	P51504 homo sapien
44	38	46.9	284	1	P100 LEIMA	P22045 leishmania
45	38	46.9	314	1	TOPI VACCV	P08585 vaccinia vi

ALIGNMENTS

RESULT 1							
ID	KV2A_MOUSE	STANDARD;	PRT;	112 AA.			
AC	P01626;						
DT	21-JUL-1986 (Rel. 01, Created)						
DT	21-JUL-1986 (Rel. 01, Last sequence update)						
DT	15-JUL-1999 (Rel. 38, Last annotation update)						
DE	Ig kappa chain V-II region MOPC 167.						
OS	Mus musculus (Mouse)						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
OX	NCBI_TaxID=10090;						
RN	[1]						
RP	SEQUENCE.						
RX	MEDLINE=79000273; PubMed=99160;						
RA	Rudikoff S., Porter M.;						
RT	"Kappa Chain variable region from M167, a phosphorylcholine binding						
RT	myeloma protein."						
RL	Biochemistry 17:2703-2707(1978).						
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT						
CC	BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY						
CC	CHAIN HAS ALSO BEEN DETERMINED.						
DR	PIR; A01908; KWS16.						
DR	HSP; P80362; IWL.						
DR	InterPro; IPR007110; Ig-like.						
DR	InterPro; IPR003596; Ig_v.						
DR	Pfam; PF00047; Ig; 1.						
DR	SMART; SM00406; IGV; 1.						
DR	PROSITE; PS50835; IG LIKE; 1.						
KW	Immunoglobulin V region.						
FT	DOMAIN 1 23						
FT	DOMAIN 24 39						
FT	DOMAIN 40 54						
FT	DOMAIN 55 61						
FT	DOMAIN 62 93						
FT	DOMAIN 94 102						
FT	DOMAIN 103 112						
FT	DISULFID 23 93						
FT	NON_TER 112 112						
SQ	SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;						
Query Match 100.0%; Score 81; DB 1; Length 112;							
Best Local Similarity 100.0%; Pred. No. 4.3e-07;							
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps							
QY	1 RSSKSLLYKDGKTYLN 16						
DB	24 RSSKSLLYKDGKTYLN 39						
RESULT 2							
ID	KV2C_MOUSE	STANDARD;	PRT;	113 AA.			
AC	P01628;						
DT	21-JUL-1986 (Rel. 01, Created)						
DT	21-JUL-1986 (Rel. 01, Last sequence update)						

DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-II region WOPC 511.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81052016; PubMed=6776396;  
 RA Appella E.;  
 RT "Amino acid sequence of the light chain variable region of M511, a  
 RT phosphorylcholine-binding murine myeloma protein.";  
 RL Mol. Immunol. 17:711-718(1980).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS PHOSPHORYLCHOLINE.  
 PIR: A01910; KWS51.  
 DR HSP; P80362; IWTL.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region.  
 FT SIGNAL 1 23  
 FT CHAIN 24 39  
 FT DOMAIN 40 54  
 FT DOMAIN 55 61  
 FT DOMAIN 62 93  
 FT DOMAIN 94 102  
 FT DOMAIN 103 112  
 FT DISULFID 23 93  
 FT NON\_TER 113  
 SQ SEQUENCE 113 AA; 12496 MW; EFBD0C4DA2ED3450 CRC64;  
  
 Query Match 100.0%; Score 81; DB 1; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 RSSKSLLYKDGKTYLN 16  
 DB 24 RSSKSLLYKDGKTYLN 39  
  
 RESULT 3  
 KV2B\_MOUSE STANDARD; PRT; 120 AA.  
 AC F01627;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-II region VKappa167 precursor.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8200223; PubMed=6791832;  
 RA Selsing E., Storb U.;  
 RT "Somatic mutation of immunoglobulin light-chain variable-region  
 RT genes";  
 RL Cell 25:47-58(1981).  
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 CC  
 DR EMBL; J00562; AAA39032.1; -;  
 DR EMBL; K02415; AAA39051.1; -;.

DR PIR: A01909; KWS67.  
 DR HSP; P80362; IWTL.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 120  
 FT DOMAIN 21 43  
 FT DOMAIN 44 59  
 FT DOMAIN 60 74  
 FT DOMAIN 75 81  
 FT DOMAIN 82 113  
 FT DOMAIN 114 120  
 FT DISULFID 43 113  
 SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;  
  
 Query Match 100.0%; Score 81; DB 1; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 RSSKSLLYKDGKTYLN 16  
 DB 44 RSSKSLLYKDGKTYLN 59  
  
 RESULT 4  
 KV2F\_HUMAN STANDARD; PRT; 133 AA.  
 AC P06310;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-II region RPMI 6410 precursor.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86041852; PubMed=2997711;  
 RA Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;  
 RT "Human immunoglobulin kappa light chain genes of subgroups II and  
 RT III";  
 RL Nucleic Acids Res. 13:6499-6513(1985).  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; Z00020; CAA77315.1; -;  
 DR PIR: A01890; K2HURP.  
 DR HSP; P80362; IWTL.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 133  
 FT DOMAIN 21 43  
 FT DOMAIN 44 59  
 FT DOMAIN 60 74  
 FT DOMAIN 75 81  
 FT DOMAIN 82 113  
 FT DOMAIN 114 120  
 FT DISULFID 43 113  
 SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;



FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 82 113 FRAMEWORK-3.  
 FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 123 132 FRAMEWORK-4.  
 FT DISULFID 43 113 BY SIMILARITY.  
 FT NON\_TER 133 133  
 SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;  
 Query Match 79.0%; Score 64; DB 1; Length 133;  
 Best Local Similarity 75.0%; Pred. No. 0.00047;  
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 RSSKSLLYKDGKTYLN 16  
 DQ 44 RSSQSLVSYDGNLYLN 59  
 RESULT 5  
 KV2B HUMAN  
 ID KV2B HUMAN STANDARD; PRT; 113 AA.  
 AC P01615;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region FR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76253627; PubMed=821524;  
 RA Riesen W.F., Jaton J.-C.;  
 RT "variable region sequence of the light chain from a Waldenström's IgM  
 RT with specificity for phosphorylcholine."  
 RL Biochemistry 15:3829-3833(1976).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
 CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.  
 DR PIR; A01886; K2HUPR.  
 DR HSSP; P01607; 1REI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 40 54 FRAMEWORK-2.  
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 62 93 FRAMEWORK-3.  
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 103 112 FRAMEWORK-4.  
 FT DISULFID 23 93 BY SIMILARITY.  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;  
 Query Match 75.3%; Score 61; DB 1; Length 113;  
 Best Local Similarity 62.5%; Pred. No. 0.0013;  
 Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RSSKSLLYKDGKTYLN 16  
 DQ 24 RSSQSLVYREGTYLB 39  
 RESULT 6  
 KV2F MOUSE  
 ID KV2F MOUSE STANDARD; PRT; 113 AA.  
 AC P01630;

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region 7S34.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83256427; PubMed=6409088;  
 RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;  
 RT "A new isotype sequence (V kappa 27) of the variable region of kappa-  
 RT light chains from a mouse hybridoma-derived anti-(streptococcal group  
 RT A polysaccharide) antibody containing an additional cysteine residue.  
 RT Application of the dimethylaminoazobenzene isothiocyanate technique  
 RT for the isolation of peptides."  
 RL Biochem. J. 211:173-180(1983).  
 CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL  
 CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.  
 DR PIR; A01913; KVM57S.  
 DR HSSP; P80362; 1WTL.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 40 54 FRAMEWORK-2.  
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 62 93 FRAMEWORK-3.  
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 103 112 FRAMEWORK-4.  
 FT DISULFID 23 93 BY SIMILARITY.  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;  
 Query Match 67.9%; Score 55; DB 1; Length 113;  
 Best Local Similarity 73.3%; Pred. No. 0.015;  
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 RSSKSLLYKDGKTYLN 15  
 DQ 24 RSSKSLLYHNGNTYL 38  
 RESULT 7  
 KV2G MOUSE  
 ID KV2G MOUSE STANDARD; PRT; 113 AA.  
 AC P01631;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region 26-10.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX STRAIN=A/J;  
 RX MEDLINE=83178921; PubMed=6404298;  
 RA Novotny J., Margolies M.N.;  
 RT "Amino acid sequence of the light chain variable region from a mouse  
 RT anti-digoxin hybridoma antibody."  
 RL Biochemistry 22:1153-1158(1983).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA  
 CC PROTEIN THAT BINDS DIGOXIN.  
 DR PIR; A01914; KVM526.  
 DR HSSP; P80362; 1WTL.  
 DR InterPro; IPR007110; Ig-like.



DE Ig kappa chain V-II region Cum.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=68242259; PubMed=5586923;  
RA Hilschmann N.;  
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722 (1967).  
RN [2]  
RP REVISIONS TO 50; 52; 96 AND 97.  
RX MEDLINE=70063440; PubMed=4188189;  
RA Hilschmann N.;  
RT "Molecular basis of antibody formation.";  
RL Naturwissenschaften 56:195-205 (1969).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PIR; B91639; K2HUCM.  
DR HSSP; P01407; 1REI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT NON\_TER 115 115 BY SIMILARITY.  
SQ SEQUENCE 115 AA; 12676 MW; 5959F90A379569EC CRC64;  
  
Query Match 57.4%; Score 46.5; DB 1; Length 115;  
Best Local Similarity 70.6%; Pred. No. 0.45; Mismatches 1; Gaps 1;  
Matches 12; Conservative 1; Indels 3;  
  
OY 1 RSSKSLLYK-DGKTYLN 16  
DB 25 RSSQSLDSDGDTNTYLN 41  
  
RESULT 11  
ID KV2E HUMAN STANDARD; PRT; 117 AA.  
AC P06309;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region GM607 precursor (fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84191506; PubMed=6325927;  
RA Klobeck H.G., Solomon A., Zachau H.G.;  
RT "Contribution of human V kappa II germ-line genes to light-chain diversity.";  
RL Nature 309:73-76 (1984).  
CC  
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CC  
CC EMBL; Z00009; -; NOT\_ANNOTATED\_CDS.  
DR

DR PIR; A01889; K2HUCM.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT NON\_TER 117 117 BY SIMILARITY.  
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;  
  
Query Match 55.8%; Score 45; DB 1; Length 117;  
Best Local Similarity 56.2%; Pred. No. 0.83; Mismatches 4; Gaps 0;  
Matches 9; Conservative 4; Indels 3;  
  
OY 1 RSSKSLLYKDGKTYLN 16  
DB 28 RSSQSLHSHNGVNYLD 43  
  
RESULT 12  
ERR1 YEAST STANDARD; PRT; 437 AA.  
ID P42222;  
AC P42222; 1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Enolase related protein 1 (EC 4.2.1.11).  
GN ERR1 OR YMR323W OR YM9924.15.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=S288C / AB972;  
MEDLINE=97313268; PubMed=9169872;  
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jags R., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;  
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.";  
RL Nature 387:90-93 (1997).  
RN [2]  
RP SEQUENCE OF 120-437 FROM N.A.  
RX STRAIN=S288C / YPI;  
MEDLINE=95304851; PubMed=7785338;  
RA Pryde F.E., Huckle T.C., Louis E.J.;  
RT "Sequence analysis of the right end of chromosome XV in Saccharomyces cerevisiae: an insight into the structural and functional significance of sub-telomeric repeat sequences.";  
RL yeast 11:371-382 (1995).  
CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2O).  
CC -!- SIMILARITY: Belongs to the enolase family.  
CC  
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CC -----  
 CC EMBL; Z54141; CAA90841.1; -  
 CC EMBL; U23472; AAC48992.1; -  
 CC DR PIR; S69881; S69881.  
 CC DR HSR; P00924; 4ENL.  
 CC DR GermOnline; 143981; -  
 CC DR SGD; S0005920; ERL1; -  
 CC DR InterPro; IPR000941; Enolase.  
 CC DR Pfam; PF00113; enolase; 1.  
 CC DR Pfam; PF03952; enolase\_N; 1.  
 CC DR PRINTS; PR00148; ENOLASE.  
 CC DR ProDom; PD000902; Enolase; 1.  
 CC DR TIGRFAMs; TIGR01060; eno; 1.  
 CC DR PROSITE; PS00164; ENOLASE; 1.  
 CC DR Lyase; Glycolysis; Magnesium.  
 CC FT ACT\_SITE 160 160 BY SIMILARITY.  
 CC FT METAL 247 247 MAGNESIUM (BY SIMILARITY).  
 CC FT METAL 296 296 MAGNESIUM (BY SIMILARITY).  
 CC FT METAL 321 321 MAGNESIUM (BY SIMILARITY).  
 CC SQ SEQUENCE 437 AA; 47312 MW; 143D6EF6FB03D13 CRC64;

Query Match 53.1%; Score 43; DB 1; Length 437;  
 Best Local Similarity 60.0%; Pred. NO. 7.9;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 SKSKLLYKDGKTYLN 16  
 : : : : :  
 Db 248 SAPSVFYKDGKTYLDN 262

RESULT 13  
 ID Y535 METJA STANDARD; PRT; 343 AA.  
 AC Q5795;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical protein MJ0535.  
 GN MJ0535.

OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 OC Methanocaldococcaceae; Methanocaldococcus.  
 OX NCBI\_TaxID=2190;

CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 CC MEDLINE=96337999; PubMed=8688087;  
 CC RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Kierlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weisscock K.G., Merrick J.M., Glodek A.,  
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 jannaschii.";  
 RL Science 273:1058-1073 (1996).

CC -!- FUNCTION: Putative deacetylase (By similarity).  
 CC -!- SIMILARITY: Belongs to the histone deacetylase family.

CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC EMBL; U67502; AAB98526.1; -  
 CC DR PIR; G64366; G64366.  
 CC DR TIGR; MJ0535; -  
 CC DR InterPro; IPR000286; His\_deacetylase.  
 CC DR Pfam; PF00850; Hist\_deacetyl; 1.  
 CC DR PRINTS; PR01270; HDASUPER.  
 CC KW Hypothetical protein; Hydrolase; Complete proteome.  
 CC SQ SEQUENCE 343 AA; 38174 MW; 8849EDB757FDC233 CRC64;

Query Match 51.9%; Score 42; DB 1; Length 343;  
 Best Local Similarity 89.2%; Pred. NO. 9;  
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 SKSKLLYKDGKTYL 15  
 : : : : :  
 Db 73 SKSFNYVDGTYL 85

RESULT 14  
 ID R31B VIBPA STANDARD; PRT; 86 AA.  
 AC Q87MCS;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE S05 ribosomal protein L31 type B.  
 GN RPME2 OR VP2331.  
 OS Vibrio parahaemolyticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=670;

CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=RIMD 2210633 / Serotype O3:K6;  
 CC MEDLINE=22508454; PubMed=12620739;  
 CC RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
 RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism  
 RT distinct from that of V. cholerae.";  
 RL Lancet 361:743-749 (2003).

CC -!- SIMILARITY: Belongs to the L31P family of ribosomal proteins.  
 CC Subfamily B.

CC -----  
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CC -----  
 CC EMBL; AP005081; BAC60594.1; -  
 CC DR HAMAP; MF\_00502; -; 1.  
 CC DR InterPro; IPR002150; Ribosomal\_L31.  
 CC DR Pfam; PF01197; Ribosomal\_L31; 1.  
 CC DR PRINTS; PR01249; RIBOSOMAL\_L31.  
 CC DR PROSITE; PS01143; RIBOSOMAL\_L31; 1.  
 CC KW Ribosomal protein; Complete Proteome.  
 CC SQ SEQUENCE 86 AA; 9995 MW; 59010EF3786573BF CRC64;

Query Match 50.6%; Score 41; DB 1; Length 86;  
 Best Local Similarity 42.9%; Pred. NO. 2.9;  
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSKSKLLYKDGKTY 14  
 : : : : :  
 Db 30 KTDRTIEWXDGKTY 43

RESULT 15  
 R31B\_HAEDU

```
ID R31B_HAEDU STANDARD; PRT; 89 AA.
AC Q7VKH9;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE 50S ribosomal protein L31 type B.
GN RPN22 OR HD1927.
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3500HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT "The complete genome sequence of Haemophilus ducreyi."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the L31P family of ribosomal proteins.
CC Subfamily B.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB017156; AAP96649.1; -.
CC HAMAP; MF_00502; -.
CC InterPro; IPR002150; Ribosomal_L31.
CC Pfam; PF01197; Ribosomal_L31; 1.
CC PROSITE; PS01143; RIBOSOMAL_L31; 1.
CC Ribosomal protein; Complete proteome
SQ SEQUENCE 89 AA; 10187 MW; 4BF9B2435E60530F CRC64;

Query Match 50.6%; Score 41; DB 1; Length 89;
Best Local Similarity 46.2%; Pred. No. 3.1;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSKSLLYKDGKTY 14
Db ::||:::|||
32 TNKSMWEDGKEY 44

Search completed: September 30, 2004, 06:01:14
Job time : 11.7627 secs
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 78.1017 Seconds  
(without alignments)  
57.883 Million cell updates/sec

Title: US-09-674-716B-3  
Perfect score: 81  
Sequence: 1 RSSKSLYKDKTYLN 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	16	3 AAY32254	Aay32254 Light cha
2	81	100.0	100	4 AAE06969	Aae06969 Mouse ger
3	81	100.0	116	3 AAY32262	Aay32262 Humanised
4	81	100.0	145	3 AAY32261	Aay32261 Mouse ant
5	77	95.1	16	2 AAW39818	Aaw39818 Light cha
6	77	95.1	113	2 AAW39882	Aaw39882 Light cha
7	77	95.1	113	2 AAW39804	Aaw39804 Variable
8	76	93.8	131	2 AAR12232	Aar12232 Mouse Mab
9	76	93.8	132	2 AAR12354	Aar12354 Light (ka
10	75	92.6	16	2 AAW39824	Aaw39824 Light cha
11	75	92.6	16	2 AAW39815	Aaw39815 Light cha
12	75	92.6	113	2 AAW39803	Aaw39803 Variable
13	75	92.6	113	2 AAW39886	Aaw39886 Light cha
14	75	92.6	113	2 AAW39802	Aaw39802 Variable
15	75	92.6	113	2 AAW39801	Aaw39801 Variable
16	69	85.2	16	2 AAW39875	Aaw39875 Light cha
17	69	85.2	16	2 AAW39839	Aaw39839 Light cha
18	69	85.2	113	2 AAW39897	Aaw39897 Light cha
19	69	85.2	114	2 AAW39805	Aaw39805 Variable
20	67	82.7	20	3 AAY70802	Aay70802 Murine an
21	67	82.7	122	3 AAY70790	Aay70790 Murine an
22	65	80.2	112	4 AAE06992	Aae06992 Human kap
23	64	79.0	91	6 ABR55905	Abr55905 Human mab
24	64	79.0	91	6 ABR55889	Abr55889 Human mab
25	64	79.0	93	3 AAY56670	Aay56670 Partial p

ALIGNMENTS

RESULT 1

AAY32254  
ID AAY32254 standard; peptide; 16 AA.

XX AAY32254;

XX 15-FEB-2000 (first entry)

XX Light chain CDR L1 of mouse anti-CD23 MAb C11.

XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.

XX Mus musculus.

XX WO958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX ) GLAXO GROUP LTD.

XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI: 2000-053101/04.

XX N-PSDB; AA234739.

XX Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

XX Claim 1; Page 40; 81pp; English.

XX This sequence represents complementarity determining region 1 (CDR L1) of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also AAY32262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents  
 XX  
 XX Sequence 16 AA;  
 SQ

Query Match 100.0%; Score 81; DB 3; Length 16;  
 Best Local Similarity 100.0%; Pred. NO. 8.1e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
 DB 1 RSSKSLLYKDGKTYLN 16

RESULT 2  
 AAEE06969  
 ID AAE06969 standard; protein; 100 AA.  
 AC AAE06969;  
 DT 16-OCT-2001 (first entry)  
 DE Mouse germline kappa light chain variable (VK) region, 167/24.  
 KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherosclerosis; attherosclerosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; VK; kappa light chain variable region.  
 OS Mus SP.  
 XX WO200157226-A1.  
 XX 09-AUG-2001.  
 XX  
 XX 02-FEB-2001; 2001WO-US003537.  
 XX  
 XX 03-FEB-2000; 2000US-00497625.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
 XX WPI; 2001-48888/53.  
 XX  
 XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
 XX disorder in a patient, comprises a binding specificity for CCR2, and a  
 XX non-human antigen binding region and human immunoglobulin.  
 XX  
 XX Disclosure; Page 151; 183pp; English.  
 XX  
 XX The patent discloses a humanised antibody or its antigen-binding  
 XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
 XX comprising an antigen binding region of non-human origin and at least a  
 XX portion of an immunoglobulin of human origin. The humanised antibodies  
 XX are useful for inhibiting the interaction of a cell expressing CCR2. They  
 XX are useful for inhibiting or treating HIV infection. The proteins of the  
 XX invention are useful for inhibiting leukocyte trafficking, for treating

CC CCR2-mediated disorders such as inflammatory disorder, autoimmune  
 CC disorders such as rheumatoid arthritis and multiple sclerosis,  
 CC atherosclerosis and atherosclerosis, and for inhibiting restenosis. They  
 CC are useful in therapy or diagnosis, and in the manufacture of a  
 CC medicament for treating CCR-2 mediated disease. They are also useful for  
 CC treating allergy, anaphylaxis, malignancy, chronic and acute  
 CC inflammation, histamine and IGE-mediated allergic reaction, shock,  
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
 CC associated with vascular intervention, including angioplasty and/or stent  
 CC placement in a mammal. Humanised antibodies are also useful for  
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated  
 CC with vascular intervention. The present sequence is mouse germline kappa  
 CC light chain variable (VK) region, 167/24  
 XX  
 XX Sequence 100 AA;  
 SQ

Query Match 100.0%; Score 81; DB 4; Length 100;  
 Best Local Similarity 100.0%; Pred. NO. 6.3e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
 DB 24 RSSKSLLYKDGKTYLN 39

RESULT 3  
 AAY32262  
 ID AAY32262 standard; protein; 116 AA.  
 XX  
 AC AAY32262;  
 XX  
 DT 15-FEB-2000 (first entry)  
 DE Humanised anti-CD23 MAB C11 light chain variable region.  
 KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX Region 1..23  
 XX /note= "framework region 1"  
 XX Region 24..39  
 XX /note= "CDR 1"  
 XX Region 40..54  
 XX /note= "framework region 2"  
 XX Region 55..61  
 XX /note= "CDR 2"  
 XX Region 62..93  
 XX /note= "framework region 3"  
 XX Region 94..102  
 XX /note= "CDR 3"  
 XX Region 103..113  
 XX /note= "framework region 4"  
 XX  
 XX WO9958679-A1.  
 XX 18-NOV-1999.  
 XX 07-MAY-1999; 99WO-GB001434.  
 XX



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PR 09-MAY-1998; 98GB-00009839.
XX (GLAX ) GLAXO GROUP LTD.
XX Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
XX DR N-PSDB; AA234747.
XX WPI; 2000-053101/04.
XX DR N-PSDB; AA234747.
XX Cell receptor specific antibodies useful for treating e.g. arthritis,
XX diabetes, multiple sclerosis and psoriasis.
XX Claim 9; Fig 3; 81pp; English.
XX This sequence represents the light chain variable region (VL) of
XX humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human
XX framework (H5IGKVII) and the light chain complementarity determining
XX regions (see AAY32254-56) of murine antibody C11. The DNA was constructed
XX by splice overlap PCR. The invention provides altered antibodies, such as
XX chimeric or humanised antibodies, which comprise sufficient of the amino
XX acid sequences of the C11 light and heavy chain complementarity
XX determining regions to render them capable of binding to the CD23 type II
XX molecule expressed on haematopoietic cells. The antibodies are used to
XX block soluble CD23 formation in human therapy, for the treatment of
XX arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
XX sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
XX syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
XX colitis, Crohn's disease, Sjogren's syndrome, allergic asthma,
XX intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
XX versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
XX bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
XX malignancies (claimed). They are also useful for studying interactions
XX between CD23 and various ligands and determining the binding agents
XX
XX Sequence 116 AA;
XX
XX Query Match 100.0%; Score 81; DB 3; Length 116;
XX Best Local Similarity 100.0%; Pred. No. 7.5e-06;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RSSKSLLYKDGKTYLN 16
XX |||||
XX Db 24 RSSKSLLYKDGKTYLN 39
XX
XX RESULT 4
XX AAY32261
XX ID AAY32261 standard; protein; 145 AA.
XX AC AAY32261;
XX
XX 15-FEB-2000 (first entry)
XX
XX Mouse anti-CD23 MAb C11 light chain variable region.
XX
XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
XX monoclonal antibody; chimeric antibody; humanised antibody;
XX complementarity determining region; CDR; autoimmune disease;
XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;
XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
XX urticaria; nephrotic syndrome; glomerulonephritis;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;
XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
XX therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX FH 55..70
XX Region /note= "CDR L1"
XX FT 83..92
XX Region /note= "CDR L2"
XX FT

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FT Region 125..134
XX /note= "CDR L3"
XX
XX WO9958679-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-GB001434.
XX
XX 09-MAY-1998; 98GB-00009839.
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
XX
XX WPI; 2000-053101/04.
XX N-PSDB; AA234746.
XX
XX Cell receptor specific antibodies useful for treating e.g. arthritis,
XX diabetes, multiple sclerosis and psoriasis.
XX
XX Claim 8; Fig 2; 81pp; English.
XX
XX This sequence represents the light chain variable region (VL) of murine
XX anti-CD23 (FCERII) monoclonal antibody C11. The invention provides
XX altered antibodies, such as chimeric or humanised antibodies (see
XX AAY32262 and AAY32263), which comprise sufficient of the amino acid
XX sequences of the C11 light and heavy chain complementarity determining
XX regions (see AAY32254-59) to render them capable of binding to the CD23
XX type II molecule expressed on haematopoietic cells. The antibodies are
XX used to block soluble CD23 formation in human therapy, for the treatment
XX of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
XX sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
XX syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
XX colitis, Crohn's disease, Sjogren's syndrome, allergic asthma,
XX intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
XX versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
XX bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
XX malignancies (claimed). They are also useful for studying interactions
XX between CD23 and various ligands and determining the binding agents
XX
XX Sequence 145 AA;
XX
XX Query Match 100.0%; Score 81; DB 3; Length 145;
XX Best Local Similarity 100.0%; Pred. No. 9.6e-06;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RSSKSLLYKDGKTYLN 16
XX |||||
XX Db 55 RSSKSLLYKDGKTYLN 70
XX
XX RESULT 5
XX AAW39818
XX ID AAW39818 standard; peptide; 16 AA.
XX
XX AC AAW39818;
XX
XX 16-JUN-1998 (first entry)
XX
XX Light chain CDR1 of catalytic antibody 6A12.
XX
XX Variable domain; lambda light chain; catalytic antibody; degradation;
XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX overdose; addiction.
XX
XX Mus sp.
XX
XX WO9749800-A1.
XX
XX 31-DEC-1997.
XX

```

PF 25-JUN-1997; 97WO-US010965.  
 PR 25-JUN-1996; 96US-00672345.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA Landry DW;  
 PI WPI; 1998-077166/07.  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX Claim 13; Page 81; 147pp; English.  
 PS AAW39818-20 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 6A12, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified  
 CC using TSAI, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)  
 XX Sequence 16 AA;  
 SQ Query Match 95.1%; Score 77; DB 2; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 3.9e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RSSKSLLYDKGKTYLN 16  
 Db 1 RSSKSLLYDKGKTYLN 16  
 RESULT 6  
 AAW39882  
 ID AAW39882 standard; protein; 113 AA.  
 XX AAW39882;  
 AC AAW39882;  
 XX 16-JUN-1998 (first entry)  
 DT Light chain of the catalytic antibody 2A10.  
 DE Variable domain; lambda light chain; catalytic antibody; degradation;  
 XX cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX Mus sp.  
 OS WO9749800-A1.  
 XX 31-DEC-1997.  
 PD 25-JUN-1997; 97WO-US010965.  
 PF 25-JUN-1996; 96US-00672345.  
 PR (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA Landry DW;  
 PI WPI; 1998-077166/07.  
 XX N-PSDB; AAW09789.  
 DR New catalytic antibodies able to decompose cocaine, single-chain  
 XX

PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX Disclosure; Fig 21; 147pp; English.  
 PS The present sequence represents the light chain of a catalytic antibody  
 CC which is capable of degrading cocaine. A series of cocaine transition  
 CC state analogues (TSAs) were prepared and used to immunise mice for  
 CC production of hybridomas. Catalytic antibodies were identified by their  
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The  
 CC antibodies reduce the concentration of cocaine in a subject, and are used  
 CC particularly for the treatment of an overdose. They are also used for  
 CC treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)  
 XX Sequence 113 AA;  
 SQ Query Match 95.1%; Score 77; DB 2; Length 113;  
 Best Local Similarity 93.8%; Pred. No. 3.5e-05;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RSSKSLLYDKGKTYLN 16  
 Db 24 RSSKSLLYDKGKTYLN 39  
 RESULT 7  
 AAW39804  
 ID AAW39804 standard; protein; 113 AA.  
 XX AAW39804;  
 AC AAW39804;  
 XX 16-JUN-1998 (first entry)  
 DT Variable domain of the Kappa light chain of catalytic antibody 2A10.  
 DE Variable domain; lambda light chain; catalytic antibody; degradation;  
 XX cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX Mus sp.  
 OS WO9749800-A1.  
 XX 31-DEC-1997.  
 PD 25-JUN-1997; 97WO-US010965.  
 PF 25-JUN-1996; 96US-00672345.  
 PR (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA Landry DW;  
 PI WPI; 1998-077166/07.  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX Claim 16; Page 73-74; 147pp; English.  
 PS AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the Kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809  
 CC represents the heavy chain) was identified using TSAI, which is an  
 CC immunogenic conjugate of a phosphate monoester transition state analogue.  
 CC Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the

CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved)  
 XX  
 SQ Sequence 113 AA;

Query Match 95.1%; Score 77; DB 2; Length 113;  
 Best Local Similarity 93.8%; Pred. No. 3.5e-05;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
 |||||:|||||  
 Db 24 RSSKSLLYEDGKTYLN 39

RESULT 8  
 AAR12354  
 ID AAR12354 standard; protein; 131 AA.

XX AC  
 XX AAR12354;  
 DT 25-MAR-2003 (revised)  
 DT 19-AUG-1991 (first entry)

XX Mouse MAb 2E12 L chain V region.  
 DE HIV-1; chimera.  
 XX  
 KW  
 XX  
 OS  
 XX  
 PN  
 XX  
 PD  
 XX  
 PF  
 XX  
 PR  
 XX  
 PA  
 PA  
 PA  
 XX  
 PI  
 XX  
 DR  
 DR  
 DR  
 XX  
 XX  
 XX  
 PT  
 PT  
 XX  
 PS  
 XX

WPI; 1991-178106/24.  
 N-PSDB; AAQ12057.  
 New chimeric mouse human antibodies - used in treatment, diagnosis and  
 prophylaxis of HIV infections.  
 Disclosure; Fig 1; 108pp; English.

The mouse VL gene product may be used to produce chimeric mouse- human  
 Abs against HIV-1 comprising human Ig constant regions and murine  
 variable regions. These novel sequence are useful in treatment, diagnosis  
 and prophylaxis of HIV infections, and may be produced by a bacterial,  
 yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct  
 PA field.) (Updated on 25-MAR-2003 to correct PI field.)

Query Match 93.8%; Score 76; DB 2; Length 131;  
 Best Local Similarity 93.8%; Pred. No. 6.1e-05;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
 |||||:|||||  
 Db 44 RSSKSLLYKDGKTYLS 59

RESULT 9  
 AAR12354  
 ID AAR12354 standard; protein; 132 AA.

XX AC  
 XX AAR12354;  
 DT 25-MAR-2003 (revised)  
 DT 15-AUG-1991 (first entry)

XX Light chain CDR1 of catalytic antibody 12H1.  
 DE  
 XX  
 KW  
 KW  
 KW  
 XX  
 OS  
 XX

WPI; 1991-178106/24.  
 N-PSDB; AAQ12057.  
 New chimeric mouse human antibodies - used to detect, kill and remove HIV  
 -1 antigen from sample.  
 Disclosure; Fig 1; 107pp; English.

This is the light (kappa)- chain variable (V) region of a mouse  
 monoclonal antibody (MAB), 2E12, and is specific for an HIV-1 viral  
 antigen. It is used in the construction of a chimeric MAB comprising  
 heavy and light chains having murine V regions and human C regions. The  
 chimeric MABs are more effective than murine MAB 2E12 since they have an  
 increased compatibility in humans. The heavy and light chain V-regions  
 are joined by manipulating their respective joining (J) regions, to  
 generate restriction enzyme recognition sites. The chimeric MABs can be  
 used as immuno- conjugates, in association with e.g. toxins for HIV  
 treatment. They can also be used in diagnosis of HIV. See also AAQ12057-  
 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003  
 to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)

Query Match 93.8%; Score 76; DB 2; Length 132;  
 Best Local Similarity 93.8%; Pred. No. 6.1e-05;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
 |||||:|||||  
 Db 44 RSSKSLLYKDGKTYLS 59

RESULT 10  
 AAR12354  
 ID AAR12354 standard; peptide; 16 AA.

XX AC  
 XX AAR12354;  
 DT 25-MAR-2003 (revised)  
 DT 15-AUG-1991 (first entry)

AC AAR12354;  
 XX 25-MAR-2003 (revised)  
 DT 15-AUG-1991 (first entry)

XX Light (kappa) chain variable region of murine 2E12 immunoglobulin.  
 XX Chimeric antibodies; immunoconjugates; HIV; AIDS.  
 XX Mus musculus.

XX WO9107493-A.  
 XX 30-MAY-1991.  
 XX 13-NOV-1989; 89US-00433730.  
 XX 13-NOV-1989; 89US-00433730.

XX (XOMA ) XOMA CORP.  
 XX (GREC ) GREEN CROSS CORP.  
 XX Better MD, Horwitz AH, Ghoshdasti P, Robinson R;  
 XX WPI; 1991-178105/24.  
 DR N-PSDB; AAQ12056.

XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV  
 -1 antigen from sample.  
 XX Disclosure; Fig 1; 107pp; English.

This is the light (kappa)- chain variable (V) region of a mouse  
 monoclonal antibody (MAB), 2E12, and is specific for an HIV-1 viral  
 antigen. It is used in the construction of a chimeric MAB comprising  
 heavy and light chains having murine V regions and human C regions. The  
 chimeric MABs are more effective than murine MAB 2E12 since they have an  
 increased compatibility in humans. The heavy and light chain V-regions  
 are joined by manipulating their respective joining (J) regions, to  
 generate restriction enzyme recognition sites. The chimeric MABs can be  
 used as immuno- conjugates, in association with e.g. toxins for HIV  
 treatment. They can also be used in diagnosis of HIV. See also AAQ12057-  
 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003  
 to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)

Query Match 93.8%; Score 76; DB 2; Length 132;  
 Best Local Similarity 93.8%; Pred. No. 6.1e-05;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
 |||||:|||||  
 Db 44 RSSKSLLYKDGKTYLS 59

RESULT 10  
 AAR12354  
 ID AAR12354 standard; peptide; 16 AA.

XX AC  
 XX AAR12354;  
 DT 25-MAR-2003 (revised)  
 DT 15-AUG-1991 (first entry)

XX Light chain CDR1 of catalytic antibody 12H1.  
 DE  
 XX  
 KW  
 KW  
 KW  
 XX  
 OS  
 XX

WPI; 1991-178105/24.  
 N-PSDB; AAQ12056.  
 New chimeric mouse-human antibodies - used to detect, kill and remove HIV  
 -1 antigen from sample.  
 Disclosure; Fig 1; 107pp; English.

This is the light (kappa)- chain variable (V) region of a mouse  
 monoclonal antibody (MAB), 2E12, and is specific for an HIV-1 viral  
 antigen. It is used in the construction of a chimeric MAB comprising  
 heavy and light chains having murine V regions and human C regions. The  
 chimeric MABs are more effective than murine MAB 2E12 since they have an  
 increased compatibility in humans. The heavy and light chain V-regions  
 are joined by manipulating their respective joining (J) regions, to  
 generate restriction enzyme recognition sites. The chimeric MABs can be  
 used as immuno- conjugates, in association with e.g. toxins for HIV  
 treatment. They can also be used in diagnosis of HIV. See also AAQ12057-  
 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003  
 to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)

Query Match 93.8%; Score 76; DB 2; Length 132;  
 Best Local Similarity 93.8%; Pred. No. 6.1e-05;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
 |||||:|||||  
 Db 44 RSSKSLLYKDGKTYLS 59

RESULT 10  
 AAR12354  
 ID AAR12354 standard; peptide; 16 AA.

XX AC  
 XX AAR12354;  
 DT 25-MAR-2003 (revised)  
 DT 15-AUG-1991 (first entry)

XX Light chain CDR1 of catalytic antibody 12H1.  
 DE  
 XX  
 KW  
 KW  
 KW  
 XX  
 OS  
 XX

WPI; 1991-178105/24.  
 N-PSDB; AAQ12056.  
 New chimeric mouse-human antibodies - used to detect, kill and remove HIV  
 -1 antigen from sample.  
 Disclosure; Fig 1; 107pp; English.

This is the light (kappa)- chain variable (V) region of a mouse  
 monoclonal antibody (MAB), 2E12, and is specific for an HIV-1 viral  
 antigen. It is used in the construction of a chimeric MAB comprising  
 heavy and light chains having murine V regions and human C regions. The  
 chimeric MABs are more effective than murine MAB 2E12 since they have an  
 increased compatibility in humans. The heavy and light chain V-regions  
 are joined by manipulating their respective joining (J) regions, to  
 generate restriction enzyme recognition sites. The chimeric MABs can be  
 used as immuno- conjugates, in association with e.g. toxins for HIV  
 treatment. They can also be used in diagnosis of HIV. See also AAQ12057-  
 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003  
 to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)

Query Match 93.8%; Score 76; DB 2; Length 132;  
 Best Local Similarity 93.8%; Pred. No. 6.1e-05;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

PN WO9749800-A1.  
 PD 31-DEC-1997.  
 XX  
 XX 25-JUN-1997; 97WO-US010965.  
 XX  
 XX 25-JUN-1996; 96US-00672345.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Landry DW;  
 XX WPI; 1998-077166/07.  
 XX  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 XX Claim 17; Page 83; 147pp; English.  
 XX  
 CC AAW39824-26 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 12H1, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified  
 CC using TSA2, and has a per minute Kcat of 0.16. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the  
 CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved)  
 XX  
 XX Sequence 16 AA;  
 SQ  
 Query Match 92.6%; Score 75; DB 2; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 8.5e-06;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RSSKSLLYKDGKTYLN 16  
 |||:||||:|||||  
 DB 1 RSSKSLLYKDGKTYLN 16  
 |||:||||:|||||  
 RESULT 11  
 AAW39815  
 ID AAW39815 standard; peptide; 16 AA.  
 XX  
 AC AAW39815;  
 XX  
 XX 16-JUN-1998 (first entry)  
 XX  
 XX Light chain CDR1 of catalytic antibody 3B9.  
 XX  
 XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX  
 OS Mus sp.  
 XX  
 XX WO9749800-A1.  
 XX  
 XX 31-DEC-1997.  
 XX  
 XX 25-JUN-1997; 97WO-US010965.  
 XX  
 XX 25-JUN-1996; 96US-00672345.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Landry DW;  
 XX WPI; 1998-077166/07.  
 XX  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 XX Claim 18; Page 73; 147pp; English.  
 XX  
 CC AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-

PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 XX Claim 11; Page 80; 147pp; English.  
 XX  
 CC AAW39815-17 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)  
 XX  
 XX Sequence 16 AA;  
 SQ  
 Query Match 92.6%; Score 75; DB 2; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 8.5e-06;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RSSKSLLYKDGKTYLN 16  
 |||:||||:|||||  
 DB 1 RSSKSLLYKDGKTYLN 16  
 |||:||||:|||||  
 RESULT 12  
 AAW39803  
 ID AAW39803 standard; protein; 113 AA.  
 XX  
 AC AAW39803;  
 XX  
 XX 16-JUN-1998 (first entry)  
 XX  
 XX Variable domain of the kappa light chain of catalytic antibody 12H1.  
 DE  
 XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX  
 OS Mus sp.  
 XX  
 XX WO9749800-A1.  
 XX  
 XX 31-DEC-1997.  
 XX  
 XX 25-JUN-1997; 97WO-US010965.  
 XX  
 XX 25-JUN-1996; 96US-00672345.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Landry DW;  
 XX WPI; 1998-077166/07.  
 XX P-PSDB; AAV09802.  
 XX  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 XX Claim 18; Page 73; 147pp; English.  
 XX  
 CC AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-



DE Variable domain of the Kappa light chain of catalytic antibody 3B9.  
 XX  
 KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9749800-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 PF 25-JUN-1997; 97WO-US010965.  
 XX  
 PR 25-JUN-1996; 96US-00672345.  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 PI Landry DW;  
 XX  
 DR WPI; 1998-077166/07.  
 DR P-PSDB; AAV09791.  
 XX  
 PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 PS Claim 12; Page 71-72; 147pp; English.  
 XX  
 CC AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the Kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806  
 CC represents the heavy chain) was identified using TSA1, which is an  
 CC immunogenic conjugate of a phosphate monoester transition state analogue.  
 CC Antibody 3B9 has a per minute Keat of 0.11. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the  
 CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved)  
 XX  
 SQ Sequence 113 AA;  
 Query Match 92.6%; Score 75; DB 2; Length 113;  
 Best Local Similarity 87.5%; Pred. No. 7.6e-05;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RSSKSLLYKDGKTYLN 16  
 Db 24 RSSRSLLYRDGKTYLN 39  
 |||:|||||  
 |||:|||||

Search completed: September 30, 2004, 06:06:09  
 Job time : 80.1017 secs

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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:01:30 ; Search time 268.475 Seconds  
(without alignments)  
19.178 Million cell updates/sec

Title: US-09-674-716B-3

Perfect score: 81  
Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubpaa/pct PUBCOMB.pcp.\*
- 2: /cgn2\_6/prodata/1/pubpaa/pct NEW PUB.pcp.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06 NEW PUB.pcp.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06 PUBCOMB.pcp.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07 NEW PUB.pcp.\*
- 6: /cgn2\_6/prodata/1/pubpaa/US07 PUBCOMB.pcp.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US08 NEW PUB.pcp.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08 PUBCOMB.pcp.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US09A PUBCOMB.pcp.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US09B PUBCOMB.pcp.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US09C PUBCOMB.pcp.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US09 NEW PUB.pcp.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US10A PUBCOMB.pcp.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US10B PUBCOMB.pcp.\*
- 15: /cgn2\_6/prodata/1/pubpaa/US10C PUBCOMB.pcp.\*
- 16: /cgn2\_6/prodata/1/pubpaa/US10 NEW PUB.pcp.\*
- 17: /cgn2\_6/prodata/1/pubpaa/US60 NEW PUB.pcp.\*
- 18: /cgn2\_6/prodata/1/pubpaa/US60 PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	100	9	US-09-840-459-32
2	81	100.0	100	16	US-10-766-773-32
3	81	100.0	100	16	US-10-766-610-32
4	81	100.0	100	16	US-10-733-563-32
5	77	95.1	16	10	US-09-940-727B-22
6	77	95.1	16	10	US-09-940-727B-25
7	77	95.1	113	10	US-09-940-727B-8
8	77	95.1	113	10	US-09-940-727B-108
9	75	92.6	16	10	US-09-940-727B-19
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13	75	92.6	113	10	US-09-940-727B-7
14	75	92.6	113	10	US-09-940-727B-100
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16	75	92.6	113	10	US-09-940-727B-112	Sequence 112, Appl
17	75	92.6	280	10	US-09-940-727B-119	Sequence 119, Appl
18	69	85.2	16	10	US-09-940-727B-43	Sequence 43, Appl
19	69	85.2	16	10	US-09-940-727B-79	Sequence 79, Appl
20	69	85.2	113	10	US-09-940-727B-116	Sequence 116, Appl
21	69	85.2	114	10	US-09-940-727B-9	Sequence 9, Appl
22	65	80.2	112	9	US-09-840-459-55	Sequence 55, Appl
23	65	80.2	112	16	US-10-766-773-55	Sequence 55, Appl
24	65	80.2	112	16	US-10-766-610-55	Sequence 55, Appl
25	65	80.2	112	16	US-10-733-563-55	Sequence 55, Appl
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27	64	79.0	100	9	US-09-840-459-23	Sequence 23, Appl
28	64	79.0	100	9	US-09-840-459-24	Sequence 24, Appl
29	64	79.0	100	12	US-10-453-698-22	Sequence 22, Appl
30	64	79.0	100	12	US-10-453-698-23	Sequence 23, Appl
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32	64	79.0	100	14	US-10-194-975-76	Sequence 76, Appl
33	64	79.0	100	14	US-10-153-382-36	Sequence 36, Appl
34	64	79.0	100	15	US-10-308-817-22	Sequence 22, Appl
35	64	79.0	100	15	US-10-308-817-23	Sequence 23, Appl
36	64	79.0	100	16	US-10-379-392-87	Sequence 87, Appl
37	64	79.0	100	16	US-10-379-392-88	Sequence 88, Appl
38	64	79.0	100	16	US-10-766-773-23	Sequence 23, Appl
39	64	79.0	100	16	US-10-766-773-24	Sequence 24, Appl
40	64	79.0	100	16	US-10-766-610-23	Sequence 23, Appl
41	64	79.0	100	16	US-10-766-610-24	Sequence 24, Appl
42	64	79.0	100	16	US-10-733-563-23	Sequence 23, Appl
43	64	79.0	100	16	US-10-733-563-24	Sequence 24, Appl
44	64	79.0	103	15	US-10-309-764-48	Sequence 48, Appl
45	64	79.0	112	9	US-09-840-459-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1  
US-09-840-459-32  
; Sequence 32, Application US/09840459  
; Patent No. US20020150576A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-840-459-32

Query Match 100.0%; Score 81; DB 9; Length 100;  
Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
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Db      24 RSSKSLLYKDGKTYLN 39

RESULT 2
US-10-766-773-32
; Sequence 32, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-773-32

Query Match      100.0%; Score 81; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSKSLLYKDGKTYLN 16
      |||||
Db      24 RSSKSLLYKDGKTYLN 39

RESULT 3
US-10-766-610-32
; Sequence 32, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/457,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-610-32

Query Match      100.0%; Score 81; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSKSLLYKDGKTYLN 16
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Db      24 RSSKSLLYKDGKTYLN 39

RESULT 4
US-10-733-563-32
; Sequence 32, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-733-563-32

Query Match      100.0%; Score 81; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSKSLLYKDGKTYLN 16
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Db      24 RSSKSLLYKDGKTYLN 39

RESULT 5
US-09-940-727B-22
; Sequence 22, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 16
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-22

Query Match      95.1%; Score 77; DB 10; Length 16;
Best Local Similarity 93.8%; Pred. No. 2e-06;
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Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
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Db 1 RSSKSLLYEDGKTYLN 16

## RESULT 6

US-09-940-727B-25  
; Sequence 25, Application US/09940727B  
; Publication No. US20030077793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-25

Query Match 95.1%; Score 77; DB 10; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
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Db 1 RSSKSLLYEDGKTYLN 16

## RESULT 7

US-09-940-727B-8  
; Sequence 8, Application US/09940727B  
; Publication No. US20030077793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-8

Query Match 95.1%; Score 77; DB 10; Length 113;  
Best Local Similarity 93.8%; Pred. No. 1.8e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
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Db 24 RSSKSLLYEDGKTYLN 39

RESULT 8  
US-09-940-727B-108  
; Sequence 108, Application US/09940727B  
; Publication No. US20030077793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 108  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-108

Query Match 95.1%; Score 77; DB 10; Length 113;  
Best Local Similarity 93.8%; Pred. No. 1.8e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
|||||:|||||  
Db 24 RSSKSLLYEDGKTYLN 39

## RESULT 9

US-09-940-727B-19  
; Sequence 19, Application US/09940727B  
; Publication No. US20030077793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-19

Query Match 92.6%; Score 75; DB 10; Length 16;  
Best Local Similarity 87.5%; Pred. No. 4.3e-06;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16  
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Db 1 RSSKSLLYEDGKTYLN 16

## RESULT 10

US-09-940-727B-28  
; Sequence 28, Application US/09940727B  
; Publication No. US20030077793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

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; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 16
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-28

Query Match          92.6%; Score 75; DB 10; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.3e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 11
US-09-940-727B-5
; Sequence 5, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-5

Query Match          92.6%; Score 75; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 12
US-09-940-727B-6
; Sequence 6, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 113
; TYPE: PRT
US-09-940-727B-100

Query Match          92.6%; Score 75; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 13
US-09-940-727B-7
; Sequence 7, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-7

Query Match          92.6%; Score 75; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 14
US-09-940-727B-100
; Sequence 100, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 113
; TYPE: PRT
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; ORGANISM: mouse
US-09-940-727B-100

Query Match      92.6%; Score 75; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
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Db 24 RSSRSLLYRDGKTYLN 39

RESULT 15
US-09-940-727B-104
; Sequence 104, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-104

Query Match      92.6%; Score 75; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
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Db 24 RSSRSLLYRDGKTYLN 39
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#### SUMMARIES

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14	75	92.6	113	2	US-08-672-345C-6
15	75	92.6	113	2	US-08-672-345C-7
16	75	92.6	113	2	US-08-672-345C-95
17	75	92.6	113	2	US-08-672-345C-96
18	75	92.6	113	2	US-08-672-345C-97
19	75	92.6	113	3	US-09-214-095D-5
20	75	92.6	113	3	US-09-214-095D-6
21	75	92.6	113	3	US-09-214-095D-7
22	75	92.6	113	3	US-09-214-095D-100
23	75	92.6	113	3	US-09-214-095D-104
24	75	92.6	113	3	US-09-214-095D-112
25	75	92.6	280	3	US-09-214-095D-119
26	69	85.2	16	2	US-08-672-345C-43
27	69	85.2	16	2	US-08-672-345C-79

28	69	85.2	16	3	US-09-214-095D-43	Sequence 43, Appl
29	69	85.2	16	3	US-09-214-095D-79	Sequence 79, Appl
30	69	85.2	113	3	US-09-214-095D-116	Sequence 116, Appl
31	69	85.2	114	2	US-08-672-345C-9	Sequence 9, Appl
32	69	85.2	114	3	US-09-214-095D-9	Sequence 9, Appl
33	69	85.2	115	2	US-08-672-345C-99	Sequence 99, Appl
34	64	79.0	100	4	US-09-472-087-113	Sequence 113, Appl
35	64	79.0	112	1	US-07-942-245-28	Sequence 28, Appl
36	64	79.0	139	4	US-09-472-087-25	Sequence 25, Appl
37	64	79.0	139	4	US-09-472-087-114	Sequence 114, Appl
38	64	79.0	222	4	US-09-479-614-26	Sequence 26, Appl
39	64	79.0	242	4	US-09-479-614-20	Sequence 20, Appl
40	59	72.8	111	4	US-09-809-739-13	Sequence 13, Appl
41	59	72.8	112	1	US-08-477-877B-89	Sequence 89, Appl
42	59	72.8	112	2	US-08-472-281A-89	Sequence 89, Appl
43	59	72.8	112	2	US-08-678-194-6	Sequence 6, Appl
44	59	72.8	112	2	US-08-477-989B-89	Sequence 89, Appl
45	59	72.8	112	3	US-08-890-011-6	Sequence 6, Appl

#### ALIGNMENTS

RESULT 1  
US-08-672-345C-22  
; Sequence 22, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P. 28,678  
; REGISTRATION NUMBER: 0575/51400  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-22

Query Match 95.1%; Score 77; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2e-06;  
Matches 15; Conservative 1; Mismatches 0; Gaps 0;

QY	1	RSSKSLLYDKGKTYLN 16
DB	1	RSSKSLLYDKGKTYLN 16

RESULT 2

US-08-672-345C-25  
; Sequence 25, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-672-345C-25

Query Match 95.1%; Score 77; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16  
| | | | | | | | | | | | | | | |  
DB 1 RSSKSLLYEDGKTYLN 16

RESULT 3  
US-09-214-095D-22  
; Sequence 22, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
; US-09-214-095D-22

Query Match 95.1%; Score 77; DB 3; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16  
| | | | | | | | | | | | | | | |  
DB 1 RSSKSLLYEDGKTYLN 16

RESULT 4  
US-09-214-095D-25  
; Sequence 25, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
; US-09-214-095D-25

Query Match 95.1%; Score 77; DB 3; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16  
| | | | | | | | | | | | | | | |  
DB 1 RSSKSLLYEDGKTYLN 16

RESULT 5  
US-08-672-345C-8  
; Sequence 8, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/672,345C  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-672-345C-8

Query Match 95.1%; Score 77; DB 2; Length 113;  
Best Local Similarity 93.8%; Pred. No. 1.5e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



```
US-08-672-345C-19
Query Match          92.6%; Score 75; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSKSLLYKDGKTYLN 16
   |||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 10
US-08-672-345C-28
; Sequence 28, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-28

Query Match          92.6%; Score 75; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSKSLLYKDGKTYLN 16
   |||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 11
US-09-214-095D-19
; Sequence 19, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19

US-08-672-345C-19
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-19

Query Match          92.6%; Score 75; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSKSLLYKDGKTYLN 16
   |||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 12
US-09-214-095D-28
; Sequence 28, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-28

Query Match          92.6%; Score 75; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSKSLLYKDGKTYLN 16
   |||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 13
US-08-672-345C-5
; Sequence 5, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-5
```



SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-672-345C-5

Query Match 92.6%; Score 75; DB 2; Length 113;  
Best Local Similarity 87.5%; Pred. No. 3.2e-05;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16  
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 14

US-08-672-345C-6  
Sequence 6 Application US/08672345C  
Patent No. 5948658  
GENERAL INFORMATION:  
APPLICANT: Landry Donald, W.  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper and Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,345C  
FILING DATE: 24-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-672-345C-6

Query Match 92.6%; Score 75; DB 2; Length 113;  
Best Local Similarity 87.5%; Pred. No. 3.2e-05;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16  
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 15

US-08-672-345C-7  
Sequence 7 Application US/08672345C  
Patent No. 5948658  
GENERAL INFORMATION:  
APPLICANT: Landry Donald, W.  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper and Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,345C  
FILING DATE: 24-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-672-345C-7

Query Match 92.6%; Score 75; DB 2; Length 113;  
Best Local Similarity 87.5%; Pred. No. 3.2e-05;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16  
Db 24 RSSRSLLYRDGKTYLN 39

Search completed: September 30, 2004, 06:38:15  
Job time : 28.1186 secs

Blank sheet

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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 7.59322 Seconds  
(without alignments)  
88.677 Million cell updates/sec

Title: US-09-674-716b-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	74	2	G30538
2	31	100.0	112	1	KWMS16
3	31	100.0	113	1	KWMS51
4	31	100.0	120	1	KWMS67
5	27	87.1	104	2	E69832
6	27	87.1	234	2	S50468
7	27	87.1	342	2	C81451
8	27	87.1	409	2	E86017
9	27	87.1	409	2	E91171
10	27	87.1	760	2	T39991
11	27	87.1	842	2	T16198
12	27	87.1	845	1	S34027
13	27	87.1	1401	2	T39225
14	26	83.9	112	2	E95905
15	26	83.9	313	2	D96028
16	26	83.9	341	1	QXFR2Y
17	26	83.9	810	2	C70791
18	26	83.9	1453	2	S21626
19	26	83.9	1464	1	CGHUIS
20	25	80.6	177	2	T51460
21	25	80.6	212	2	S09623
22	25	80.6	212	2	T05936
23	25	80.6	326	2	T26647
24	25	80.6	341	2	T39105
25	25	80.6	390	2	E88925
26	25	80.6	511	2	C56849
27	25	80.6	532	2	A04533
28	25	80.6	565	2	B72660
29	25	80.6	627	2	F95867

## ALIGNMENTS

### RESULT 1

G30538

IG kappa chain V region (253.15E2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 16-Aug-1996

C:Accession: G30538

R:Clafalin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988

A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum

A:Reference number: A30534; MUID:89035545; PMID:3141511

A:Accession: G30538

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar

A:Molecule type: mRNA

A:Residues: 1-74 <CLA>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 74;

Best Local Similarity 100.0%; Pred. No. 0.75; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LMSTRAS 7

Db 24 LMSTRAS 30

### RESULT 2

KWMS16

IG kappa chain V region (M167) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 16-Aug-1996

C:Accession: A01908

R:Rudikoff, S.; Potter, M.

Biochemistry 17, 2703-2707, 1978

A:Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prote

A:Reference number: A01908; MUID:79000273; PMID:99160

A:Accession: A01908

A:Molecule type: protein

A:Residues: 1-112 <RUD>

C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine. 7

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-95/Domain: immunoglobulin homology <IMM>

F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 112;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LMSTRAS 7

alcohol oxidase (B  
probable membrane  
probable ATP-depen  
rifamycin polyketi  
gene MHC DO-beta 1  
hypothetical prote  
conserved hypotet  
hypothetical prote  
hypothetical prote  
IB18-4 protein [i  
hypothetical prote  
cytolysin II opero  
emopalin-binding p  
periplasmic immuno  
conserved hypotet  
Cof family protein

Db 55 LMSTRAS 61

## RESULT 3

KVMS61  
Ig kappa chain V region (M511) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000  
C:Accession: A01910  
R:Appella, E.  
Mol Immunol. 17, 711-718, 1980  
A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine  
A:Reference number: A01910; MUID:81052016; PMID:6776396  
A:Accession: A01910  
A:Molecule type: protein  
A:Residues: 1-113 <APP>  
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-95/Domain: immunoglobulin homology <IMM>  
F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 113;

Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 55 LMSTRAS 61

## RESULT 4

KVMS67  
Ig kappa chain precursor V region (VK167) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 21-Jan-2000  
C:Accession: A01909  
R:Seisang, E.; Storb, U.  
Cell 25, 47-58, 1981  
A:Title: Somatic mutation of immunoglobulin light-chain variable-region genes.  
A:Reference number: A01909; MUID:82002223; PMID:6791832  
A:Accession: A01909  
A:Molecule type: DNA  
A:Residues: 1-120 <SEL>  
A:Note: the sequence was determined from the germline gene  
C:Genetics: 17/1  
A:Introns: 17/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>  
F:36-115/Domain: immunoglobulin homology <IMM>  
F:43-113/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 120;

Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 75 LMSTRAS 81

## RESULT 5

E69832  
conserved hypothetical protein yhgB - Bacillus subtilis  
N:Alternate names: hypothetical protein y (pbpf 5' region)  
C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Oct-1999  
C:Accession: E69832; C40614

R:Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero  
C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue  
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror,  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A:Authors: Yoshikawa, H.P.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69590; MUID:98044033; PMID:9384377  
A:Accession: E69832  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-104 <KUN>  
A:Cross-references: GB:Z99109; GB:AL009126; NID:G2633260; PIDN:CAB12849.1; PID:e1183011;  
A:Experimental source: strain 168  
R:Popham, D.L.; Setlow, P.  
J. Bacteriol. 175, 4870-4876, 1993  
A:Title: Cloning, nucleotide sequence, and regulation of the Bacillus subtilis pbpf gene,  
A:Reference number: A40614; MUID:93328693; PMID:8335642  
A:Accession: C40614  
A:Molecule type: DNA  
A:Residues: 1-67 <POP>  
A:Cross-references: GB:L10630  
C:Genetics:  
A:Gene: yhgB

Query Match 87.1%; Score 27; DB 2; Length 104;

Best Local Similarity 85.7%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 38 LMSTRAS 44

## RESULT 6.

S50468  
hypothetical protein YER010c - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 28-May-1993 #sequence\_revision 24-Feb-1995 #text\_change 19-Apr-2002  
C:Accession: S50468  
R:Dietrich, F.S.

Submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae cosmid 9537, 9581, 9495, 9867, and lambda c

A:Reference number: S50433

A:Accession: S50468

A:Molecule type: DNA

A:Residues: 1-234 <DIE>

A:Cross-references: EMBL:U18778; NID:G603592; PID:G603602; GSPDB:GN00005; MIPS:YER010C

C:Genetics:

A:Gene: MIPS:YER010C

A:Cross-references: SGD:S0000812

A:Map position: 5R

Query Match 87.1%; Score 27; DB 2; Length 234;

Best Local Similarity 100.0%; Pred. No. 26; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 6

Db 102 LMSTRAS 107

## RESULT 7

A;Residues: 1-409 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BAB37764.1.; PTD:g13363815; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain RMD 0509952  
C;Genetics:  
A;Gene: ECs4341  
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-protein]  
  
Query Match 87.1%; Score 27; DB 2; Length 409;  
Best Local Similarity 100.0%; Pred.No. 46;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 MSTRAS 7  
Db 77 MSTRAS 82

RESULT 10  
T16198  
miniChromosome maintenance protein mcm7p [imported] - fission yeast (Schizosaccharomyces N;Alternate names: cell division control protein 47 homolog  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequences\_revision 03-Dec-1999 #text\_change 28-Jul-2000  
C;Accession: T16198; T45282  
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Whitthead, S.; Chillingworth, T.; Churcher, C. submitted to the EMBL Data Library, July 1998  
A;Reference number: Z21897  
A;Accession: T39991  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-760 <LYN>  
A;Cross-references: EMBL:AL031158; PIDN:CAA20099.1; GSPDB:GN00067; SPDB:SPBC25D12.03c  
A;Experimental source: strain 972h-; cosmid c25D12  
R;Liag, D.T.; Forsburg, S.L.  
submitted to the EMBL Data Library, June 1998  
A;Description: Fission yeast mcm7+ is an essential gene required for normal DNA replication  
A;Reference number: Z22955  
A;Accession: T45282  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-760 <LIA>  
A;Cross-references: EMBL:AF070481; PIDN:AAC23693.1  
A;Experimental source: strain Sp.011  
C;Genetics:  
A;Gene: SPBC25D12.03c; mcm7  
A;Map position: 2  
C;Function:  
A;Description: essential replication factor  
C;Superfamily: replication licensing factor MCM7; MCM homology  
F;170-662/Domain: MCM homology <MCM>

Query Match 87.1%; Score 27; DB 2; Length 760;  
Best Local Similarity 100.0%; Pred.No. 85;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 MSTRAS 7  
Db 243 MSTRAS 248

RESULT 11  
T16198  
hypothetical protein F28B4.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 18-Aug-2000  
C;Accession: T16198  
submitted to the EMBL Data Library, December 1995  
A;Description: The sequence of C. elegans cosmid F28B4.  
A;Reference number: Z18475  
A;Accession: T16198  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-842 <LEI>

A;Cross-references: EMBL:U42834; NID:g1125756; PID:g1125758; PIDN:AAA83583.1; CESP:F28B4  
 C;Genetics:  
 A;Gene: CBSP:F28B4.2  
 A;Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2  
 C;Superfamily: CDC25-type guanine nucleotide exchange activator homology  
 F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>  
  
 Query Match 87.1%; Score 27; DB 2; Length 842;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 MSTRAS 7  
 |||||  
 Db 650 MSTRAS 655  
  
 RESULT 12  
 S34027  
 replication licensing factor MCM7 [validated] - yeast (Saccharomyces cerevisiae)  
 N;Alternate names: cell division control protein CDC47; protein YBR1441; protein YBR202W  
 C;Species: Saccharomyces cerevisiae  
 C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 21-Jul-2000  
 C;Accession: S34027; S46074; S34925; S56049  
 submitted to the EMBL Data Library, January 1993  
 R;Jacquet, M.  
 A;Reference number: S34022  
 A;Accession: S34027  
 A;Molecule type: DNA  
 A;Residues: 1-845 <JAC>  
 A;Cross-references: EMBL:Z21487; NID:g311665; PIDN:CAA79689.1; PID:g311678  
 R;Bussereau, F.; Demolis, N.; Jacquet, M.; Mallet, L.  
 submitted to the Protein Sequence Database, August 1994  
 A;Reference number: S46054  
 A;Accession: S46074  
 A;Molecule type: DNA  
 A;Residues: 1-845 <BUS>  
 A;Cross-references: EMBL:Z36071; NID:g536576; PIDN:CAA8166.1; PID:g536577; GSPDB:GN0000  
 R;Bussereau, F.; Mallet, L.; Gaillon, L.; Jacquet, M.  
 Yeast 9, 797-806, 1993  
 A;Title: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of chromosome II  
 A;Reference number: S34925; MUID:93377417; PMID:8368014  
 A;Accession: S34925  
 A;Molecule type: DNA  
 A;Residues: 407-620 <BU2>  
 A;Cross-references: EMBL:Z21487  
 R;Dalton, S.  
 submitted to the EMBL Data Library, September 1994  
 A;Description: Cdc47 and Cdc54 belong to a family of proteins essential for initiation o  
 A;Reference number: S56049  
 A;Accession: S56049  
 A;Molecule type: DNA  
 A;Residues: 1-551, 'G', 553-555, 'TLN', 559-573, 'Y', 575-845 <DAL>  
 A;Cross-references: EMBL:U14730; NID:g608168; PIDN:AAA86309.1; PID:g608169  
 C;Comment: The complex of six MCM proteins is one of several proteins that must be bound  
 phosphorylated and dissociate from the chromatin.  
 C;Genetics:  
 A;Gene: SGD:CDC47; MIPS:YBR202W  
 A;Cross-references: SGD:S0000406; MIPS:YBR202W  
 A;Map position: 2R  
 C;Complex: The predominant form is a heterohexamer of MCM2 (PIR:S45757), MCM3 (PIR:A3637  
 component of replication licensing factor.  
 C;Function:  
 A;Description: MCM7 is a component of the replication licensing factor that permits DNA  
 C;Superfamily: replication licensing factor MCM7; MCM homology  
 C;Keywords: cell cycle control; DNA replication initiation; heterohexamer; nucleus; phos  
 F;227-719/Domain: MCM homology <MCM>  
  
 Query Match 87.1%; Score 27; DB 1; Length 845;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 MSTRAS 7  
 |||||  
 Db 650 MSTRAS 655

Db 300 MSTRAS 305  
  
 RESULT 13  
 T39225  
 MAP kinase kinase - fission yeast (Schizosaccharomyces pombe)  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Jan-2000  
 C;Accession: T39225  
 R;Churcher, C.M.; Gentles, S.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
 submitted to the EMBL Data Library, August 1997  
 A;Reference number: Z21837  
 A;Accession: T39225  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-1401 <CHU>  
 A;Cross-references: EMBL:Z98763; PIDN:CAB11500.1; GSPDB:GN00066; SPDB:SPAC9G1.02  
 A;Experimental source: strain 972h-; cosmid c9G1  
 C;Genetics:  
 A;Gene: SPDB:SPAC9G1.02  
 A;Map position: 1  
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
  
 Query Match 87.1%; Score 27; DB 2; Length 1401;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 LMSTRAS 7  
 |||||  
 Db 81 LMSTRAS 87  
  
 RESULT 14  
 E95905  
 Hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymb  
 C;Species: Sinorhizobium meliloti  
 C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
 C;Accession: E95905  
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
 A;Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo  
 A;Reference number: A95842; MUID:21396508; PMID:11481431  
 A;Accession: E95905  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-112 <KUR>  
 A;Cross-references: GB:AL591985; PIDN:CAC48909.1; PID:g15140382; GSPDB:GN00167  
 A;Experimental source: strain 1021, megaplasmid pSymb  
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
 L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
 A;Reference number: A96039; MUID:21368234; PMID:11474104  
 A;Contents: annotation  
 C;Genetics:  
 A;Gene: SMB20530  
 A;Genome: plasmid  
  
 Query Match 83.9%; Score 26; DB 2; Length 112;  
 Best Local Similarity 71.4%; Pred. No. 23;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 LMSTRAS 7  
 |||||  
 Db 5 LMSTRAS 11  
  
 RESULT 15  
 D96028  
 probable transcription activator of the pca operon, LysR family protein [imported] - Sinc

C:Species: *Sinorhizobium meliloti*  
 C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
 C:Accession: D96028  
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
 A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo  
 A:Reference number: A95842; MUID:21396508; PMID:11481431  
 A:Accession: D96028  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-313 <KUR>  
 A:Cross-references: GB:AL591985; PIDN:CAC49892.1; PID:gl5141380; GSPDB:GN00167  
 A:Experimental source: strain 1021, megaplasmid pSymB  
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
 L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
 A:Reference number: A96039; MUID:21368234; PMID:11474104  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: pcaQ; SMD20580  
 A:Genome: plasmid

Query Match 83.9%; Score 26; DB 2; Length 313;  
 Best Local Similarity 85.7%; Pred. No. 63;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 |||||  
 Db 199 LMPTRAS 205

Search completed: September 30, 2004, 06:00:33  
 Job time : 9.59322 secs

Blank Sheet



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 4.27119 Seconds  
(without alignments)  
85.337 Million cell updates/sec

Title: US-09-674-716B-5  
Perfect score: 31  
Sequence: 1 LMSTRAS 7

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	112	1 KV2A_MOUSE	P01626 mus musculus
2	31	100.0	113	1 KV2C_MOUSE	P01628 mus musculus
3	31	100.0	120	1 KV2B_MOUSE	P01627 mus musculus
4	27	87.1	104	1 YHGB_BACSU	P38048 bacillus su
5	27	87.1	234	1 YK00_YEAST	P40011 saccharomyc
6	27	87.1	760	1 MCW7_SCHPO	O75001 schizosach
7	27	87.1	845	1 CC47_YEAST	P38132 saccharomyc
8	27	87.1	1401	1 W1S4_SCHPO	O14299 schizosach
9	26	83.9	193	1 RS3A_SULTO	Q97579 sulfolobus
10	26	83.9	341	1 NU2M_DROME	P03896 drosophila
11	26	83.9	341	1 NU2M_DROYA	P03895 drosophila
12	26	83.9	1453	1 C111_MOUSE	P11087 mus musculus
13	26	83.9	1460	1 C111_CANFA	Q9xsi7 canis famli
14	26	83.9	1464	1 C111_HUMAN	P02452 homo sapien
15	25	80.6	212	1 AG11_WHEAT	P10968 triticum ae
16	25	80.6	212	1 AG11_HORVU	P15312 hordeum vul
17	25	80.6	463	1 D2DR_FUGRU	P53453 fugu rubrip
18	25	80.6	565	1 TP6B_AERPE	Q9ye64 aeropyrum p
19	25	80.6	664	1 ALOX_PICAN	P04841 pichia angu
20	25	80.6	778	1 YK85_YEAST	P43610 saccharomyc
21	25	80.6	887	1 YAY5_SCHPO	O10213 schizosach
22	24	77.4	176	1 Y0S9_NPVOP	O10316 oryza psu
23	24	77.4	228	1 EBP_CAVPO	Q60490 cavia porce
24	24	77.4	230	1 EBP_MOUSE	P70245 mus musculus
25	24	77.4	250	1 PP26_BRUME	Q57099 bruceella me
26	24	77.4	259	1 PP26_BRUAB	Q44642 bruceella ab
27	24	77.4	312	1 YG37_YEAST	P53275 saccharomyc
28	24	77.4	339	1 G3P_MYCTU	O06822 mycobacteri
29	24	77.4	436	1 LIP7_CANAL	Q9p4e7 candida alb
30	24	77.4	443	1 FBL4_CRIGR	O55058 cricetus
31	24	77.4	443	1 FBL4_HUMAN	O95967 homo sapien
32	24	77.4	443	1 FBL4_MOUSE	Q9wvj9 mus musculus
33	24	77.4	463	1 SAH1_CAUCR	Q9abn0 caulobacter

34	24	77.4	543	1 NFL_HUMAN	P07196 homo sapien
35	24	77.4	548	1 NFL_PIG	P02547 sus scrofa
36	24	77.4	584	1 PARF_PARTE	P47244 paramectium
37	24	77.4	636	1 CAL3_RAT	P13941 rattus norv
38	24	77.4	766	1 METE_YEAST	P05694 saccharomyc
39	24	77.4	825	1 FTSK_BRAJA	Q89wr2 bradyrhizob
40	24	77.4	859	1 ALRI_YEAST	Q08269 saccharomyc
41	24	77.4	882	1 CHD3_DROME	O16102 drosophila
42	24	77.4	909	1 Y4G1_RHISN	P55465 rhizobium s
43	24	77.4	925	1 YBK4_YEAST	P38164 saccharomyc
44	24	77.4	1359	1 STH1_YEAST	P32597 saccharomyc
45	24	77.4	1373	1 HRP1_SCHPO	Q9ue25 schizosacch

## ALIGNMENTS

RESULT 1				
ID	KV2A_MOUSE	STANDARD;	PRT;	112 AA.
AC	P01626;			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	15-JUL-1999	(Rel. 38, Last annotation update)		
DE	Ig kappa chain V-II region MOPC 167.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=79000273; PubMed=99160;			
RA	Rudikoff S., Potter M.;			
RT	"kappa Chain variable region from M167, a phosphorylcholine binding			
RT	myeloma protein.";			
RL	Biochemistry 17:2703-2707(1978).			
CC	-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT			
CC	BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY			
CC	CHAIN HAS ALSO BEEN DETERMINED.			
DR	PIR; A01908; KVM516.			
DR	HSSP; P80362; 1WTL.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; Ig; 1.			
DR	PROSITE; PS50835; IG LIKE; 1.			
KW	Immunoglobulin V region.			
FT	DOMAIN	1	23	FRAMEWORK-1.
FT	DOMAIN	24	39	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	40	54	FRAMEWORK-2.
FT	DOMAIN	55	61	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	62	93	FRAMEWORK-3.
FT	DOMAIN	94	102	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	103	112	FRAMEWORK-4.
FT	DISULFID	23	93	BY SIMILARITY.
FT	NON_TER	112	112	
SQ	SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;			
Query Match 100.0%; Score 31; DB 1; Length 112;				
Best Local Similarity 100.0%; Pred. No. 0.39;				
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 LMSTRAS 7			
DB	55 LMSTRAS 61			
RESULT 2				
KV2C_MOUSE				
ID	KV2C_MOUSE	STANDARD;	PRT;	113 AA.
AC	P01628;			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		

DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region WOPC 511.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81052016; PubMed=6776396;  
 RA Appella E.;  
 RT "Amino acid sequence of the light chain variable region of Mb11, a  
 RT phosphorylcholine-binding murine myeloma protein.";  
 RL Mol. Immunol. 17:711-718(1980).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS PHOSPHORYLCHOLINE.  
 DR HSP; A01910; KWS51.  
 DR HSP; P80362; IWTL.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR Immunoglobulin V region.  
 KW IMUNOGLOBULIN V REGION; SIGNAL.  
 FT CHAIN 1 20  
 FT SIGNAL 1 20  
 FT CHAIN 21 120  
 FT DOMAIN 21 43  
 FT DOMAIN 44 59  
 FT DOMAIN 60 74  
 FT DOMAIN 75 81  
 FT DOMAIN 82 113  
 FT DOMAIN 114 120  
 FT DISULFID 43 113  
 FT BY SIMILARITY.  
 SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;  
 Query Match 100.0%; Score 31; DB 1; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 DB 75 LMSTRAS 81  
 RESULT 4  
 YHGB BACSU  
 ID YHGB BACSU STANDARD; PRT; 104 AA.  
 AC P38048;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical protein yhgB.  
 GN YHGB OR BSU10090.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98240224; PubMed=9579061;  
 RA Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.,  
 RA Wedler H., Venema G., Bron S.;  
 RT "The 172 kb prkA-adjAB region from 83 degrees to 97 degrees of the  
 RT Bacillus subtilis chromosome contains several dysfunctional genes,  
 RT the glyB marker, many genes encoding transporter proteins, and the  
 RT ubiquitous hit gene";  
 RL Microbiology 144:859-875(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerth I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,  
 RA Etian K.D., Exington J., Fabret C., Ferrari E., Foulger D.,  
 RA Frits C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Ghim S.Y., Glaser P., Goifeau A., Golligly E.J., Grandi G.,  
 RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Renaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogilvie A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region WOPC 511.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81052016; PubMed=6776396;  
 RA Appella E.;  
 RT "Amino acid sequence of the light chain variable region of Mb11, a  
 RT phosphorylcholine-binding murine myeloma protein.";  
 RL Mol. Immunol. 17:711-718(1980).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS PHOSPHORYLCHOLINE.  
 DR HSP; A01910; KWS51.  
 DR HSP; P80362; IWTL.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR Immunoglobulin V region.  
 KW IMUNOGLOBULIN V REGION; SIGNAL.  
 FT CHAIN 1 23  
 FT DOMAIN 24 39  
 FT DOMAIN 40 54  
 FT DOMAIN 55 61  
 FT DOMAIN 62 93  
 FT DOMAIN 94 102  
 FT DOMAIN 103 112  
 FT DISULFID 23 93  
 FT NON TER 113 113  
 SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;  
 Query Match 100.0%; Score 31; DB 1; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 0.39; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 DB 55 LMSTRAS 61  
 RESULT 3  
 KV2B MOUSE  
 ID KV2B MOUSE STANDARD; PRT; 120 AA.  
 AC P01627;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region VKappa167 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82002223; PubMed=6791832;  
 RA Selsing E., Storb U.;  
 RT "Somatic mutation of immunoglobulin light-chain variable-region  
 RT genes";  
 RL Cell 25:47-58(1981).  
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 CC  
 DR EMBL; J00562; AAA39032.1; -  
 DR EMBL; K02415; AAA39051.1; -

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RA Presecan E., Pujic P., Purnelle B., Rappoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi B., Takagi T., Takahashi H., Takenaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [3]
RN SEQUENCE OF 1-67 FROM N.A.
RP STRAIN=168;
RX MEDLINE=93328693; PubMed=8335642;
RA Popham D.L., Setlow P.;
RT "Cloning, nucleotide sequence, and regulation of the Bacillus
RT subtilis pbpF gene, which codes for a putative class A
RT high-molecular-weight penicillin-binding protein."
RL J. Bacteriol. 175:4870-4876(1993).
CC -----
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CC -----
DR EMBL; Y14083; CAA74515.1; -
DR EMBL; Z99109; CAB12849.1; -
DR EMBL; L10630; AAA71940.2; -
DR PIR; E59832; E59832.
DR Subtilist; BG10426; yhgB.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 104 AA; 11998 MW; 6B44CD77B52FDP968 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 104;
Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 38 LMSTRCS 44

RESULT 5
YEKO YEAST STANDARD; PRT; 234 AA.
AC P40011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 23.6 kDa protein in NTF2-SRPI intergenic region.
GN YEKO10C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=S288C / AB972;
RC MEDLINE=97313264; PubMed=9169868;
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
RA Hunkeler-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Mossdale D., Nakahara K., Namath A., Norgren R., Oefner P.,
RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
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RL Nature 387:78-81(1997).
CC -----
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CC -----
DR EMBL; U18778; AAB64543.1; -
DR PIR; S50468; S50468.
DR Germonline; 139090; -
DR SGD; S0000812; YER010C.
DR InterPro; IPR005493; Methyltransf_6.
DR Pfam; PF03737; Methyltransf_6; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25563 MW; EC109F224240F980 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6
DB 102 LMSTRA 107

RESULT 6
MCM7 SCHPO STANDARD; PRT; 760 AA.
ID MCM7 SCHPO
AC O75001; P87302;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA replication licensing factor mcm7 (Minichromosome maintenance
DE protein 7).
DN MCM7 OR SPBC25D12.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RN SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RP STRAIN=SP011;
RX MEDLINE=21518581; PubMed=11606526;
RA Liang D.T., Forsburg S.L.;
RT "Characterization of Schizosaccharomyces pombe mcm7(+) and cdc23(-)
RT (MCM10) and interactions with replication checkpoints."
RL Genetics 159:471-486(2001).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Feat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Grentley S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Wellens L., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Weiler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
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RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Spakovski G.V., Usery D., Barrell B.G., Nurse P.,  
RA "The genome sequence of Schizosaccharomyces pombe.",  
RL Nature 415:871-880(2002).  
RN [3]  
RN SEQUENCE OF 367-466 FROM N.A.  
RP STRAIN=972;  
RX MEDLINE=98031880; PubMed=9366552;  
RA Adachi Y., Usukura J., Yanagida M.,  
RT "A globular complex formation by Ndc1 and the other five members of  
RT the MCM protein family in fission yeast.",  
RL Genes Cells 2:467-479(1997).  
CC -1- FUNCTION: Required for the progression of S phase.  
CC -1- SUBUNIT: Heterodimer. The heterodimers of mcm4/mcm6 and  
CC mcm3/mcm5 interact with mcm2 and mcm7.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: Belongs to the MCM family.  
CC  
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CC  
CC EMBL; AF070481; AAC23693.1; -;  
CC EMBL; AL031158; CAA20099.1; -;  
CC EMBL; AJ000065; CAA03898.1; -;  
CC PIR; T39991; T39991.  
CC GeneDB Spombe; SPBC25D12.03c; -;  
CC InterPro; IPR003593; AAA\_ATPase.  
CC InterPro; IPR001208; MCM.  
CC InterPro; IPR008050; MCM\_7.  
CC Pfam; PF00493; MCM; 1.  
CC PRINTS; PR01657; MCMFAMILY.  
CC PRINTS; PR01663; MCMFAMILY.  
CC ProDom; PD001041; MCM; 1.  
CC SMART; SM00382; AAA; 1.  
CC SMART; SM00350; MCM; 1.  
CC PROSITE; PS00847; MCM; 1.  
CC PROSITE; PS00051; MCM; 2; 1.  
CC Transcription regulation; DNA-binding; Nuclear protein;  
CC DNA replication; Cell cycle; ATP-binding.  
CC DOMAIN 353 559 MCM.  
CC NP\_BIND 403 410 ATP (POTENTIAL).  
CC CONFLICT 457 457 V -> I (IN REF. 3).  
CC SEQUENCE 760 AA; 85622 MW; 2141F8F9C80BAA34 CRC64;  
  
Query Match 87.1%; Score 27; DB 1; Length 760;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 MSTRAS 7  
DB 243 MSTRAS 248  
  
RESULT 7  
ID CC47 YEAST STANDARD; PRT; 845 AA.  
AC P38132;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE DNA replication licensing factor CDC47 (Cell division control protein  
DE 47).  
DE CDC47 OR YBR202W OR YBR1441.  
DE Saccharomyces cerevisiae (Baker's yeast).  
OS

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RN SEQUENCE FROM N.A.  
RA Dalton S.,  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=S288C;  
RX MEDLINE=93377417; PubMed=8368014;  
RA Bussereau F., Mallet L., Gaillon L., Jacquet M.,  
RT "A 12.8 kb segment, on the right arm of chromosome II from  
RT Saccharomyces cerevisiae including part of the DURI.2 gene, contains  
RT five putative new genes.",  
RL Yeast 9:797-806(1993).  
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -1- SIMILARITY: Belongs to the MCM family.  
CC  
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CC  
CC EMBL; U14730; AAA86309.1; -;  
CC EMBL; Z21487; CAA79689.1; -;  
CC EMBL; Z36071; CAA85166.1; -;  
CC PIR; S34027; S34027.  
CC GeneOnline; 138745; -;  
CC GK; P38132; -;  
CC SGD; S0000406; CDC47.  
CC GO; GO:0005737; Cytoplasm; IDA.  
CC GO; GO:0005634; C:nucleus; IDA.  
CC GO; GO:0005566; C:pre-replicative complex; IDA.  
CC GO; GO:0005524; F:ATP binding; IDA.  
CC GO; GO:0006267; P:pre-replicative complex formation and maint. . .; IPI.  
CC InterPro; IPR003593; AAA\_ATPase.  
CC InterPro; IPR001208; MCM.  
CC InterPro; IPR008050; MCM\_7.  
CC Pfam; PF00493; MCM; 1.  
CC PRINTS; PR01657; MCMFAMILY.  
CC PRINTS; PR01663; MCMFAMILY.  
CC ProDom; PD001041; MCM; 1.  
CC SMART; SM00382; AAA; 1.  
CC SMART; SM00350; MCM; 1.  
CC PROSITE; PS00847; MCM; 1; 1.  
CC PROSITE; PS00051; MCM; 2; 1.  
CC Transcription regulation; DNA-binding; Nuclear protein;  
CC DNA replication; Cell cycle; ATP-binding.  
CC DOMAIN 410 617 MCM.  
CC NP\_BIND 460 467 ATP (POTENTIAL).  
CC CONFLICT 552 552 G -> V (IN REF. 2).  
CC CONFLICT 556 558 TLN -> NPG (IN REF. 2).  
CC CONFLICT 574 574 Y -> I (IN REF. 2).  
CC SEQUENCE 845 AA; 94942 MW; ADA56C719D96DB4A CRC64;  
  
Query Match 87.1%; Score 27; DB 1; Length 845;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 MSTRAS 7  
DB 300 MSTRAS 305  
  
RESULT 8  
ID WIS4 SCHPO STANDARD; PRT; 1401 AA.  
AC O14299; P87062; Q92384;  
DT 16-OCT-2001 (Rel. 40, Created)  
OS

DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DT 28-FEB-2003 (Rel. 41, last annotation update)  
 DE MAP kinase kinase kinase wis4 (EC 2.7.1.1-) (MAP kinase kinase kinase  
 DE waki) (MAP kinase kinase kinase waki).  
 GN WIS4 OR WAK1 OR WIK1 OR SPAC9G1.02.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC NCBI TaxID=4896;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=98026892; PubMed=9321395;  
 RX Samejima I., Mackie S., Fantes P.A.;  
 RT "Multiple modes of activation of the stress-responsive MAP kinase  
 RT pathway in fission yeast.";  
 RL EMBO J. 16:6162-6170(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,  
 RA Welljens I., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Cabell C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Carlson A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F.F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe";  
 RL Nature 415:871-880(2002).  
 RN [3]  
 RP SEQUENCE OF 96-1401 FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=97282620; PubMed=9136929;  
 RA Shieh J.C., Wilkinson M., Buck V., Morgan B., Makino K.,  
 RA Willar J.B.A.;  
 RT "The Mca4 response regulator coordinately controls the stress-  
 RT activated Waki-Wis1-Styl1 MAP kinase pathway and fission yeast cell  
 RT cycle.";  
 RL Genes Dev. 11:1008-1022(1997).  
 RN [4]  
 RP SEQUENCE OF 457-543 FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=97331762; PubMed=9188094;  
 RA Shiozaki K., Shiozaki M., Russell P.;  
 RT "Mca4 mitotic catastrophe suppressor regulates the fission yeast cell  
 RT cycle through the Waki-Wis1-Spc1 kinase cascade.";  
 RL Mol. Biol. Cell 8:409-419(1997).  
 CC -1- FUNCTION: Involved in a signal transduction pathway that is  
 CC activated in under conditions of heat shock, oxidative stress or  
 CC limited nutrition. Unlike wisk, it is not activated by changes in  
 CC the osmolarity of the extracellular environment. Activates the  
 CC wisk MAP kinase kinase by phosphorylation.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. MAP  
 CC kinase kinase subfamily.  
 CC -----

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EMBL; Z98763; CAB11500.1; --  
 EMBL; Y07750; CAA69030.1; ALT\_INIT.  
 DR EMBL; Y11989; CAA72718.1; --  
 DR EMBL; U11521; AAB39762.1; --  
 DR PIR; T39225; T39225.  
 DR HSP; P24941; ICKP.  
 DR GeneDB SPombe; SPAC9G1.02; --  
 DR GO; GO:0007049; P:cell cycle; ISS.  
 DR GO; GO:0000165; P:MAPKK cascade; ISS.  
 DR GO; GO:0007165; P:signal transduction; ISS.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD000001; Prot\_kinase; 1.  
 DR SMART; SMO0220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding.  
 FT DOMAIN 1037 1306 PROTEIN\_KINASE.  
 FT NP\_BIND 1043 1051 ATP (BY SIMILARITY).  
 FT BINDING 1066 1066 ATP (BY SIMILARITY).  
 FT ACT\_SITE 1161 1161 RL -> SP (IN REF. 3).  
 FT CONFLICT 484 485 D -> V (IN REF. 1).  
 FT CONFLICT 1346 1346 D -> V (IN REF. 1).  
 SQ SEQUENCE 1401 AA; 160537 MW; 529A989D2B627F3D CRC64;

Query Match 87.1%; Score 27; DB 1; Length 1401;  
 Best Local Similarity 85.7%; Pred.No. 72;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 DB 81 LMSTRTS 87

RESULT 9  
 RS3A\_SULTO  
 ID RS3A\_SULTO STANDARD; PRT; 193 AA.  
 AC Q975F8;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 30S ribosomal protein S3Ae.  
 GN RP3Ae OR ST0453.  
 OS Sulfolobus tokodaii.  
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
 OC Sulfolobus.  
 OX NCBI TaxID=111955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JCM 10545 / 7;  
 RX MEDLINE=21456156; PubMed=11572479;  
 RA Kawabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
 RA Sekine M., Baba S.-I., Ankaï A., Kosugi H., Hosoyama A., Fukui S.,  
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,  
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,  
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
 RA Oshima T., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic thermoacidophilic  
 RT Crenarchaeon, Sulfolobus tokodaii strain7.";  
 RL DNA Res. 8:123-140(2001).

```
CC -!- SIMILARITY: Belongs to the S3AE family of ribosomal proteins.
CC -----
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CC -----
CC EMBL; AF000982; BAB65443.1; -.
CC DR HAMAF; MF 00359; -.
CC DR InterPro; IPR001593; Ribosomal_S3AE.
CC DR Pfam; PF01015; Ribosomal_S3AE; 1.
CC DR ProDom; PD003035; Ribosomal_S3AE; 1.
CC DR PROSITE; PS01191; RIBOSOMAL_S3AE; FALSE NEG.
CC KW Ribosomal protein; Complete proteome.
CC SQ SEQUENCE 193 AA; 22180 MW; 78A94B87B961D751 CRC64;
CC -----
CC Query Match 83.9%; Score 26; DB 1; Length 193;
CC Best Local Similarity 71.4%; Pred. No. 15;
CC Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 1 LMSTRAS 7
CC Db 142 ILSTRAS 148
CC -----
CC RESULT 10
CC NU2M DROME
CC ID NU2M_DROME STANDARD; PRT; 341 AA.
CC AC P03896;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
CC GN ND2.
CC OS Drosophila melanogaster (Fruit fly).
CC OG Mitochondrion.
CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC OC Ephydroidea; Drosophilidae; Drosophila.
CC OX NCBI_TaxID=7227;
CC [1]
CC SEQUENCE FROM N.A.
CC RX MEDLINE=96423163; PubMed=8825764;
CC RA Lewis D.L., Farr C.L., Kaguni L.S.;
CC RT "Drosophila melanogaster mitochondrial DNA: completion of the
CC RT nucleotide sequence and evolutionary comparisons.";
CC RL Insect Mol. Biol. 4:263-278(1995).
CC [2]
CC SEQUENCE OF 56-341 FROM N.A.
CC RX MEDLINE=83245048; PubMed=6408489;
CC RA de Bruijn M.H.L.;
CC RT "Drosophila melanogaster mitochondrial DNA, a novel organization and
CC RT genetic code.";
CC RL Nature 304:234-241(1993).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- SIMILARITY: Belongs to the complex I subunit 2 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U37541; AAC47811.1; -.
CC DR EMBL; J01404; AAB59238.1; -.
CC PIR; A00419; QXFF2M.
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DR FlyBase; FBgn0013680; mt:ND2.
DR InterPro; IPR003917; NADHub_oxred2.
DR InterPro; IPR001750; Oxidored q1.
DR Pfam; PF00361; oxidored q1; 1.
DR PRINTS; PR01436; NADHDHGNASE2.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ SEQUENCE 341 AA; 39773 MW; 2B8E9528C28007D8 CRC64;
CC -----
CC Query Match 83.9%; Score 26; DB 1; Length 341;
CC Best Local Similarity 85.7%; Pred. No. 28;
CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 1 LMSTRAS 7
CC Db 51 LMSTRAS 57
CC -----
CC RESULT 11
CC NU2M DROVA
CC ID NU2M_DROVA STANDARD; PRT; 341 AA.
CC AC P03895;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
CC GN ND2.
CC OS Drosophila yakuba (Fruit fly).
CC OG Mitochondrion.
CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC OC Ephydroidea; Drosophilidae; Drosophila.
CC OX NCBI_TaxID=7245;
CC [1]
CC SEQUENCE FROM N.A.
CC RX STRAIN=2317.6 Ivory Coast;
CC RX MEDLINE=86089137; PubMed=3001325;
CC RA Clary D.O., Wolstenholme D.R.;
CC RT "The mitochondrial DNA molecular of Drosophila yakuba: nucleotide
CC RT sequence, gene organization, and genetic code.";
CC RL J. Mol. Evol. 22:252-271(1985).
CC [2]
CC SEQUENCE FROM N.A.
CC RX MEDLINE=84041489; PubMed=6314262;
CC RA Clary D.O., Wolstenholme D.R.;
CC RT "Genes for cytochrome c oxidase subunit I, URF2, and three tRNAs in
CC RT Drosophila mitochondrial DNA.";
CC RL Nucleic Acids Res. 11:6859-6872(1983).
CC [3]
CC SEQUENCE OF 1-56 FROM N.A.
CC RX MEDLINE=83090428; PubMed=6294611;
CC RA Clary D.O., Goddard J.M., Martin S.C., Fauron C.M.-R.,
CC RA Wolstenholme D.R.;
CC RT "Drosophila mitochondrial DNA: a novel gene order.";
CC RL Nucleic Acids Res. 10:6619-6637(1982).
CC [4]
CC SEQUENCE OF 1-56 FROM N.A.
CC RX MEDLINE=88011348; PubMed=3116271;
CC RA Clary D.O., Wolstenholme D.R.;
CC RT "Drosophila mitochondrial DNA: conserved sequences in the A + T-rich
CC RT region and supporting evidence for a secondary structure model of the
CC RT small ribosomal RNA.";
CC RL J. Mol. Evol. 25:116-125(1987).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- SIMILARITY: Belongs to the complex I subunit 2 family.
CC -----
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CC -----
CC EMBL; U37541; AAC47811.1; -.
CC DR EMBL; J01404; AAB59238.1; -.
CC PIR; A00419; QXFF2M.
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CC -----
CC EMBL; X03240; CAA26985.1; -.
CC EMBL; X05915; CAA29342.1; -.
CC PIR; B93488; OXFERY.
CC FlyBase; FBgn0013184; Dyakmt.ND2.
CC InterPro; IPR003917; NADhub_oxred2.
CC InterPro; IPR001750; Oxidored_g1.
CC Pfam; PF00361; oxidored_g1; 1.
CC PRINTS; PR01436; NADHDHGNASE2.
CC Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
CC SEQUENCE 341 AA; 39495 MW; E6117DE50BE9D4AF CRC64;
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Query Match 83.9%; Score 26; DB 1; Length 341;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 LMSTRAS 7
Db 51 LMSTAS 57
RESULT 12
CALL_MOUSE
ID CALL_MOUSE STANDARD; PRT; 1453 AA.
AC P11067; G60635;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagen alpha 1(I) chain precursor.
GN COL1A1 OR COL1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RX MEDLINE=96033240; PubMed=8535610;
RA Li S.W., Killian J., Prockop D.J.;
RT "The complete cDNA coding sequence for the mouse pro alpha 1(I) chain
of type I procollagen.";
RL Matrix Biol. 14:593-595(1995).
RN [2]
RP SEQUENCE OF 518-1128 FROM N.A.
RX MEDLINE=86137403; PubMed=3841523;
RA French B.T., Lee W.-H., Maul G.G.;
RT "Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I)
collagen protein.";
RL Gene 39:311-312(1985).
RN [3]
RP SEQUENCE OF 735-1130 FROM N.A.
RX MEDLINE=83141374; PubMed=6298597;
RA Monson J.M., Friedman J., McCarthy B.J.;
RT "DNA sequence analysis of a mouse pro alpha 1(I) procollagen gene:
evidence for a mouse B1 element within the gene.";
RL Mol. Cell. Biol. 2:1362-1371(1982).
RN [4]
RP SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
RX MEDLINE=83157109; PubMed=6219867;
RA Monson J.M., McCarthy B.J.;
RT "Identification of a Balb/c mouse pro alpha 1(I) procollagen gene:
evidence for insertions or deletions in gene coding sequences.";
RL DNA 1:59-69(1981).
RN [5]
RP SEQUENCE OF 1442-1453 FROM N.A.
RX MEDLINE=88124276; PubMed=3340560;
RA Moosleher K., Harbers K.;
RT "Two mRNAs of mouse pro alpha 1(I) collagen gene differ in the size
of the 3'-untranslated region.";
RL Nucleic Acids Res. 16:773-773(1988).
CC -/- FUNCTION: Type I collagen is a member of group I collagen
(fibrillar forming collagen).

```

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CC -/- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
CC -/- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and
CC bones. In bones the fibrils are mineralized with calcium
CC hydroxyapatite.
CC -/- PTM: Prolines at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -/- SIMILARITY: Contains 1 VWFC domain.
CC -----
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CC -----
CC EMBL; U08020; AAA88912.1; -.
CC EMBL; X15896; CAA33904.1; -.
CC EMBL; M14423; AAA37333.1; -.
CC EMBL; M17491; AAA37334.1; -.
CC EMBL; X06753; CAA29927.1; -.
CC EMBL; X03036; AAA37332.1; -.
CC EMBL; X03029; AAA37332.1; JOINED.
CC EMBL; X03030; AAA37332.1; JOINED.
CC EMBL; X03031; AAA37332.1; JOINED.
CC EMBL; X03032; AAA37332.1; JOINED.
CC EMBL; X03033; AAA37332.1; JOINED.
CC EMBL; X03034; AAA37332.1; JOINED.
CC EMBL; X03035; AAA37332.1; JOINED.
CC PIR; S57243; S21626.
CC MGD; MGI:88467; Colla1.
CC InterPro; IPR008161; C1g_helix.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR000885; Fib_collagen_C.
CC InterPro; IPR002181; Fibrinogen_C.
CC InterPro; IPR001007; VWFC_C.
CC Pfam; PF01410; COLFI; 1.
CC ProDom; PD000007; C1g_helix; 1.
CC ProDom; PD002078; Fib_collagen_C; 1.
CC SMART; SM00038; COLFI; 1.
CC SMART; SM00214; VWFC; 1.
CC PROSITE; PS01208; VWFC_1; 1.
CC PROSITE; PS0184; VWFC_2; 1.
CC Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
CC Glycoprotein; Collagen; Signal.
FT SIGNAL 1 22
FT PROPEP 23 151 AMINO-TERMINAL PROPEPTIDE.
FT CHAIN 152 1207 COLLAGEN ALPHA 1(I) CHAIN.
FT PROPEP 1208 1453 CARBOXYL-TERMINAL PROPEPTIDE.
FT DOMAIN 29 87 VWFC.
FT DOMAIN 152 167 NONHELICAL REGION (N-TERMINAL).
FT DOMAIN 168 1181 TRIPLE-HELICAL REGION.
FT DOMAIN 1182 1207 NONHELICAL REGION (C-TERMINAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1354 1354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 734 736 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 1082 1084 CELL ATTACHMENT SITE (POTENTIAL).
FT CONFLICT 1450 1450 A -> V (IN REF. 5).
SQ SEQUENCE 1453 AA; 137944 MW; 3B802E53DF81808 CRC64;
Query Match 83.9%; Score 26; DB 1; Length 1453;
Best Local Similarity 85.7%; Pred. No. 144+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 LMSTRAS 7
Db 1346 LMSTAS 1352
RESULT 13
CALL_CANFA
ID CALL_CANFA STANDARD; PRT; 1460 AA.

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AC QXKSJ7;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Collagen alpha 1(I) chain precursor.  
 GN COL1A1  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND VARIANT OI ALA-208.  
 RC TISSUE=Skin;  
 RX MEDLINE=21033337; PubMed=11147834;  
 RA Campbell B.G., Wootton J.A.M., Macleod J.N., Minor R.R.;  
 RT "Sequence of normal canine COL1A1 cDNA and identification of a  
 RT heterozygous normal(I) collagen Gly208Ala mutation in a severe case  
 RT of canine osteogenesis imperfecta.";  
 RL Arch. Biochem. Biophys. 384:137-46(2000).  
 CC -I- FUNCTION: Type I collagen is a member of group I collagen  
 CC (fibrillar forming collagen).  
 CC -I- SUBUNIT: Trimer of one alpha 2(I) and two alpha 1(I) chains.  
 CC -I- PTM: Prolines at the third position of the tripeptide repeating  
 CC unit (G-X-Y) are hydroxylated in some or all of the chains.  
 CC -I- DISEASE: Defects in COL1A1 are a cause of osteogenesis imperfecta  
 CC (OI).  
 CC -I- SIMILARITY: Contains 1 VWFC domain.  
 CC  
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 CC  
 CC EMBL; AF153062; AAD34619.1; -;  
 DR InterPro; IPR008161; Clg helix.  
 DR InterPro; IPR008160; Collagen.  
 DR InterPro; IPR000885; Fib collagen\_C.  
 DR InterPro; IPR002181; Fibrinogen\_C.  
 DR InterPro; IPR001007; VWFC\_C.  
 DR Pfam; PF01410; COLFI; 1.  
 DR Pfam; PF01391; Collagen; 18.  
 DR ProDom; PD000007; Clg helix; 2.  
 DR ProDom; PD002078; Fib collagen\_C; 1.  
 DR SMART; SM00038; COLFI\_1.  
 DR SMART; SM00214; VWC; 1.  
 DR PROSITE; PS01208; VWFC\_1; 1.  
 DR PROSITE; PS0184; VWFC\_2; 1.  
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;  
 KW Glycoprotein; Collagen; Signal; Disease mutation.  
 FT SIGNAL 1 22  
 FT PROPEP 23 157 AMINO-TERMINAL PROPEPTIDE.  
 FT CHAIN 158 1214 COLLAGEN ALPHA 1(I) CHAIN.  
 FT PROPEP 1215 1460 CARBOXYL-TERMINAL PROPEPTIDE.  
 FT DOMAIN 34 92 VWFC.  
 FT DOMAIN 158 174 NONHELICAL REGION (N-TERMINAL).  
 FT DOMAIN 175 1188 TRIPLE-HELICAL REGION.  
 FT DOMAIN 1189 1214 NONHELICAL REGION (C-TERMINAL).  
 FT SITE 741 743 CELL ATTACHMENT SITE (POTENTIAL).  
 FT SITE 1089 1091 CELL ATTACHMENT SITE (POTENTIAL).  
 FT CARBOHYD 1361 1361 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARIANT 208 208 G -> A (in OI; severe).  
 SQ SEQUENCE 1460 AA; 138762 MW; 58E3674D2B570697 CRC64;  
 Query Match 83.9%; Score 26; DB 1; Length 1460;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 DB 1353 LMSTRAS 1359

RESULT 14  
 CALL HUMAN STANDARD; PRT; 1464 AA.  
 AC P02452; Q14037; Q15176;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Collagen alpha 1(I) chain precursor.  
 GN COL1A1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 1-472 FROM N.A.  
 RX MEDLINE=89025644; PubMed=3178743;  
 RA Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,  
 RA Jaenisch R., Prockup D.J.;  
 RT "Structure of a full-length cDNA clone for the prepro alpha 1(I)  
 RT chain of human type I procollagen.";  
 RL Biochem. J. 253:919-922(1988).  
 RN [2]  
 RP SEQUENCE OF 1-181 FROM N.A.  
 RX MEDLINE=84270697; PubMed=6462220;  
 RA Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,  
 RA Myers J., Williams C., Ramirez F.;  
 RT "Human pro alpha 1(I) collagen gene structure reveals evolutionary  
 RT conservation of a pattern of introns and exons.";  
 RL Nature 310:337-340(1984).  
 RN [3]  
 RP SEQUENCE OF 162-301.  
 RC TISSUE=Skin;  
 RX MEDLINE=71038625; PubMed=5529814;  
 RA Click E.M., Bornstein P.;  
 RT "Isolation and characterization of the cyanogen bromide peptides from  
 RT the alpha 1 and alpha 2 chains of human skin collagen.";  
 RL Biochemistry 9:4699-4706(1970).  
 RN [4]  
 RP SEQUENCE OF 263-268.  
 RC TISSUE=Skin;  
 RX MEDLINE=71001508; PubMed=4319110;  
 RA Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;  
 RT "A comparative study of glycopeptides derived from selected  
 RT vertebrate collagens. A possible role of the carbohydrate in fibril  
 RT formation.";  
 RL J. Biol. Chem. 245:5042-5048(1970).  
 RN [5]  
 RP SEQUENCE OF 425-1464 FROM N.A.  
 RX MEDLINE=84080385; PubMed=6689127;  
 RA Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,  
 RA Prockup D.J.;  
 RT "Nucleotide sequences of complementary deoxyribonucleic acids for the  
 RT pro alpha 1 chain of human type I procollagen. Statistical evaluation  
 RT of structures that are conserved during evolution.";  
 RL Biochemistry 22:5213-5223(1983).  
 RN [6]  
 RP SEQUENCE OF 1229-1454 FROM N.A.  
 RC TISSUE=Bone;  
 RX MEDLINE=88124208; PubMed=3340531;  
 RA Mäkelä J.K., Raasina M., Virta A., Vuorio E.;  
 RT "Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide  
 RT domain.";  
 RL Nucleic Acids Res. 16:349-349(1988).  
 RN [7]  
 RP SEQUENCE OF 1-34 FROM N.A.  
 RX MEDLINE=88097389; PubMed=3480516;  
 RA Bornstein P., McKay J., Wörishima J.K., Devarayalu S., Gelinas R.E.;  
 RT "Regulatory elements in the first intron contribute to  
 RT transcriptional control of the human alpha 1(I) collagen gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8869-8873(1987).  
 RN [8]



RP SEQUENCE OF 1-34 FROM N.A.  
 RX MEDLINE=85130970; PubMed=2857713;  
 RA Chu M.-L., de Wet W.J., Bernard M.P., Ramirez F.;  
 RT "Fine structural analysis of the human pro-alpha 1 (I) collagen gene.  
 RT Promoter structure, Alu repeats, and polymorphic transcripts.";  
 RL J. Biol. Chem. 260:2315-2320(1985).  
 RN [9]  
 RP SEQUENCE OF 1-44 FROM N.A.  
 RX MEDLINE=88033098; PubMed=2822714;  
 RA Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez F.,  
 RA de Wet W.J.;  
 RT "DNA sequences in the first intron of the human pro-alpha 1(I)  
 RT collagen gene enhance transcription.";  
 RL J. Biol. Chem. 262:15151-15157(1987).  
 RN [10]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=91184577; PubMed=2010058;  
 RA Kuivaniemi H., Tromp G., Prockop D.J.;  
 RT "Mutations in collagen genes: causes of rare and some common diseases  
 RT in humans.";  
 RL FASEB J. 5:2052-2060(1991).  
 RN [11]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=97255959; PubMed=9101290;  
 RA Kuivaniemi H., Tromp G., Prockop D.J.;  
 RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-  
 RT associated collagen (type IX), and network-forming collagen (type X)  
 RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";  
 RL Hum. Mutat. 9:300-315(1997).  
 RN [12]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=97169399; PubMed=9016532;  
 RA Dalglish R.;  
 RT "The human type I collagen mutation database.";  
 RL Nucleic Acids Res. 25:181-187(1997).  
 RN [14]  
 RP VARIANT OI-II CYS-1166.  
 RX MEDLINE=86287390; PubMed=3016737;  
 RA Cohn D.H., Byers P.H., Steinmann B., Gelinas R.E.;  
 RT "Lethal osteogenesis imperfecta resulting from a single nucleotide  
 RT change in one human pro alpha 1(I) collagen allele.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6045-6047(1986).  
 RN [15]  
 RP VARIANT OI-II ARG-569.  
 RX MEDLINE=8722295; PubMed=3108247;  
 RA Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G.;  
 RT "Lethal perinatal osteogenesis imperfecta due to the substitution of  
 RT arginine for glycine at residue 391 of the alpha 1(I) chain of type I  
 RT collagen.";  
 RL J. Biol. Chem. 262:7021-7027(1987).  
 RN [16]  
 RP VARIANT OI-II CYS-926.  
 RX MEDLINE=88033031; PubMed=3667599;  
 RA Vogel B.E., Minor R.R., Freund M., Prockop D.J.;  
 RT "A point mutation in a type I procollagen gene converts glycine 748  
 RT of the alpha 1 chain to cysteine and destabilizes the triple helix in  
 RT a lethal variant of osteogenesis imperfecta.";  
 RL J. Biol. Chem. 262:14737-14744(1987).  
 RN [17]  
 RP VARIANT OI-II ARG-842.  
 RX MEDLINE=88298628; PubMed=3403550;  
 RA Bateman J.F., Lamané S.R., Dahl H.H., Chan D., Cole W.G.;  
 RT "Substitution of arginine for glycine 664 in the collagen alpha 1(I)  
 RT chain in lethal perinatal osteogenesis imperfecta. Demonstration of  
 RT the peptide defect by in vitro expression of the mutant cDNA.";  
 RL J. Biol. Chem. 263:11627-11630(1988).  
 RN [18]

RP VARIANT OI CYS-1195.  
 RX MEDLINE=89218628; PubMed=3244312;  
 RA Labhard M.E., Wirtz M.K., Pope F.M., Nicholls A.C., Hollister D.W.;  
 RT "A cysteine for glycine substitution at position 1017 in an alpha  
 RT 1(I) chain of type I collagen in a patient with mild dominantly  
 RT inherited osteogenesis imperfecta.";  
 RL Mol. Biol. Med. 5:197-207(1988).  
 RN [19]  
 RP VARIANT OI-II VAL-434.  
 RX MEDLINE=89255493; PubMed=2470760;  
 RA Patterson E., Smiley E., Bonadio J.;  
 RT "RNA sequence analysis of a perinatal lethal osteogenesis imperfecta  
 RT mutation.";  
 RL J. Biol. Chem. 264:10083-10087(1989).  
 RN [20]  
 RP VARIANT OI-IV SER-1010.  
 RX MEDLINE=89308591; PubMed=2745420;  
 RA Marini J.C., Grange D.K., Gottesman G.S., Lewis M.B., Koepplin D.A.;  
 RT "Osteogenesis imperfecta type IV. Detection of a point mutation in  
 RT one alpha 1(I) collagen allele (COL1A1) by RNA/RNA hybrid analysis.";  
 RL J. Biol. Chem. 264:11893-11900(1989).  
 RN [21]  
 RP VARIANTS OI-II ALA-1106; VAL-1151; ARG-1154 AND VAL-1184.  
 RX MEDLINE=89380165; PubMed=2777764;  
 RA Lamané S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;  
 RT "Characterization of point mutations in the collagen COL1A1 and  
 RT COL1A2 genes causing lethal perinatal osteogenesis imperfecta.";  
 RL J. Biol. Chem. 264:15809-15812(1989).  
 RN [22]  
 RP VARIANT OI SER-1022.  
 RX MEDLINE=90062068; PubMed=2511192;  
 RA Pack M., Constantinou C.D., Kallia K., Nielsen K.B., Prockop D.J.;  
 RT "Substitution of serine for alpha 1(I)-glycine 844 in a severe  
 RT variant of osteogenesis imperfecta minimally destabilizes the triple  
 RT helix of type I procollagen. The effects of glycine substitutions on  
 RT thermal stability are either position of amino acid specific.";  
 RL J. Biol. Chem. 264:19694-19699(1989).  
 RN [23]  
 RP VARIANT OI-II CYS-1082.  
 RX MEDLINE=89109573; PubMed=2913053;  
 RA Constantinou C.D., Nielsen K.B., Prockop D.J.;  
 RT "A lethal variant of osteogenesis imperfecta has a single base  
 RT mutation that substitutes cysteine for glycine 904 of the alpha 1(I)  
 RT chain of type I procollagen. The asymptomatic mother has an  
 RT unidentified mutation producing an overmodified and unstable type I  
 RT procollagen.";  
 RL J. Clin. Invest. 83:574-584(1989).  
 RN [24]  
 RP VARIANTS OI CYS-272; CYS-704 AND CYS-896.  
 RX MEDLINE=90009313; PubMed=2794057;  
 RA Staman B.J., Eyre D., Charbonneau H., Harrylock M., Weis M.A.,  
 RA Weiss L., Graham J.M., Byers P.H.;  
 RT "Osteogenesis imperfecta. The position of substitution for glycine by  
 RT cysteine in the triple helical domain of the pro alpha 1(I) chains of  
 RT type I collagen determines the clinical phenotype.";  
 RL J. Clin. Invest. 84:1206-1214(1989).  
 RN [25]  
 RP VARIANT OI-II CYS-422.

Query Match 83.9%; Score 26; DB 1; Length 1464;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7

Db 1357 LMSTEAS 1363

RESULT 15

AG11 WHEAT

ID AG11 WHEAT STANDARD; PRT; 212 AA.

AC P10968;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Agglutinin isolectin 1 precursor (WGA1) (Isolectin A).  
 OS Triticum aestivum (Wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticaceae; Triticum.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=91370843; PubMed=2491677;  
 RX Smith J.J., Raikhel N.V.;  
 RA "Nucleotide sequences of cDNA clones encoding wheat germ agglutinin  
 RT isolectins A and D.";  
 RL Plant Mol. Biol. 13:601-603(1989).  
 RN [2]  
 RN SEQUENCE OF 27-197.  
 RP TISSUE=Germ;  
 RX MEDLINE=89279931; PubMed=2499688;  
 RA Wright C.S., Raikhel N.V.;  
 RT "Sequence variability in three wheat germ agglutinin isolectins:  
 RT products of multiple genes in polyploid wheat.";  
 RL J. Mol. Evol. 28:327-336(1989).  
 RN [3]  
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RP MEDLINE=91039324; PubMed=2231724;  
 RX Wright C.S.;  
 RA "2.2-A resolution structure analysis of two refined  
 RT N-acetylneuraminyl-lactose-wheat germ agglutinin isolectin  
 RT complexes.";  
 RL J. Mol. Biol. 215:635-651(1990).  
 RN [4]  
 RN X-RAY CRYSTALLOGRAPHY.  
 RP MEDLINE=90064507; PubMed=2585496;  
 RX Wright C.S.;  
 RA "Comparison of the refined crystal structures of two wheat germ  
 RT isolectins.";  
 RL J. Mol. Biol. 209:475-487(1989).  
 CC -1- FUNCTION: N-acetyl-D-glucosamine / N-acetyl-D-neuraminic acid  
 CC binding lectin.  
 CC -1- SUBUNIT: Homodimer, u-shaped.  
 CC -1- MISCELLANEOUS: The 4 sites proposed for binding to carbohydrates  
 CC (N-acetyl-D-glucosamine) of receptor molecules are on the surface  
 CC of the agglutinin molecule.  
 CC -1- SIMILARITY: THERE ARE THREE VARIANTS OF WGA; VARIABILITY AMONG  
 CC THEM IS OBSERVED AT A TOTAL OF 10 POSITIONS.  
 CC -1- SIMILARITY: Contains 4 chitin-binding domains.  
 CC -1- SIMILARITY: Contains 4 chitin-binding type-1 domains.  
 CC -----  
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 CC -----  
 DR EMBL: M25536; AAA34256.1; --  
 DR F1R; S09623; S09623.  
 DR PDB; 7WGA; 15-OCT-90.  
 DR PDB; 1WGC; 15-OCT-90.  
 DR PDB; 2CWG; 31-JAN-94.  
 DR InterPro; IPR001002; Chitin\_binding\_1.  
 DR Pfam; PF00187; Chitin\_bind\_1; 4.  
 DR PRINTS; PR00451; CHITINBINDING.  
 DR ProDom; PD000609; Chitin\_binding\_1; 4.  
 DR SWART; SMO0270; ChEBI; 4.  
 DR PROSITE; PS00941; CHIT\_BIND\_I\_2; 4.  
 DR PROSITE; PS00026; CHIT\_BIND\_I\_1; 4.  
 KW Lectin; Repeat; Chitin-binding; 3D-structure; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 197 AGGLUTININ ISOLECTIN 1.  
 FT PROPEP 198 212

FT DOMAIN 27 68  
 FT DOMAIN 69 111  
 FT DOMAIN 112 154  
 FT DOMAIN 155 197  
 FT DISULFID 29 44  
 FT DISULFID 38 50  
 FT DISULFID 43 57  
 FT DISULFID 61 66  
 FT DISULFID 72 87  
 FT DISULFID 81 93  
 FT DISULFID 86 100  
 FT DISULFID 104 109  
 FT DISULFID 115 130  
 FT DISULFID 124 136  
 FT DISULFID 129 143  
 FT DISULFID 147 152  
 FT DISULFID 158 173  
 FT DISULFID 167 179  
 FT DISULFID 172 186  
 FT DISULFID 190 195  
 FT CONFLICT 63 63  
 FT STRAND 30 30  
 FT HELIX 31 33  
 FT TURN 34 35  
 FT STRAND 36 37  
 FT HELIX 39 41  
 FT STRAND 43 44  
 FT TURN 46 47  
 FT STRAND 50 52  
 FT HELIX 54 57  
 FT TURN 59 60  
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 FT STRAND 73 73  
 FT HELIX 74 76  
 FT TURN 77 78  
 FT STRAND 79 79  
 FT TURN 83 84  
 FT STRAND 86 87  
 FT TURN 89 90  
 FT STRAND 92 95  
 FT HELIX 97 100  
 FT TURN 102 103  
 FT STRAND 106 106  
 FT STRAND 114 114  
 FT STRAND 116 116  
 FT HELIX 117 119  
 FT TURN 120 121  
 FT STRAND 122 122  
 FT HELIX 125 127  
 FT STRAND 129 130  
 FT TURN 132 133  
 FT STRAND 135 138  
 FT HELIX 140 143  
 FT TURN 145 146  
 FT STRAND 149 149  
 FT STRAND 159 159  
 FT HELIX 160 162  
 FT TURN 163 164  
 FT STRAND 165 165  
 FT HELIX 168 170  
 FT STRAND 172 173  
 FT TURN 175 176  
 FT STRAND 179 181  
 FT HELIX 183 186  
 FT TURN 188 189  
 FT STRAND 192 192  
 FT SEQUENCE 212 AA; 21239 MW; EC7B6F007DDC15EB CRC64;

N -&gt; D (IN REF. 2 AND 3).

Query Match 80.6%; Score 25; DB 1; Length 212;  
 Best Local Similarity 83.3%; Pred. No. 31;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LMSTRA 6  
:|||||  
Db 3 MMSTRA 8

Search completed: September 30, 2004, 06:01:16  
Job time : 6.27119 secs

Blank sheet

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 22.8983 Seconds  
(without alignments)  
96.454 Million cell updates/sec

Title: US-09-674-716b-5  
Perfect score: 31  
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	90.3	847	16 Q7UW5	Q7UW5 rhodopirell
2	27	87.1	124	15 Q8EEB9	Q8EEB9 shewanella
3	27	87.1	342	16 Q9P110	Q9P110 campylobact
4	27	87.1	409	16 Q8X5U5	Q8X5U5 escherichia
5	27	87.1	409	16 Q8FJ15	Q8FJ15 escherichia
6	27	87.1	505	16 Q7UQP6	Q7UQP6 rhodopirell
7	27	87.1	541	5 Q868T1	Q868T1 anopheles g
8	27	87.1	544	11 Q8BX14	Q8BX14 mus musculu
9	27	87.1	579	5 Q7YV69	Q7YV69 cryptospori
10	27	87.1	657	11 Q8BLC8	Q8BLC8 mus musculu
11	27	87.1	860	5 Q198S2	Q198S2 caenorhabdi
12	27	87.1	1024	11 Q9ESJ5	Q9ESJ5 mus musculu
13	27	87.1	1049	2 Q9XBP6	Q9XBP6 myxococcus
14	27	87.1	1141	10 Q8LJU7	Q8LJU7 cryza sativ
15	26	83.9	112	16 Q92K36	Q92K36 rhizobium m
16	26	83.9	114	6 Q862S4	Q862S4 bos taurus

17	26	83.9	212	6 Q862R9	Q862R9 bos taurus
18	26	83.9	284	4 Q160S0	Q160S0 homo sapien
19	26	83.9	287	6 Q5NND8	Q5NND8 bos taurus
20	26	83.9	313	16 Q92TL9	Q92TL9 rhizobium m
21	26	83.9	325	11 Q60785	Q60785 mus musculu
22	26	83.9	338	8 Q9B2J6	Q9B2J6 chrysomya c
23	26	83.9	338	8 Q9MFQ0	Q9MFQ0 cochliomyia
24	26	83.9	340	8 Q9XMP1	Q9XMP1 ceratitis c
25	26	83.9	341	8 Q9MGL3	Q9MGL3 drosophila
26	26	83.9	341	8 Q9MGN7	Q9MGN7 drosophila
27	26	83.9	341	8 Q9MGN2	Q9MGN2 drosophila
28	26	83.9	341	8 Q9MDS9	Q9MDS9 drosophila
29	26	83.9	341	8 Q9MGP1	Q9MGP1 drosophila
30	26	83.9	341	8 Q9MD72	Q9MD72 drosophila
31	26	83.9	341	8 Q9WJC9	Q9WJC9 drosophila
32	26	83.9	341	8 Q9MD83	Q9MD83 drosophila
33	26	83.9	420	16 Q8E9A1	Q8E9A1 shewanella
34	26	83.9	437	16 Q7V3T8	Q7V3T8 prochloroco
35	26	83.9	481	13 Q90YJ1	Q90YJ1 brachydanio
36	26	83.9	531	10 Q8L4V1	Q8L4V1 cryza sativ
37	26	83.9	589	11 Q99LL6	Q99LL6 mus musculu
38	26	83.9	718	16 Q8D859	Q8D859 vibrio vuln
39	26	83.9	810	16 Q69650	Q69650 mycobacteri
40	26	83.9	810	16 Q7TVY3	Q7TVY3 mycobacteri
41	26	83.9	1453	11 Q63079	Q63079 ratus norv
42	26	83.9	1453	11 Q810J9	Q810J9 mus musculu
43	26	83.9	1461	4 Q76045	Q76045 homo sapien
44	26	83.9	1464	4 Q8N473	Q8N473 homo sapien
45	25	80.6	135	2 Q8RQ37	Q8RQ37 bacillus ce

ALIGNMENTS

RESULT 1  
Q7UW5 PRELIMINARY; PRT; 847 AA.  
AC Q7UW5; 2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN R81802.  
OS Rhodopirellula baltica.  
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
OC Planctomycetaceae; Pirellula.  
OX NCBI\_TaxID=117;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1;  
RX MEDLINE=22735913; PubMed=12835416;  
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,  
RA Schlesner H., Amann R., Reinhardt R.;  
RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
strain 1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).  
DR EMBL; BX294135; CAD72277.1;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 847 AA; 89847 MW; 437EF2BCED0B2812 CRC64;

Query Match 90.3%; Score 28; DB 16; Length 847;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 177 LMSTRAS 183

RESULT 2  
Q8EEB9 PRELIMINARY; PRT; 124 AA.  
ID Q8EEB9

Q8EBB9;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Adhesion-related protein.  
 GN SO2467.  
 OS Shewanella oneidensis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 OC Alteromonadaceae; Shewanella.  
 OX NCBI\_TaxID=70863;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NR-1;  
 RX MEDLINE=2297686; PubMed=12368813;  
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,  
 RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,  
 RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,  
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,  
 RA Madupu R., Peterson J.D., Unayam L.A., White O., Wolf A.M.,  
 RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,  
 RA Mueller J., Khouri H., Gill J., Uterback T.R., McDonald L.A., C.M.;  
 RA Feldblyum T.V., Smith H.O., Venter J.C., Neelson K.H., Fraser C.M.;  
 RA "Genome sequence of the dissimilatory metal ion-reducing bacterium  
 RT Shewanella oneidensis.";  
 RL Nat. Biotechnol. 20:1118-1123 (2002).  
 DR EMBL; AB015688; AAN55499.1; -.  
 DR TIGR; SO2467; -.  
 KW Complete proteome.  
 SQ SEQUENCE 124 AA; 13061 MW; D77E2F6F42DEF735 CRC64;  
 Query Match 87.1%; Score 27; DB 16; Length 124;  
 Best Local Similarity 85.7%; Pred. No. 38;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 Db 83 LMSTRAS 89

RESULT 3  
 Q9PIIO PRELIMINARY; PRT; 342 AA.  
 AC Q9PIIO;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Flagellar motor switch protein.  
 GN FLIG OR CJ0319.  
 OS Campylobacter jejuni.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 OC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=197;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCCT 11168;  
 RX MEDLINE=20150912; PubMed=10688204;  
 RA Parkhill J., Wren B.W., Mungall K., Kettle J.M., Churcher C.,  
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,  
 RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,  
 RA Quail M.A., Rajadream M.A., Rutherford K.M., van Vliet A.H.M.,  
 RA Whitehead S., Barrall B.G.;  
 RA "The genome sequence of the food-borne pathogen Campylobacter jejuni  
 RT reveals hypervariable sequences.";  
 RL Nature 403:665-668 (2000).  
 DR EMBL; AL139074; CAB72786.1; -.  
 DR PIR; C81451; C81451.  
 DR HSP; Q9WY63; IQC7.  
 DR GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.  
 DR GO; GO:0003774; F:motor activity; IEA.  
 DR GO; GO:0006935; P:chemotaxis; IEA.  
 DR GO; GO:0001529; P:ciliary/flagellar motility; IEA.  
 DR InterPro; IPR000090; FLG\_Motor\_Flag.  
 DR Pfam; PF01706; FLIG-C; 1.

DR PRINTS; PRO0954; FLGMOTORFLIG.  
 DR TIGRFams; TIGR00207; flIG; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 342 AA; 38429 MW; ED4D214417C1524C CRC64;  
 Query Match 87.1%; Score 27; DB 16; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 MSTRAS 7  
 Db 289 MSTRAS 294

RESULT 4  
 Q8XSU5 PRELIMINARY; PRT; 409 AA.  
 ID Q8XSU5  
 AC Q8XSU5;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Putative beta-ketoacyl-ACP synthase (Putative 3-oxoacyl-(acyl-carrier-  
 DE protein) synthase II).  
 GN Z4866 OR EC34341.  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.R., Plunkett G., III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
 RL Nature 409:529-533 (2001).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / RIMD 050952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.,  
 RA "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";  
 RL DNA Res. 8:11-22 (2001).  
 DR EMBL; AE005571; AAG58601.1; -.  
 DR EMBL; AP002565; BAB37764.1; -.  
 DR PIR; E86017; E86017.  
 DR PIR; E91171; E91171.  
 DR GO; GO:0003824; F:catalytic activity; IEA.  
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
 DR InterPro; IPR000794; Ketoacyl synth.  
 DR Pfam; PF00109; ketoacyl-synt; 1.  
 DR Pfam; PF02801; ketoacyl-synt C; 1.  
 DR PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 409 AA; 44148 MW; A4DAB0AFALIED883 CRC64;

Query Match 87.1%; Score 27; DB 16; Length 409;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 MSTRAS 7  
 Db 77 MSTRAS 82

```
RESULT 5
Q8FJ15 ID Q8FJ15 PRELIMINARY; PRT; 409 AA.
AC Q8FJ15;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-ketoacyl-ACP synthase.
GN Cll86.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=06:HI / CF7073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=124711157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AB016758; AAN79648.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0006533; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR000794; K:Ketoacyl-synth.
DR Pfam; PF00109; ketoacyl-synth.
DR Pfam; PF02801; ketoacyl-synth_C; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
KW Complete proteome.
SQ SEQUENCE 409 AA; 44133 MW; FEDAA0651B6E1239 CRC64;

Query Match 87.1%; Score 27; DB 16; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTRAS 7
Db 77 MSTRAS 82

RESULT 6
Q7UQF6 ID Q7UQF6 PRELIMINARY; PRT; 505 AA.
AC Q7UQF6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable iron-sulfur protein.
GN RB6355.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL; BX294144; CAD74747.1; -.
KW Complete proteome.
SQ SEQUENCE 505 AA; 55994 MW; 22B90195A3E1D941 CRC64;

Query Match 87.1%; Score 27; DB 16; Length 505;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTRAS 7
Db 77 MSTRAS 82

RESULT 7
Q868T1 ID Q868T1 PRELIMINARY; PRT; 541 AA.
AC Q868T1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gag-like protein (Fragment).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22531580; PubMed=12644555;
RA Kojima K.K., Fujiwara H.;
RT "Evolution of Target Specificity in R1 Clade Non-LTR
Retrotransposons.";
RL Mol. Biol. Evol. 20:351-361 (2003).
DR EMBL; AB090812; BAC57899.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_C2HC; 2.
DR PROSITE; PS50158; ZF_CCHC; 2.
FT NON_TER;
SQ SEQUENCE 541 AA; 60221 MW; 6CB5F551260FDF55 CRC64;

Query Match 87.1%; Score 27; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTRAS 7
Db 37 MSTRAS 42

RESULT 8
Q8BX14 ID Q8BX14 PRELIMINARY; PRT; 544 AA.
AC Q8BX14;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RAP guanine nucleotide exchange factor homolog.
GN C030018K18RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK049228; BAC33622.1; -.
DR MGD; MGI:1924777; C030018K18RIK.
DR GO; GO:0005085; F:guanyl-nucleotide exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR000651; RasGEFN.
DR InterPro; IPR008937; Ras_GEF.
```

DR Pfam; PF00027; cNMP\_binding; 1.  
 DR Pfam; PF00618; RasGEFN; 1.  
 DR SMART; SM00100; cNMP; 1.  
 DR SMART; SM00229; RasGEFN; 1.  
 DR PROSITE; PS50042; cNMP\_BINDING\_3; 2.  
 DR PROSITE; PS50212; RasGEFN; 1.  
 DR PROSITE; PS50212; RasGEFN; 1.  
 SQ SEQUENCE 544 AA; 82255 MW; B8285479CB5ACEF5 CRC64;

Query Match 87.1%; Score 27; DB 11; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6  
 DB 48 LMSTRA 53

RESULT 9

ID Q7YV69 PRELIMINARY; PRT; 579 AA.  
 AC Q7YV69;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN 56k.15.  
 OS Cryptosporidium parvum.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
 OC Cryptosporididae; Cryptosporidium.  
 OX NCBI\_TaxID=5807;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Iowa;  
 RA Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M.,  
 RA Vogel C., Teichmann S.A., Ivens A., Dear P.H.;  
 RT "Integrated mapping, chromosomal sequencing and sequence analysis of  
 RT Cryptosporidium parvum";  
 RL Genome Res. 0:0-0(2003).  
 KW EMBL; BX538350; CAD98618.1; --  
 SQ SEQUENCE 579 AA; 67569 MW; 3F153FD2678AEC75 CRC64;

Query Match 87.1%; Score 27; DB 5; Length 579;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 DB 393 LMSTRAS 399

RESULT 10

ID Q8BLC8 PRELIMINARY; PRT; 657 AA.  
 AC Q8BLC8;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE RAP guanine nucleotide exchange factor homolog (fragment).  
 GN C030018K18RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium.  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).

DR EMBL; AK045540; BAC32411.1; --  
 DR MGD; MGI:1924777; C030018K18RIK.  
 DR GO; GO:0005885; P:guanyl-nucleotide exchange factor activity; IEA.  
 DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.  
 DR InterPro; IPR000595; cNMP\_binding.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR000651; RasGEFN.  
 DR InterPro; IPR008937; RasGEF.  
 DR Pfam; PF00027; cNMP\_binding; 1.  
 DR Pfam; PF00595; PDZ\_1.  
 DR Pfam; PF00618; RasGEFN; 1.  
 DR SMART; SM00100; cNMP; 1.  
 DR SMART; SM00228; PDZ; 1.  
 DR SMART; SM00229; RasGEFN; 1.  
 DR PROSITE; PS50042; cNMP\_BINDING\_3; 2.  
 DR PROSITE; PS50106; PDZ\_1.  
 DR PROSITE; PS50212; RasGEFN; 1.  
 DR PROSITE; PS50212; RasGEFN; 1.  
 FT NON\_TER 657  
 SQ SEQUENCE 657 AA; 74726 MW; C531B0D1FB4E4D9A CRC64;

Query Match 87.1%; Score 27; DB 11; Length 657;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6  
 DB 48 LMSTRA 53

RESULT 11

ID Q19852 PRELIMINARY; PRT; 860 AA.  
 AC Q19852;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN F2884.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Leimbach D.;  
 RT "The sequence of C. elegans cosmid F2884.";  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;  
 RT "Direct Submission";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U42834; AAA83583.2; --  
 DR PIR; T16198; T16198.  
 DR HSSP; Q61193; 1BLF.  
 DR WormPep; F2884.2; CE28222.  
 DR GO; GO:0005885; P:guanyl-nucleotide exchange factor activity; IEA.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.  
 DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.  
 DR InterPro; IPR000651; RasGEFN.  
 DR InterPro; IPR001895; RasGEF.  
 DR InterPro; IPR008937; RasGEF.  
 DR InterPro; IPR008937; RasGEF.  
 DR InterPro; IPR00159; RA\_Domain.



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DR Pfam; PF00788; RA; 1.
DR Pfam; PF00617; RasGEF; 1.
DR Pfam; PF00618; RasGEF; 1.
DR SMART; SM00314; RA; 1.
DR SMART; SM00147; RasGEF; 1.
DR SMART; SM00229; RasGEF; 1.
DR SMART; PS00300; RA; 1.
DR PROSITE; PS00720; RasGEF; 1.
DR PROSITE; PS00009; RasGEF; 1.
DR PROSITE; PS0212; RasGEF_NTER; 1.
KW Hypothetical protein.
SQ SEQUENCE 860 AA; 96122 MW; 16088524FBC65CA5 CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 5; Length 860;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTRAS 7
Db 668 MSTRAS 673

RESULT 12
Q9ESJ5 PRELIMINARY; PRT; 1024 AA.
AC Q9ESJ5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE GluR-delta2 philic-protein.
GN GRID2IP OR DELPHILIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Miyagi Y., Yamashita T., Okuda K., Mishina M., Kawamoto S.;
RT "Delphinin: A novel PDZ-containing protein associates with the Glur-
delta2 subunit.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AF099933; AAG31020.1; -.
DR HSSP; P29476; IQAV.
DR MGD; MGI:2176213; Grid2ip.
DR GO; GO:0019717; C:synapto some; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR003104; FH2.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF02181; FH2; 1.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00498; FH2; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS0106; PDZ; 1.
SQ SEQUENCE 1024 AA; 112578 MW; E318AFDE02F846A CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 11; Length 1024;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 53 LVSTRAS 59

RESULT 13
Q9XBP6 PRELIMINARY; PRT; 1049 AA.
AC Q9XBP6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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DE Serine/threonine kinase PKN8.
GN PKN8.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cyctobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DZFl;
RA Inouye S., Jain R., Ueki T., Nariya H., Xu C., Hsu M.,
RA Munoz-Dorado J., Farex-Vidal E., Inouye M.;
RT "Sequence Analysis of 13 Eukaryotic-like Protein Ser/Thr Kinases of
RT Myxococcus xanthus, a Developmental Bacterium and Significance of
RT Their Coexistence with Protein His Kinases.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159691; AAD42856.1; -.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001440; TPR-like.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00515; TPR; 5.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 1049 AA; 114313 MW; 7752862DAA25338C CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 2; Length 1049;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1002 LMSTRAS 1008

RESULT 14
Q8LJJ7 PRELIMINARY; PRT; 1141 AA.
AC Q8LJJ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative chromodomain-helicase-DNA-binding protein.
GN P0018C10.33.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0018C10.33";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003227; BAC06232.1; -.
DR Gramene; Q8LJJ7; -.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
DR GO; GO:0003682; F:chromatin binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006333; P:chromatin assembly/disassembly; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000953; Chromo.

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DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002464; DEAH_box.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR000330; SNF2_N.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00385; Chromo; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00176; SNF2_N; 1.
DR SMART; SM00298; CHROMO; 2.
DR SMART; SM00487; DEXDG; 1.
DR SMART; SM00490; HELIC; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS00013; CHROMO_2; 2.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
DR PROSITE; PS01359; ZF_PHD_1; 1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
KW ATP-binding; DNA-binding; Helicase; Hydrolase.
SQ SEQUENCE 1141 AA; 128517 MW; 47B812CC0ABC2649 CRC64;

Query Match      87.1%; Score 27; DB 10; Length 1141;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6
Db 908 LMSTRA 913

RESULT 15
Q92W36 PRELIMINARY; PRT; 112 AA.
ID Q92W36
AC Q92W36;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein RB0509.
GN RB0509 OR SMB20530.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymB (megaplasmid 2).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_taxid=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Gouzy J.,
RA Vorhoeelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
DR EMBL; AL603643; CAC48509.1; -.
DR FIR; E95905; E95905.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 112 AA; 11488 MW; 95FD54B0FC5CA90E CRC64;

Query Match      83.9%; Score 26; DB 16; Length 112;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 5 INSTRSS 11

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 34.1695 Seconds  
(without alignments)  
57.863 Million cell updates/sec

Title: US-09-674-716B-5  
Perfect score: 31  
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Genesep 29Jan04: \*  
1: Genesep1980s: \*  
2: Genesep1990s: \*  
3: Genesep2000s: \*  
4: Genesep2001s: \*  
5: Genesep2002s: \*  
6: Genesep2003as: \*  
7: Genesep2003bs: \*  
8: Genesep2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	2 AAW39825	AAW39825 Light cha
2	31	100.0	7	2 AAW39822	AAW39822 Light cha
3	31	100.0	7	2 AAW39819	AAW39819 Light cha
4	31	100.0	7	3 AAV32255	AAV32255 Light cha
5	31	100.0	100	4 AAE06959	AAE06959 Mouse ger
6	31	100.0	113	2 AAW39803	AAW39803 Variable
7	31	100.0	113	2 AAW39886	AAW39886 Light cha
8	31	100.0	113	2 AAW39802	AAW39802 Variable
9	31	100.0	113	2 AAW39882	AAW39882 Light cha
10	31	100.0	113	2 AAW39804	AAW39804 Variable
11	31	100.0	116	3 AAV32262	AAV32262 Humanised
12	31	100.0	145	3 AAV32261	AAV32261 Mouse ant
13	28	90.3	7	2 AAW39816	AAW39816 Light cha
14	28	90.3	113	2 AAW39801	AAW39801 Variable
15	28	90.3	274	2 AAW39899	AAW39899 Single ch
16	28	90.3	979	7 ADB64292	ADB64292 Human pro
17	27	87.1	7	2 AAW39876	AAW39876 Light cha
18	27	87.1	68	4 AAW4213	AAW4213 Propionib
19	27	87.1	68	6 ABM50732	ABM50732 Propionib
20	27	87.1	119	6 ABU00435	ABU00435 Human nov
21	27	87.1	123	4 ABM54742	ABM54742 Propionib
22	27	87.1	123	6 ABM51261	ABM51261 Propionib
23	27	87.1	131	2 AAR12232	AAR12232 Mouse Mab
24	27	87.1	132	2 AAR12354	AAR12354 Light (ka
25	27	87.1	140	4 AAM95756	AAM95756 Human rep

26	27	87.1	218	5	ABG77402	ABG77402 Selected
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28	27	87.1	342	6	ABU26357	ABU26357 Protein e
29	27	87.1	409	4	ABBS2717	ABBS2717 Escherich
30	27	87.1	809	5	ABP73372	ABP73372 Candida a
31	27	87.1	845	6	ABR53640	ABR53640 Protein s
32	26	83.9	77	4	AU39838	AU39838 Propionib
33	26	83.9	77	6	ABM36357	ABM36357 Propionib
34	26	83.9	115	4	AAU41133	AAU41133 Peptide #
35	26	83.9	115	4	ABB33078	ABB33078 Peptide #
36	26	83.9	115	4	AAW26539	AAW26539 Peptide #
37	26	83.9	115	4	ABB27906	ABB27906 Human pep
38	26	83.9	115	4	ABBI8546	ABBI8546 Protein #
39	26	83.9	115	4	AAW66263	AAW66263 Human bon
40	26	83.9	115	4	AAW53875	AAW53875 Human bra
41	26	83.9	115	4	ABG47927	ABG47927 Human liv
42	26	83.9	115	4	AAU01871	AAU01871 Peptide #
43	26	83.9	115	5	ABG35910	ABG35910 Human pep
44	26	83.9	133	7	ADB64310	ADB64310 Human pro
45	26	83.9	134	4	ABG10627	ABG10627 Novel hum

ALIGNMENTS

RESULT 1  
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ID AAW39825 standard; peptide; 7 AA.  
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AC AAW39825;  
XX  
DT 16-JUN-1998 (first entry)  
XX  
DE Light chain CDR2 of catalytic antibody 12H1.  
XX  
KW Variable domain; lambda light chain; catalytic antibody; degradation;  
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
KW overdose; addiction.  
XX  
OS Mus sp.  
XX  
PN WO9749800-A1.  
XX  
PD 31-DEC-1997.  
XX  
PF 25-JUN-1997; 97WO-US010965.  
XX  
PR 25-JUN-1996; 96US-00672345.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Laundry DW;  
XX  
DR WPI; 1998-077166/07.  
XX  
PT New catalytic antibodies able to decompose cocaine, single-chain  
PT analogues - used to treat cocaine overdose and addiction, required in far  
PT smaller doses than antibodies that antagonise cocaine by simply binding.  
XX  
PS Claim 17; Page 83; 147pp; English.  
XX  
CC AAW39824-26 represent the sequences of the light chain complementarity  
CC determining regions (CDRs) of the catalytic antibody 12H1, which is able  
CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
CC were prepared and used to immunise mice for production of hybridomas.  
CC Catalytic antibodies were identified by their capacity to release 3H-  
CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified  
CC using TSA2, and has a per minute Kcat of 0.16. The antibodies reduce the  
CC concentration of cocaine in a subject, and are used particularly for the  
CC treatment of an overdose. They are also used for treating addiction (by  
CC reducing the in vivo concentration that can be achieved)

SQ Sequence 7 AA;  
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 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
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 Db 1 LMSTRAS 7

RESULT 2  
 AAW39822  
 ID AAW39822 standard; peptide; 7 AA.  
 XX  
 AC AAW39822;  
 XX  
 DT 16-JUN-1998 (first entry)  
 XX  
 DE Light chain CDR2 of catalytic antibody 2A10.  
 XX  
 KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9749800-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 PF 25-JUN-1997; 97WO-US010965.  
 XX  
 PR 25-JUN-1996; 96US-00672345.  
 XX  
 PS (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 PI Landry DW;  
 XX  
 DR WPI; 1998-077166/07.  
 XX  
 PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 PS Claim 15; Page 82; 147pp; English.  
 XX  
 CC AAW39821-23 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 2A10, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

SQ Sequence 7 AA;  
 Query Match 100.0%; Score 31; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 |||||  
 Db 1 LMSTRAS 7

RESULT 3  
 AAW39822  
 ID AAW39822 standard; peptide; 7 AA.  
 XX  
 AC AAW39822;  
 XX  
 DT 15-FEB-2000 (first entry)  
 XX  
 DE Light chain CDR L2 of mouse anti-CD23 Mab C11.  
 XX  
 KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;

AAW39819  
 ID AAW39819 standard; peptide; 7 AA.  
 XX  
 AC AAW39819;  
 XX  
 DT 16-JUN-1998 (first entry)  
 XX  
 DE Light chain CDR2 of catalytic antibody 6A12.  
 XX  
 KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9749800-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 PF 25-JUN-1997; 97WO-US010965.  
 XX  
 PR 25-JUN-1996; 96US-00672345.  
 XX  
 PS (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 PI Landry DW;  
 XX  
 DR WPI; 1998-077166/07.  
 XX  
 PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 PS Claim 13; Page 81; 147pp; English.  
 XX  
 CC AAW39818-20 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 6A12, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

SQ Sequence 7 AA;  
 Query Match 100.0%; Score 31; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 |||||  
 Db 1 LMSTRAS 7

RESULT 4  
 AAW32255  
 ID AAW32255 standard; peptide; 7 AA.  
 XX  
 AC AAW32255;  
 XX  
 DT 15-FEB-2000 (first entry)  
 XX  
 DE Light chain CDR L2 of mouse anti-CD23 Mab C11.  
 XX  
 KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;

XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
KW

[illegible]

XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
KW

KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX Mus sp.  
 XX WO9749800-A1.  
 XX 31-DEC-1997.  
 XX 25-JUN-1997; 97WO-US010965.  
 XX 25-JUN-1996; 96US-00672345.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Landry DW;  
 XX WPI; 1998-077166/07.  
 XX P-PSDB; AAV09802.  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX Claim 18; Page 73; 147pp; English.  
 XX AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808  
 CC represents the heavy chain) was identified using TSA2, and has a per  
 CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine  
 CC in a subject, and are used particularly for the treatment of an overdose.  
 CC They are also used for treating addiction (by reducing the in vivo  
 CC concentration that can be achieved)  
 XX Sequence 113 AA;  
 SQ Query Match 100.0%; Score 31; DB 2; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 Db 55 LMSTRAS 61  
 RESULT 7  
 AAW39896  
 ID AAW39886 standard; protein; 113 AA.  
 XX AAW39886;  
 XX 18-JUN-1998 (first entry)  
 XX Light chain of the catalytic antibody 6A12.  
 XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX Mus sp.  
 XX WO9749800-A1.  
 XX 31-DEC-1997.  
 XX 25-JUN-1997; 97WO-US010965.  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX Claim 14; Page 72; 147pp; English.

PR 25-JUN-1996; 96US-00672345.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Landry DW;  
 XX WPI; 1998-077166/07.  
 XX N-PSDB; AAV09793.  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX Disclosure; Fig 19; 147pp; English.  
 XX The present sequence represents the light chain of a catalytic antibody  
 CC which is capable of degrading cocaine. A series of cocaine transition  
 CC state analogues (TSAs) were prepared and used to immunise mice for  
 CC production of hybridomas. Catalytic antibodies were identified by their  
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The  
 CC antibodies reduce the concentration of cocaine in a subject, and are used  
 CC particularly for the treatment of an overdose. They are also used for  
 CC treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)  
 XX Sequence 113 AA;  
 SQ Query Match 100.0%; Score 31; DB 2; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 Db 55 LMSTRAS 61  
 RESULT 8  
 AAW39802  
 ID AAW39802 standard; protein; 113 AA.  
 XX AAW39802;  
 XX 16-JUN-1998 (first entry)  
 XX Variable domain of the kappa light chain of catalytic antibody 6A12.  
 XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX Mus sp.  
 XX WO9749800-A1.  
 XX 31-DEC-1997.  
 XX 25-JUN-1997; 97WO-US010965.  
 XX 25-JUN-1996; 96US-00672345.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Landry DW;  
 XX WPI; 1998-077166/07.  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX Claim 14; Page 72; 147pp; English.

CC AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the Kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 6A12 antibody (AAW39807  
 CC represents the heavy chain) was identified using TSA1, which is an  
 CC immunogenic conjugate of a phosphate monoester transition state analogue.  
 CC Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the  
 CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved)  
 XX  
 XX Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 |||||  
 Db 55 LMSTRAS 61

RESULT 9  
 AAW39882  
 ID AAW39882 standard; protein; 113 AA.

XX  
 AC AAW39882;

DT 16-JUN-1998 (first entry)

DE Light chain of the catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX N-PSDB; AAV09789.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX Disclosure; Fig 21; 147pp; English.

XX The present sequence represents the light chain of a catalytic antibody  
 CC which is capable of degrading cocaine. A series of cocaine transition  
 CC state analogues (TSAs) were prepared and used to immunise mice for  
 CC production of hybridomas. Catalytic antibodies were identified by their  
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The  
 CC antibodies reduce the concentration of cocaine in a subject, and are used  
 CC particularly for the treatment of an overdose. They are also used for  
 CC treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

XX Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 |||||  
 Db 55 LMSTRAS 61

RESULT 10  
 AAW39804  
 ID AAW39804 standard; protein; 113 AA.

XX  
 AC AAW39804;

DT 16-JUN-1998 (first entry)

DE Variable domain of the Kappa light chain of catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX Claim 16; Page 73-74; 147pp; English.

XX AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the Kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809  
 CC represents the heavy chain) was identified using TSA1, which is an  
 CC immunogenic conjugate of a phosphate monoester transition state analogue.  
 CC Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the  
 CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved)

XX Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 |||||  
 Db 55 LMSTRAS 61

RESULT 11  
 AAY32262

ID AAY32262 standard; protein; 116 AA.  
 AC AAY32262;  
 XX 15-FEB-2000 (first entry)  
 DT  
 XX Humanised anti-CD23 Mab C11 light chain variable region.  
 DE  
 XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.  
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 XX Homo sapiens.  
 OS  
 OS Synthetic.  
 XX  
 XX  
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 FT Region 24. .39  
 FT /note= "CDR 1"  
 FT Region 40. .54  
 FT /note= "framework region 2"  
 FT Region 55. .61  
 FT /note= "CDR 2"  
 FT Region 62. .93  
 FT /note= "framework region 3"  
 FT Region 94. .102  
 FT /note= "CDR 3"  
 FT Region 103. .113  
 FT /note= "framework region 4"  
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 XX WO9958679-A1.  
 XX  
 XX 18-NOV-1999.  
 XX  
 XX 07-MAY-1999; 99WO-GB001434.  
 XX  
 XX 09-MAY-1998; 98GB-00009839.  
 XX  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX  
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 XX WPI; 2000-053101/04.  
 DR N-PSDB; AA234747.  
 XX  
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.  
 XX  
 XX Claim 9; Fig 3; 81pp; English.  
 PS  
 XX  
 XX This sequence represents the light chain variable region (VL) of  
 CC humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human  
 CC framework (H5IGKVII) and the light chain complementarity determining  
 CC regions (see AAY32254-56) of murine antibody C11. The DNA was constructed  
 CC by splice overlap PCR. The invention provides altered antibodies, such as  
 CC chimeric or humanised antibodies, which comprise sufficient of the amino  
 CC acid sequences of the C11 light and heavy chain complementarity  
 CC determining regions to render them capable of binding to the CD23 type II  
 CC molecule expressed on haematopoietic cells. The antibodies are used to  
 CC block soluble CD23 formation in human therapy, for the treatment of  
 CC arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-

CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents  
 XX  
 SQ Sequence 116 AA;  
 Query Match 100.0%; Score 31; DB 3; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 Db 55 LMSTRAS 61  
 |||||  
 |||||  
 RESULT 12  
 AAY32261  
 ID AAY32261 standard; protein; 145 AA.  
 XX  
 AC AAY32261;  
 XX  
 XX 15-FEB-2000 (first entry)  
 DT  
 XX Mouse anti-CD23 Mab C11 light chain variable region.  
 DE  
 XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.  
 XX  
 XX Mus musculus.  
 OS  
 OS  
 FH Key Location/Qualifiers  
 FT Region 55. .70  
 FT /note= "CDR L1"  
 FT Region 83. .92  
 FT /note= "CDR L2"  
 FT Region 125. .134  
 FT /note= "CDR L3"  
 XX  
 XX WO9958679-A1.  
 XX  
 XX 18-NOV-1999.  
 XX  
 XX 07-MAY-1999; 99WO-GB001434.  
 XX  
 XX 09-MAY-1998; 98GB-00009839.  
 XX  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX  
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 XX WPI; 2000-053101/04.  
 DR N-PSDB; AA234746.  
 XX  
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.  
 XX  
 XX Claim 8; Fig 2; 81pp; English.  
 PS  
 XX  
 XX This sequence represents the light chain variable region (VL) of murine  
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides  
 CC altered antibodies, such as chimeric or humanised antibodies (see  
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions (see AAY32254-59) to render them capable of binding to the CD23



CC type II molecule expressed on haematopoietic cells. The antibodies are  
 CC used to block soluble CD23 formation in human therapy, for the treatment  
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents  
 CC

XX SQ Sequence 145 AA;

Query Match 100.0%; Score 31; DB 3; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 Db 86 LMSTRAS 92  
 |||||

RESULT 13  
 AAW39816

ID AAW39816 standard; peptide; 7 AA.

XX AC AAW39816;

XX DT 16-JUN-1998 (first entry)

XX DE Light chain CDR2 of catalytic antibody 3B9.

XX KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX PS WPI; 1998-077166/07.

XX PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS Claim 11; Page 80; 147pp; English.

XX CC AAW39815-17 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

SQ Sequence 7 AA;

Query Match 90.3%; Score 28; DB 2; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 Db 1 LMSTRSS 7  
 |||||

RESULT 14

ID AAW39801 standard; protein; 113 AA.

XX AC AAW39801;

XX DT 16-JUN-1998 (first entry)

XX DE Variable domain of the Kappa light chain of catalytic antibody 3B9.

XX KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX DR P-FSDB; AAW09791.

XX PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS Claim 12; Page 71-72; 147pp; English.

XX CC AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the Kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806  
 CC represents the heavy chain) was identified using TSA1, which is an  
 CC immunogenic conjugate of a phosphate monoester transition state analogue.  
 CC Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the  
 CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved)

XX SQ Sequence 113 AA;

Query Match 90.3%; Score 28; DB 2; Length 113;  
 Best Local Similarity 85.7%; Pred. No. 65;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 Db 55 LMSTRSS 61  
 |||||

RESULT 15  
 AAW39899 standard; protein; 274 AA.  
 XX AC AAW39899;  
 XX DT 16-JUN-1998 (first entry)  
 XX DE Single chain Fv region of the catalytic antibody 3B9.  
 XX KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX OS Mus sp.  
 XX FH Key  
 XX FT Region  
 XX FT Location/Qualifiers  
 XX FT 32..37  
 XX FT /note= "complementarity determining region 1 of the heavy  
 XX FT chain"  
 XX FT 52..67  
 XX FT /note= "complementarity determining region 2 of the heavy  
 XX FT chain"  
 XX FT 99..106  
 XX FT /note= "complementarity determining region 3 of the heavy  
 XX FT chain"  
 XX FT 120..134  
 XX FT /note= "linker"  
 XX FT 159..174  
 XX FT /note= "complementarity determining region 1 of the light  
 XX FT chain"  
 XX FT 186..192  
 XX FT /note= "complementarity determining region 2 of the light  
 XX FT chain"  
 XX FT 225..233  
 XX FT /note= "complementarity determining region 3 of the light  
 XX FT chain"  
 XX FT 259..263  
 XX FT /note= "Flag epitope sequence"  
 XX PN WO9749800-A1.  
 XX PD 31-DEC-1997.  
 XX PF 25-JUN-1997; 97WO-US010965.  
 XX PR 25-JUN-1996; 96US-00672345.  
 XX PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX PI Landry DW;  
 XX PI WPI; 1998-077166/07.  
 XX DR  
 XX PT New catalytic antibodies able to decompose cocaine, single-chain  
 XX PT analogues - used to treat cocaine overdose and addiction, required in far  
 XX PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX PS Disclosure; Fig 27; 147pp; English.  
 XX PT  
 XX CC The present sequence represents the single chain Fv region of the  
 XX CC monoclonal catalytic antibody 3B9, which is capable of degrading cocaine.  
 XX CC A series of cocaine transition state analogues (TSAs) were prepared and  
 XX CC used to immunise mice for production of hybridomas. Catalytic antibodies  
 XX CC were identified by their capacity to release 3H-benzoic acid from 3H-  
 XX CC phenyl cocaine. The antibodies reduce the concentration of cocaine in a  
 XX CC subject, and are used particularly for the treatment of an overdose. They  
 XX CC are also used for treating addiction (by reducing the in vivo  
 XX CC concentration that can be achieved)  
 XX SQ Sequence 274 AA;

Search completed: September 30, 2004, 06:06:12  
 Job time : 37.1695 secs

Query Match 90.3%; Score 28; DB 2; Length 274;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 Db 186 LMSTRSS 192



```

; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
; US-09-940-727B-26

```

Query Match	100.0%;	Score 31;	DB 10;	Length 7;
Best Local Similarity	100.0%;	Pred. No. 1.2e+06;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;

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RESULT 3
US-09-940-727B-29
; Sequence 29, Application US/09940727B
; Publication NO. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landiv, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-29

```

```
Query Match      100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4  
US-09-840-459-32  
; Sequence 32, Application US/03840459  
; Patent No. US20020190576A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran H.  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

```

, TITLE OF INVENTION: METHODS OF USE THEREFOR
,
, FILE REFERENCE: 1855, 1052-012
,
, CURRENT APPLICATION NUMBER: US/09/840,459
,
, CURRENT FILING DATE: 2001-02-02
,
, PRIOR APPLICATION NUMBER: PCT/US01/03537
,
, PRIOR FILING DATE: 2001-02-02
,
, PRIOR APPLICATION NUMBER: 09/497,625
,
, PRIOR FILING DATE: 2000-02-03
,
, PRIOR APPLICATION NUMBER: 09/359,193
,
, PRIOR FILING DATE: 1999-07-22
,
, PRIOR APPLICATION NUMBER: 09/121,781
,
, PRIOR FILING DATE: 1998-07-23
,
, NUMBER OF SEQ ID NOS: 107
,
, SOFTWARE: FastSeq for Windows Version 3.0
,
, SEQ ID NO 32
,
, LENGTH: 100
,
, TYPE: PRT
,
, ORGANISM: Mus musculus
,
, US-09-840-459-32

```

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Query Match      100.0%; Score 31; DB 9; Length 100;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

RESULT 5
US-10-766-773-32
; Sequence 32, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-773-32

```

```

Query Match      100.0%; Score 31; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
         |||||
Db      55 LMSTRAS 61

```

RESULT 6  
US-10-766-610-32  
; Sequence 32, Application US/10766610  
; Publication NO. US20040132980A1  
; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.  
 ; APPLICANT: Horvath, Christopher  
 ; APPLICANT: Newman, Walter  
 ; APPLICANT: Jones, S. Tarran  
 ; APPLICANT: O'Brien, Siobhan H.  
 ; APPLICANT: O'Keefe, Theresa  
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
 ; METHODS OF USE THEREFOR  
 ; FILE REFERENCE: 1855-1052-029  
 ; CURRENT APPLICATION NUMBER: US/10/766,610  
 ; PRIOR FILING DATE: 2004-01-27  
 ; PRIOR APPLICATION NUMBER: 09/840,459  
 ; PRIOR FILING DATE: 2001-04-23  
 ; PRIOR APPLICATION NUMBER: PCT/US01/03537  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: 09/497,625  
 ; PRIOR FILING DATE: 2000-02-03  
 ; PRIOR APPLICATION NUMBER: 09/359,193  
 ; PRIOR FILING DATE: 1999-07-22  
 ; PRIOR APPLICATION NUMBER: 09/121,781  
 ; PRIOR FILING DATE: 1998-07-23  
 ; NUMBER OF SEQ ID NOS: 107  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 32  
 ; LENGTH: 100  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-766-610-32

Query Match 100.0%; Score 31; DB 16; Length 100;  
 Best Local Similarity 100.0%; Pred. NO. 10;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 DB 55 LMSTRAS 61

RESULT 7  
 US-10-733-563-32  
 ; Sequence 32, Application US/10733563  
 ; Publication No. US20040151721A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: O'Keefe, Theresa  
 ; APPLICANT: Ponath, Paul  
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
 ; METHODS OF USE THEREOF  
 ; FILE REFERENCE: 10448-213001  
 ; CURRENT APPLICATION NUMBER: US/10/733,563  
 ; PRIOR FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: US 10/272,899  
 ; PRIOR FILING DATE: 2002-10-17  
 ; PRIOR APPLICATION NUMBER: US 60/392,364  
 ; PRIOR FILING DATE: 2002-06-26  
 ; PRIOR APPLICATION NUMBER: US 60/350,166  
 ; PRIOR FILING DATE: 2001-10-19  
 ; NUMBER OF SEQ ID NOS: 122  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 32  
 ; LENGTH: 100  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-733-563-32

Query Match 100.0%; Score 31; DB 16; Length 100;  
 Best Local Similarity 100.0%; Pred. NO. 10;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 DB 55 LMSTRAS 61

RESULT 8  
 US-09-940-727B-6  
 ; Sequence 6, Application US/09940727B  
 ; Publication No. US2003007793A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald W  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 0575/51400-B  
 ; CURRENT APPLICATION NUMBER: US/09/940,727B  
 ; CURRENT FILING DATE: 2002-09-04  
 ; PRIOR APPLICATION NUMBER: 09/214,095  
 ; PRIOR FILING DATE: 1998-12-28  
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965  
 ; PRIOR FILING DATE: 1997-06-25  
 ; PRIOR APPLICATION NUMBER: 08/672,345  
 ; PRIOR FILING DATE: 1996-06-25  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 113  
 ; TYPE: PRT  
 ; ORGANISM: mouse  
 US-09-940-727B-6

Query Match 100.0%; Score 31; DB 10; Length 113;  
 Best Local Similarity 100.0%; Pred. NO. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 DB 55 LMSTRAS 61

RESULT 9  
 US-09-940-727B-7  
 ; Sequence 7, Application US/09940727B  
 ; Publication No. US2003007793A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald W  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 0575/51400-B  
 ; CURRENT APPLICATION NUMBER: US/09/940,727B  
 ; CURRENT FILING DATE: 2002-09-04  
 ; PRIOR APPLICATION NUMBER: 09/214,095  
 ; PRIOR FILING DATE: 1998-12-28  
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965  
 ; PRIOR FILING DATE: 1997-06-25  
 ; PRIOR APPLICATION NUMBER: 08/672,345  
 ; PRIOR FILING DATE: 1996-06-25  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 113  
 ; TYPE: PRT  
 ; ORGANISM: mouse  
 US-09-940-727B-7

Query Match 100.0%; Score 31; DB 10; Length 113;  
 Best Local Similarity 100.0%; Pred. NO. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 DB 55 LMSTRAS 61

RESULT 10  
 US-09-940-727B-8  
 ; Sequence 8, Application US/09940727B  
 ; Publication No. US2003007793A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald W  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 0575/51400-B  
 CURRENT APPLICATION NUMBER: US/09/940,727B  
 CURRENT FILING DATE: 2002-09-04  
 PRIOR APPLICATION NUMBER: 09/214,095  
 PRIOR FILING DATE: 1998-12-28  
 PRIOR APPLICATION NUMBER: PCT/US97/10965  
 PRIOR FILING DATE: 1997-06-25  
 PRIOR APPLICATION NUMBER: 08/672,345  
 PRIOR FILING DATE: 1996-06-25  
 NUMBER OF SEQ ID NOS: 121  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 8  
 LENGTH: 113  
 TYPE: PRT  
 ORGANISM: mouse  
 US-09-940-727B-8

Query Match 100.0%; Score 31; DB 10; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 Db 55 LMSTRAS 61

RESULT 11  
 US-09-940-727B-104  
 ; Sequence 104, Application US/09940727B  
 ; Publication No. US2003007793A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald W  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 0575/51400-B  
 ; CURRENT APPLICATION NUMBER: US/09/940,727B  
 ; CURRENT FILING DATE: 2002-09-04  
 ; PRIOR APPLICATION NUMBER: 09/214,095  
 ; PRIOR FILING DATE: 1998-12-28  
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965  
 ; PRIOR FILING DATE: 1997-06-25  
 ; PRIOR APPLICATION NUMBER: 08/672,345  
 ; PRIOR FILING DATE: 1996-06-25  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 104  
 ; LENGTH: 113  
 ; TYPE: PRT  
 ; ORGANISM: mouse  
 US-09-940-727B-104

Query Match 100.0%; Score 31; DB 10; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 Db 55 LMSTRAS 61

RESULT 12  
 US-09-940-727B-108  
 ; Sequence 108, Application US/09940727B  
 ; Publication No. US2003007793A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald W  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 0575/51400-B  
 ; CURRENT APPLICATION NUMBER: US/09/940,727B  
 ; CURRENT FILING DATE: 2002-09-04  
 ; PRIOR APPLICATION NUMBER: 09/214,095  
 ; PRIOR FILING DATE: 1998-12-28  
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965  
 ; PRIOR FILING DATE: 1997-06-25

PRIOR APPLICATION NUMBER: 08/672,345  
 PRIOR FILING DATE: 1996-06-25  
 NUMBER OF SEQ ID NOS: 121  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 108  
 LENGTH: 113  
 TYPE: PRT  
 ORGANISM: mouse  
 US-09-940-727B-108

Query Match 100.0%; Score 31; DB 10; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 Db 55 LMSTRAS 61

RESULT 13  
 US-09-940-727B-112  
 ; Sequence 112, Application US/09940727B  
 ; Publication No. US2003007793A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landry, Donald W  
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
 ; FILE REFERENCE: 0575/51400-B  
 ; CURRENT APPLICATION NUMBER: US/09/940,727B  
 ; CURRENT FILING DATE: 2002-09-04  
 ; PRIOR APPLICATION NUMBER: 09/214,095  
 ; PRIOR FILING DATE: 1998-12-28  
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965  
 ; PRIOR FILING DATE: 1997-06-25  
 ; PRIOR APPLICATION NUMBER: 08/672,345  
 ; PRIOR FILING DATE: 1996-06-25  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 112  
 ; LENGTH: 113  
 ; TYPE: PRT  
 ; ORGANISM: mouse  
 US-09-940-727B-112

Query Match 100.0%; Score 31; DB 10; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 Db 55 LMSTRAS 61

RESULT 14  
 US-10-424-599-191879  
 ; Sequence 191879, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 191879  
 ; LENGTH: 63  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_15287C.1.pep

US-10-424-599-191879

Query Match 93.5%; Score 29; DB 12; Length 63;  
Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
Db 24 IMSTRAS 30

RESULT 15

US-09-940-727B-20  
; Sequence 20; Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-20

Query Match 90.3%; Score 28; DB 10; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
Db 1 LMSTRSS 7

Search completed: September 30, 2004, 06:54:51  
Job time : 117.458 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 30, 2004, 08:41:28 ; Search time 32.6509 Seconds  
(without alignments)  
4221.672 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 2405

Sequence: 1 gaggtgcagctggggagtc.....ccctgtctcgggtaaatga 1335

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:\*

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3: /cgn2\_6/ptodata/2/iaa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PTCUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2161.5	89.9	478	3	US-08-487-550-8 Sequence 8, Appli
2	2161.5	89.9	478	4	US-09-526-098-8 Sequence 8, Appli
3	2151.5	89.5	453	3	US-08-466-151-8 Sequence 8, Appli
4	2151.5	89.5	453	4	US-08-466-163B-8 Sequence 8, Appli
5	2151.5	89.5	453	4	US-09-802-096-8 Sequence 8, Appli
6	2150.5	89.4	451	2	US-08-887-352B-18 Sequence 18, Appli
7	2150.5	89.4	451	3	US-09-109-207C-18 Sequence 18, Appli
8	2150.5	89.4	451	3	US-09-282-505-2 Sequence 2, Appli
9	2150.5	89.4	451	3	US-09-054-255-2 Sequence 2, Appli
10	2150.5	89.4	451	3	US-09-296-005-18 Sequence 18, Appli
11	2150.5	89.4	451	4	US-09-282-846-2 Sequence 2, Appli
12	2150.5	89.4	451	4	US-09-680-145-2 Sequence 2, Appli

13	2150.5	89.4	451	4	US-09-920-171-18 Sequence 18, Appli
14	2148	89.3	452	3	US-09-027-449-71 Sequence 71, Appli
15	2148	89.3	452	3	US-09-026-985-71 Sequence 71, Appli
16	2148	89.3	452	4	US-09-121-952A-71 Sequence 71, Appli
17	2148	89.3	452	4	US-09-234-340A-71 Sequence 71, Appli
18	2147.5	89.3	451	2	US-08-887-352B-14 Sequence 14, Appli
19	2147.5	89.3	451	2	US-08-887-352B-16 Sequence 16, Appli
20	2147.5	89.3	451	3	US-08-466-151-65 Sequence 65, Appli
21	2147.5	89.3	451	3	US-09-109-207C-14 Sequence 14, Appli
22	2147.5	89.3	451	3	US-09-109-207C-16 Sequence 16, Appli
23	2147.5	89.3	451	3	US-09-296-005-14 Sequence 14, Appli
24	2147.5	89.3	451	3	US-09-296-005-16 Sequence 16, Appli
25	2147.5	89.3	451	4	US-09-920-171-14 Sequence 14, Appli
26	2147.5	89.3	451	4	US-09-920-171-16 Sequence 16, Appli
27	2143	89.2	449	4	US-09-679-397-2 Sequence 2, Appli
28	2145	89.2	449	4	US-09-680-148-2 Sequence 2, Appli
29	2145	89.2	449	4	US-09-304-465A-2 Sequence 2, Appli
30	2144	89.1	459	1	US-08-157-101A-7 Sequence 7, Appli
31	2065.5	85.9	449	1	US-08-458-516-13 Sequence 13, Appli
32	2051	85.3	446	3	US-08-397-411-7 Sequence 7, Appli
33	2044.5	85.0	476	2	US-08-378-939-10 Sequence 10, Appli
34	2042.5	84.9	468	4	US-09-485-737B-67 Sequence 67, Appli
35	2042.5	84.9	711	4	US-09-485-737B-90 Sequence 90, Appli
36	2040	84.8	467	1	US-08-704-744-81 Sequence 81, Appli
37	2034	84.6	467	3	US-09-049-672A-8 Sequence 8, Appli
38	2033.5	84.6	476	3	US-08-487-550-12 Sequence 12, Appli
39	2033.5	84.6	476	4	US-09-526-098-12 Sequence 12, Appli
40	2029	84.4	473	3	US-09-049-672A-4 Sequence 4, Appli
41	2028.5	84.3	472	4	US-08-793-450-8 Sequence 8, Appli
42	2026	84.2	463	4	US-09-472-087-4 Sequence 4, Appli
43	2026	84.2	463	4	US-09-472-087-68 Sequence 68, Appli
44	2020.5	84.0	464	4	US-09-472-087-2 Sequence 2, Appli
45	2020.5	84.0	464	4	US-09-472-087-66 Sequence 66, Appli

ALIGNMENTS

RESULT 1  
US-08-487-550-8  
; Sequence 8, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,550  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:

QY	1	GAGTGTGACGTGGTGGAGTCTGTGGGGAGCGCTTGTTGTAAGCCCGGGGGGTCCTTTAGACTC	60
Db	20	GUUValGlnLeuValGlnUSeSerGlyGlyLeuValGlnProGlyGlySerLeuArgVal	39
QY	61	TCCTGTGACGCTAGCGGATTCACATTTTCAGTGGCTACTCGATGTCCTCGGTCGCCCAAGGCT	120
Db	40	SerCysAlaValSerGlyPheThrPheSerAspHisTyrMetTyrTrpPheArgGlnAla	59
QY	121	CCAGGGAGGGGCTCGATGGGTGCTGCAATTAGATTGAAATCTGTAATATATGCAACA	180
Db	60	ProGlyLysGlyProGluTrpValGlyPheIleArgAsnLysProAsnGlyGlyThrThr	79
QY	181	CATTATGGCGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAATATCTAGA	240
Db	80	GluTyrAlaAlaSerValLysAspArgPheThrIleSerArgAspSerLysSerIle	99
QY	241	CTGTATCTGCANATCAAACAGCTGAAACCGAGACACACCGCTGATTTACTGTACAGAT	300
Db	100	AlaTyrLeuGlnMetSerSerLeuLysIleGluAspThrAlaValTyrCysThrThr	119
QY	301	-----TTCATAGACTCGGGC	315
Db	120	SerTyrIleSerHisCysArgGlyValCysTyrGlyGlyTyrPheGluPheTrpGly	139
QY	316	CAGGAAACATAGTCACCGTCTCTCAGCTCCACCAAGGGCCCATCGTCTCCCGCTG	375
Db	140	GlnGlyAlaLeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeu	159
QY	376	GCACCTCTCTCCAAGACGACCTCTGGGGGGCACAGCGCCCTGGGCTGCCTGTGTCAGAGAC	435
Db	160	AlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAsp	179
QY	436	TACTTCCCGACCGGTACCGCTGCTGTGAACCTCAGCGCCCTGACCCAGCGCGTGCAC	495
Db	180	TyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHis	199
QY	496	ACCTTCCCGGTGTCTTACAGTCTCAGGACTCTACTCCCTCAGACGCTGTGACCGTG	555
Db	200	ThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrVal	219
QY	556	CCCTCCACGCTGGGACCCAGACCTTCATCTGCAACGTGAATCACAGCCCAACAC	615
Db	220	ProSerSerSerLeuGlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsn	239
QY	516	ACCAAGGTGGACAAGAAAGTGGAGCCCAATCTTTGTGCACAAAACCTCACATATGCCACCG	675
Db	240	ThrLysValAspLysLysAlaGluProLysSerCysAspLysThrHisThrCysProPro	259
QY	576	TGCCACGACCTGAACTCGGGGGGACCGTCAGTCTTCCTCTCCCGCCCAAAACCCCAAG	735
Db	260	CysProAlaProGluLeuLeuGlyLysProSerValPheLeuPheProLysLysProLys	279
QY	736	GACACCTCATGATCCCGGACCCCTGAGTCACTGCTGCTGTGGTGGAGCGTGAAGCCAC	795
Db	280	AspThrLeuMetIleSerArgThrProGluValThrCysValValValAspValSerHis	299
QY	796	GAAGACCTTGAGTCAAGTTCAACTGGTACGTGACCGGCTGGAGGTGCAATGTCAAG	855

TELEFAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 478 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-526-098-8

Alignment Scores:  
 Pred. No.: 1,24e-152 Length: 478  
 Score: 2161.50 Matches: 412  
 Percent Similarity: 91.29% Conservative: 7  
 Best Local Similarity: 89.76% Mismatches: 25  
 Query Match: 89.88% Indels: 15  
 DB: 4 Gaps: 1

US-09-674-716B-18 (1-1335) x US-09-526-098-8 (1-478)

QY 1 GAGGTGACAGTGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGTCCCTTAGACTC 60  
 DB 20 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuVal 39  
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 DB 40 SerCysAlaValSerGlyPheThrPheSerAspHisTyrMetTyrPheArgGlnAla 59  
 QY 121 CCAGGAGGGGCTCGAGTGGTCTGAAATTAGATTGAATCTGATAATTATGCAACA 180  
 DB 60 ProGlyLysGlyProGluTrpValGlyPheLeuArgAsnLysProAsnGlyGlyThr 79  
 QY 181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240  
 DB 80 GluTyrAlaAlaSerValLysAspArgPheThrLeuSerArgAspSerLysSerile 99  
 QY 241 CTGATCTGCAATGAACAGCTGAAACCCAGGACAGCCGCTGATTACTGTACAGAT 300  
 DB 100 AlaTyrLeuGlnMetSerSerLeuLysileGluAspThrAlaValTyrTyrCysThr 119  
 QY 301 -----TTCATAGACTGGGGC 315  
 DB 120 SerTyrIleSerHisCysArgGlyGlyValCysTyrGlyGlyTyrPheGluPheTrpGly 139  
 QY 316 CAGGAAACACTAGTCAACCGTCTCTACGCTCCACCAAGGGCCCATCGGTCTTCCCGCTG 375  
 DB 140 GlnGlyAlaLeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeu 159  
 QY 376 GCACCTCTCTCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGTGCTGCTCAAGGAC 435  
 DB 160 AlaProSerSerLysSerThrSerGlyThrAlaAlaLeuGlyCysLeuValLysAsp 179  
 QY 436 TACTTCCCGAACCCGGTGACGGTGTGCTGGAACCTCAGCGCCCTGACAGCGGGGTGCAC 495  
 DB 180 TyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHis 199  
 QY 496 ACCTTCCCGGCTCTCTACAGTCTCTCAGACTCTACTCCCTCAGCAGCGGTGTCACCGT 555  
 DB 200 ThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrVal 219  
 QY 556 CCCTCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAAGCAAC 615  
 DB 220 ProSerSerSerLeuGlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsn 239  
 QY 616 ACCAAGGTGGAACAAGATGGAGGCCAAATCTTGACAAACTCACAATGCCCAAGC 675  
 DB 240 ThrLysValAspLysLysAlaGluProLysSerCysAspLysThrHisThrCysProPro 259  
 QY 676 TSCCCAGACCTGAACCTCGCGGGGCACGTCAGTCTTCTCTCCCGCCCAAAACCCCAAG 735  
 DB 260 CysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLys 279  
 QY 736 GACACCTCATGATCTCCGGGACCCCTGAGTGCATACGTCGTCGTCGTCGTCGTCGTCGTC 795

DB 280 AspThrLeuMetIleSerArgThrProGluValThrCysValValValAspValSerHis 299  
 QY 796 GAAGACCTGAGGTCAAGTTCACTGCTAGCTGGAGCGCGGTGAGGTGATATGCAAG 855  
 DB 300 GluAspProGluValLysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLys 319  
 QY 856 ACAAGCCCGGGAGGAGGAGTACACACAGTACCGTGTGTGTCAGCGCTCTCACCGTTC 915  
 DB 320 ThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValValSerValLeuThrVal 339  
 QY 916 CTCACACAGACTGCTGAATGCAAGAGTCAAGTCAAGTCAAGTCTCCAAACAAAGCCCTC 975  
 DB 340 LeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeu 359  
 QY 976 CCAGCCCCCATCGAGAAACCATCTCCAAAGCAAGAGGCGAGCCCGAGAACCCACAGGTG 1035  
 DB 360 ProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnProArgGluProGlnVal 379  
 QY 1036 TACACCTCGCCCCCATCCCGGATGAGTGCACAGAACCCAGGTCAAGCTGACCTGCCTG 1095  
 DB 380 TyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnValSerLeuThrCysLeu 399  
 QY 1096 GTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGCAATGGCAGCCGGAG 1155  
 DB 400 ValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGlu 419  
 QY 1156 AACCACTACAAGACCAACGCTCCCGTGGTGGACTCCGAGCGGTCTCTTCTCTCTACAGC 1215  
 DB 420 AsnAsnTyrLysThrThrProValLeuAspSerAspGlySerPheLeuTyrSer 439  
 QY 1216 AGCTCAGCGTGACAAAGAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1275  
 DB 440 LysLeuThrValAspLysSerArgTrpGlnGlnGlnValPheSerCysSerValMet 459  
 QY 1276 CATGAGCTCTGCACACCACTACAGCAGAGAGCTCTCCCTGTCTCCGGGTAAA 1332  
 DB 460 HisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 478

RESULT 3

US-08-466-151-8  
 Sequence 8, Application US/08466151  
 Patent No. 6037453  
 GENERAL INFORMATION:  
 APPLICANT: Jardieu, Paula M.  
 APPLICANT: Presta, Leonard G.  
 TITLE OF INVENTION: Immunoglobulin Variants  
 NUMBER OF SEQUENCES: 65  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,151  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/466163  
 FILING DATE: 06-Jun-1995  
 APPLICATION NUMBER: 08/405617  
 FILING DATE: 15-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/185899  
 FILING DATE: 26-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/879495

FILING DATE: 07-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744768

FILING DATE: 14-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Svoboda, Craig G.

REGISTRATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: P0718P2C1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1489

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 453 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-466-151-8

Alignment Scores:

Pred. No.: 6,77e-152 Length: 453  
Score: 2151.50 Matches: 410  
Percent Similarity: 92.76% Conservative: 13  
Best Local Similarity: 89.91% Mismatches: 18  
Query Match: 89.46% Indels: 15  
DB: 3 Gaps: 4

US-09-674-716b-18 (1-1335) x US-08-466-151-8 (1-453)

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Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
QY 61 TCCTGTGCGAGTACGGATCTCTTC---AGTGGCTACTGATCTCTGGTCCGCCAG 117  
Db 21 SerCysAlaValSerGlySerIleThrSerGlyTyrSerTrpAsnTrpIleArgGln 40  
QY 118 GTCACAGGAAGGGGCTCGAGTGGTGTGTAATAGATTGAAATCTGATAATTATGCA 177  
Db 41 AlaProGlyGlyGlyLeuGluTrpValAlaSerIleThrTyrAspGly-----Ser 57  
QY 178 ACACATTATGGGAGTCTGTGAAGGGAAATTCACATCTCAAGAGATGATCAAAATCT 237  
Db 58 ThrAsnTyrAlaAspSerValIysGlyArgPheThrIleSerArgAspSerIysAsn 77  
QY 238 AGACTGTATCTGCAATGAACAGCTGAAACCCGAGGACACAGCGCTGTATTACTGTACA 297  
Db 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAla 97  
QY 298 -----GATTTCTAGACTGGGCGCAGGGAACACTAGTCT 330  
Db 98 ArgGlySerHisTyrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117  
QY 331 ACGTCTCTCAGCTCCACC-----AAGGCCCATCGTCTCCCTCCCTGGCACCTCC 384  
Db 118 ThrValSerSerAlaSerThrIysGlyGlyGlyProSerValPheProLeuAlaProSer 137  
QY 385 TCCAGAGCACCTCTGGGGGACAGCGGCTGGCTGGCTGGTCAAGGACTACTTCCC 444  
Db 138 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValIysAspTyrPhePro 157  
QY 445 GRACCGGTACGGTCTGGGAACCTCAGCGGCTCCCTGACCGGGGCTGCACACTCCCG 504  
Db 158 GluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhePro 177  
QY 505 GTGTCTCTCAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGGTGCCCTCCAGC 564  
Db 178 AlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSer 197  
QY 565 AGCTGGGGACCCAGACCTACATCTGCAACGTGATATCAAGCCCGACCAACCCAGGTG 624  
Db 198 SerLeuGlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrIysVal 217  
QY 625 GACAGAAAGTGGAGCCCAAAATCTTGTGCAAAACTCACAATGCCCCACCGTCCCGACGA 684

Db 218 AspyLysValGluProLysSerCysAspLysThrHisThrCysProCysProAla 237  
QY 685 CCTGAACCTCGGGGGCAGCGTCTTCCTTCTCCCTCCCAAAACCCCAAGACACCTTC 744  
Db 238 ProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeu 257  
QY 745 ATGATCTCCGGACCCCTGAGGTCAATCGGTGGTGGTGGAGCTGAGCCAGCAAGCCCT 804  
Db 258 MetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAspPro 277  
QY 805 GAGTCAAGTTCACTGTCAGTGGACGGTGGAGGTGCATAATCCCAAGCAAAAGCCG 864  
Db 278 GluValIysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrIysPro 297  
QY 865 CGGAGGAGCAGTACCAAGCAGCTACCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 924  
Db 298 ArgGluGluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGln 317  
QY 925 GACTGCTGATCGCAAGGAGTACAGTCAAGGTCTCCCAAGAGCCCTCCAGCCGCC 984  
Db 318 AspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaPro 337  
QY 985 ATCGAGAAACCATCTCCAAAGCCAAAGGCGCAGCCCGAGAACCCAGAGTGTACACCTG 1044  
Db 338 IleGluLysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeu 357  
QY 1045 CCCCCATCCCGGATGAGTACCAAGAACAGGTGAGGTGAGGTGAGGTGAGGTGAGGTG 1104  
Db 358 ProProSerArgGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGly 377  
QY 1105 TTCTATCCAGCAGCACATCGCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACAACTAC 1164  
Db 378 PheTyrProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyr 397  
QY 1165 AAGACACGCTCCCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1224  
Db 398 LysThrThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThr 417  
QY 1225 GTGCAAGAGCAGGTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1284  
Db 418 ValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMethHisGluAla 437  
QY 1285 CTGCACACCACTACCGCAGAGAGCCCTCTCCCTCTCCCGGGTAAA 1332  
Db 438 LeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 453

RESULT 4

US-08-466-163B-8  
; Sequence 8, Application US/08466163B  
; Patent No. 6329509  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; FILE REFERENCE: P0718P2C1D1  
; CURRENT APPLICATION NUMBER: US/08/466,163B  
; PRIOR FILING DATE: 1995-06-06  
; CURRENT APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 8  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized mae11, version 1 heavy chain

US-08-466-163B-8

## Alignment Scores:

Pred. No.: 6,77e-152 Length: 453  
Score: 2151.50 Matches: 410  
Percent Similarity: 92.76% Conservative: 13  
Best Local Similarity: 89.91% Mismatches: 18  
Query Match: 89.46% Indels: 15  
DB: 4 Gaps: 4

US-09-674-716B-18 (1-1335) x US-08-466-163B-8 (1-453)

Qy 1 GAGGTGACGTGCTGAGTCTGGGGAGGCTGTGTAAGCCGGGGGCTCCCTAGACTC 60  
Db 1 GluValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
Qy 61 TCTGTGACGTAGCGGATTCACCTTC---AGTGCTACTGGATGCTCGGTGGCGGAC 117  
Db 21 SerCysAlaValSerGlyTyrSerIleThrSerGlyTyrSerTrpAsnTrpIleArgGln 40  
Qy 118 GCTCCAGGAGGGGCTCGAGTGGCTTGTGTAATGATTGAATCTGTAATATTGCA 177  
Db 41 AlaProGlyLysGlyLeuGlnTrpValAlaSerIleThrTyrAspGly-----Ser 57  
Qy 178 ACACATTATGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCT 237  
Db 58 ThrAsnTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspSerLysAsn 77  
Qy 238 AGACTGTATCTCAATGAACAGCTGAAACCCGAGGACACAGCGGTGTATTACTGTACA 297  
Db 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysala 97  
Qy 298 -----GATTTCATAGACTGGGGCCAGGGACACTAGTC 330  
Db 98 ArgGlySerHisTyrPheGlyHisThrPheAlaValTrpGlyGlnGlyThrLeuVal 117  
Qy 331 ACCGTCTCTAGCTCCACCC-----AAGGCCCATCGGTCTTCCCGCTGCGACCCCTCC 384  
Db 118 ThrValSerSerAlaSerThrLysGlyLysGlyProSerValPheProLeuAlaProSer 137  
Qy 385 TCCAGAGACACCTGGGGGCACGGCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 444  
Db 138 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 157  
Qy 445 GAACCGGTGACCGGTGCTGGAACCTCAGCGCCCTGACCGGGCGGTGCACACCTTCCCG 504  
Db 158 GluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhePro 177  
Qy 505 GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGTACCGTCCCTCCAGC 564  
Db 178 AlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSer 197  
Qy 565 AGCTTGGGCACCCAGACCTTACATCTGCAACGTGAATCAAGCCCAAGCAACACCAAGGTG 624  
Db 198 SerLeuGlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysVal 217  
Qy 625 GACAGAAAGTGGAGCCCAATCTTGTAACAAATCTACATGCCACCGTGGCCAGCA 684  
Db 218 AspLysLysValGluProLysSerCysAspLysThrHisThrCysProProCysProAla 237  
Qy 685 CCTGAACCTCGGGGCGCACCGTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 744  
Db 238 ProGluLeuLeuGlyLysProSerValPheLeuPheProProLysProLysAspThrLeu 257  
Qy 745 ATGATCTCCGGACCCCTGAGTCACTACATCGGTGGTGGAGGTGAGCAGCAAGACCT 804  
Db 258 MetIleSerArgThrProGluValThrCysValValValValAspValSerHisGluAspPro 277  
Qy 805 GAGGTCAAGTTCACCTGTGACGCGGTGGAGGTGCATATGATGCCAAGCAAGCCG 864  
Db 278 GluValLysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysPro 297  
Qy 865 CGGGAGGAGCAGTACACAGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 924

Db 298 ArgGluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGln 317  
Qy 925 GACTGGCTGAATGCGCAAGGAGTACAAAGTCTCAAGGTCTCCAAACAAGCCCTCCAGCCCCC 984  
Db 318 AspTrpLeuAsnGlyLysGlnTyrLysCysLysValSerAsnLysAlaLeuProAlaPro 337  
Qy 985 ATGAGAAACCATCTCCAAAGCCAAAGGCGACCCCGAGAACACAGGTGTACACCTG 1044  
Db 338 IleGluLysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeu 357  
Qy 1045 CCCCCATCCCGGATGAGCTGACCAAGAACCAAGCTCAGCTGACCTGCTGCTGCTGCTGCT 1104  
Db 358 ProProSerArgGluGlnMetThrLysAsnGlnValSerLeuThrCysLeuValLysGly 377  
Qy 1105 TTCTATCCCGAGCAGATCGCCGTGGAGTGGAGAGCAATGGGAGCGGAGAGCAACTAC 1164  
Db 378 PheTyrProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyr 397  
Qy 1165 AAGACACAGCCTCCCGTGTGGACTCCGACGGGTCTCTTCTCTCTACAGCAAGCTCAC 1224  
Db 398 LysThrThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThr 417  
Qy 1225 GTGACAAAGAGCAGGTGGCAGCGGGAACGCTTCTTCTCATGCTCCGTGATGAGGCT 1284  
Db 418 ValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAla 437  
Qy 1285 CTGCACACCACTACACGACAGAGAGCCCTCTCCCTGCTCTCCGGGTAAA 1332  
Db 438 LeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 453  
RESULT 5  
US-09-802-096-8  
; Sequence 8, Application US/09802096  
; Patent No. 6685939  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)  
; FILE REFERENCE: P0718P2C3US  
; CURRENT APPLICATION NUMBER: US/09/802,096  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 8  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized mael1, version 1 heavy chain  
US-09-802-096-8  
Alignment Scores:  
Pred. No.: 6,77e-152 Length: 453  
Score: 2151.50 Matches: 410  
Percent Similarity: 92.76% Conservative: 13  
Best Local Similarity: 89.91% Mismatches: 18  
Query Match: 89.46% Indels: 15  
DB: 4 Gaps: 4  
US-09-674-716B-18 (1-1335) x US-09-802-096-8 (1-453)  
Qy 1 GAGGTGACGTGCTGAGTCTGGGGAGGCTGTGTAAGCCGGGGGCTCCCTAGACTC 60



QY 118 GCTCCAGGGAAGGGCTCGAGTGGTCTGTAATGATTGAAATCTGATAATTATGCA 177  
DB 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTyrSerGlyGlu----- 57  
QY 178 ACACATTATGCGGAGCTGTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCT 237  
DB 58 ThrLysTyrAsnProSerValLysGlyArgIleThrLeuSerArgAspSerLysAsn 77  
QY 238 AGACTGTATCTCAATGACAGCTGAAACCGGAGGACACAGCGGTGATTACTGTACA 297  
DB 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAla 97  
QY 298 -----GATTTCATAGACTGGGCCAGGACACTAGTC 330  
DB 98 ArgGlySerHisTyrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117  
QY 331 ACCGTCTCTCAGCTCCACAGGCGCCCATCGTCTCCCGCTGGACCCCTCTCCCAAG 390  
DB 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137  
QY 391 AGCACCTCTGGGGGACACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGAACCG 450  
DB 138 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 157  
QY 451 GTGAGGCTGTCTGGAACCTCAGCGGCCCTGACACAGCGGCTGCACACCTTCCCGCTCTC 510  
DB 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177  
QY 511 CTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGTCCCTCCAGCAGCTTG 570  
DB 178 LeuGlnSerSerGlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeu 197  
QY 571 GGCACCCAGACCTACATCTGCAACGTGATCAACAGCCCGACCAAGGTGGACAAAG 630  
DB 198 GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217  
QY 631 AAAGTGGACCCCAATCTGTGACAACTCACAATCCACATCCCGCTGGCCGACCTGAA 690  
DB 218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237  
QY 691 CTCGCGGGGGACCGCTCAGTCTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATC 750  
DB 238 LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIle 257  
QY 751 TCCCGACCCCTGAGTCACTGCGTGTGTGTGAGTGGAGCCAGACACCTGAGTGC 810  
DB 258 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 277  
QY 811 AAGTTCAACTGTTACGTGACGCGGTGGAGGTGCATAATGCCAAGAACAGCCGCGGAG 870  
DB 278 LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297  
QY 871 GAGCAGTACAACAGCAGTACCGTGTGTGTCAGCGTCTCACCCTGCTCCACGAGCTGG 930  
DB 298 GluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrp 317  
QY 931 CTGAATGGCAGGAGTACAGTGCAGGCTCCCAACAGACCTCCCGACCCCGCTCCAG 990  
DB 318 LeuAsnGlyGlyGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337  
QY 991 AAAACCATCTCCAAAGCCAAAGGCGACCGCCCGAGACCAAGGTGTACACCTCGCCCGCA 1050  
DB 338 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro 357  
QY 1051 TCCCGGATGAGTGCACCAAGAACAGTCAAGCTGACCTGCTGGTCAAGGCTTCTAT 1110  
DB 358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 377  
QY 1111 CCAGCGCATCCCGTGGAGTGGGAGAGCAATGGGACCGGAGAACCAACTACAGACCC 1170  
DB 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr 397

QY 1171 ACCTCTCCCGTGTGAGTCTCCGACGGCTCTTCTCTTCTTACAGCAAGCTCACCGTGGAC 1230  
DB 398 ThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAsp 417  
QY 1231 AAGACAGGTGGCAGACAGGGGACGCTTCTCTCATGCTCGGTGATGCATGAGGCTCTGCAC 1290  
DB 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437  
QY 1291 AACCACTACACGACAGAGAGCTCTCCCTGTCTCCCGGTAAA 1332  
DB 438 AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 451  
RESULT 7  
US-09-109-207C-18  
; Sequence 18, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 18  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-451  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-109-207C-18  
Alignment Scores:  
Pred. No.: 8,02e-152 Length: 451  
Score: 2150.50 Matches: 408  
Percent Similarity: 92.51% Conservative: 12  
Best Local Similarity: 89.87% Mismatches: 21  
Query Match: 89.42% Indels: 13  
DB: 3 Gaps: 3  
US-09-674-716B-18 (1-1335) x US-09-109-207C-18 (1-451)  
QY 1 GAGGTGACGTGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGCTCCCTAGATCT 60  
DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
QY 61 TCCTGTGACGCTAGCGGATTCACCTTC---AGTGGTACTCGGATGTCTCGGTCCGCCAG 117  
DB 21 SerCysAlaValSerGlyTyrSerIleThrSerGlyTyrSerTrpAsnTrpIleArgGln 40  
QY 118 GCTCCAGGGAAGGGCTCGAGTGGTGTGCTGAAATAGATTGAATCTGATAATTATGCA 177  
DB 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTyrSerGlyGlu----- 57  
QY 178 ACACATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCT 237  
DB 58 ThrLysTyrAsnProSerValLysGlyArgIleThrLeuSerArgAspSerLysAsn 77  
QY 238 AGACTGTATCTGCAATGACAGCTGAAACCGGAGGACACAGCGGTGATTACTGTACA 297  
DB 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAla 97  
QY 298 -----GATTTCATAGACTGGGCCAGGACACTAGTC 330  
DB 98 ArgGlySerHisTyrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117  
QY 331 ACCGTCTCTCAGCTCCACAGGCGCCCATCGTCTCCCGCTGGACCCCTCTCCCAAG 390  
DB 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137

391 AGCACCTCTGGGGGCACAGCGGCGCTGGCTGGTCAAGGACTACTTCCCGCAACG 450  
Db SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspThrPheProGluPro 157  
451 GTACGGTGTCTGGAACTCAGCGGCGCTGACAGCGGGTGCACACTTCCCGGCTGC 510  
Db ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177  
511 CTACAGTCCCTCAGGACTCTACTCCCTCAGCAGGCTGTGACCGTCCCTCCAGCGCTG 570  
Db LeuGlnSerSerGlyLeuThrValProSerSerValThrValProSerSerLeu 197  
571 GGCACCCAGCCTACATCTGCAACGTAATCAACAGCCCAAGCAACCAAGGTGGACAA 630  
Db GlyThrGlnThrTrpIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217  
631 AAAGTGGAGCCCAATCTGTGACAACTCAGACATGCCACCGTCCCGCAGCCTGAA 690  
Db LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237  
691 CTCGCGGGGCGCACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 750  
Db LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIle 257  
751 TCCCGGACCCCTCAGGTACATCGCTGTGTGGTGGAGCTGAGCCACGACCTGAGTGC 810  
Db SerArgThrProGluValThrCysValValAspValSerHisGluAspProGluVal 277  
811 AAGTCAACTGGTACCTGACGCGGTGGAGTGCATAATGCAAGCAAGCGCGGGAG 870  
Db LysPheAsnTrpTrpValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297  
871 GACAGTACAAAGCAGTACCTGCTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 930  
Db GluGlnTrpAsnSerThrTrpArgValValSerValLeuThrValLeuHisGlnAspTrp 317  
931 CTCAAGTGGCAAGGAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 990  
Db LeuAsnGlyLysGluTrpLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337  
991 AAAACCATCTCCAAAGCCAAAGGCGCCCGCAGAACCAAGTGTACACCTGCGCCCA 1050  
Db LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValThrLeuProPro 357  
1051 TCCCGGAGTACGTCACCAAGACCAAGTACAGTACAGTACAGTACAGTACAGTAC 1110  
Db SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTrp 377  
1111 CCCAGCGCATCCCGTGGAGTGGAGAGCAATGGCGAGCGGAGCAACCAACCAAGACC 1170  
Db ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTrpLysThr 397  
1171 ACCCTCCCGTGTGAGTCCGACGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230  
Db ThrProProValLeuAspSerAspGlySerPhePheLeuTrpSerLysLeuThrValAsp 417  
1231 AAGAGCAGGTGGCAGCAGGGAACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1290  
Db LysSerArgTrpGlnGlnGlnValPheSerCysSerValMetHisGluAlaLeuHis 437  
1291 AACCATACACGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332  
Db AsnHisThrGlnLysSerLeuSerLeuSerProGlyLys 451

## RESULT 8

US-09-282-505-2  
; Sequence 2, Application US/09282505A  
; Patent No. 6194551  
; GENERAL INFORMATION:  
; APPLICANT: Esche Ekinaduse Idusogie et al.  
; TITLE OF INVENTION: Polypeptide Variants  
; FILE REFERENCE: P1266R1  
; CURRENT APPLICATION NUMBER: US/09/282,505A

; CURRENT FILING DATE: 1999-03-31  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 2  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Artificial Sequence  
; LOCATION: 1-451  
; OTHER INFORMATION: Sequence is completely synthesized  
; Patent No. 6194551  
US-09-282-505-2  
Alignment Scores:  
Seq. No.: 8.02e-152 Length: 451  
Score: 2150.50 Matches: 408  
Percent Similarity: 92.51% Conservativeness: 12  
Best Local Similarity: 89.87% Mismatches: 21  
Query Match: 89.42% Indels: 13  
DB: 3 Gaps: 3  
US-09-674-716B-18 (1-1335) x US-09-282-505-2 (1-451)  
QY 1 GAGTGCAGCTGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
QY 61 TCCGTGTGAGTACCGGATTCACTTTC--AGTGGCTACTGTGATGCTCTGGTCCGCCAG 117  
Db 21 SerCysAlaValSerGlyTrpSerIleThrSerGlyTrpSerTrpAsnTrpIleArgGln 40  
QY 118 GCTCCAGGAGGAGGCTGCGAGTGGCTGCTGAAATAGATTGAAATCTGATAATTATGCA 177  
Db 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTrpSerGlyGlu----- 57  
QY 178 ACATATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCT 237  
Db 58 ThrLysTrpAsnProSerValLysGlyArgIleThrIleSerArgAspSerLysAsn 77  
QY 238 AGACTGTATCTGCAATGAACAGCTGAAACCCAGAGACACAGCCGTGATTACTGTACA 297  
Db 78 ThrPheTrpLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTrpCysAla 97  
QY 298 -----GATTTCATAGACTGGGGCCAGGGAACACTAGTC 330  
Db 98 ArgGlySerHisTrpPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117  
QY 331 ACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCCTCTCCAAG 390  
Db 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerLys 137  
QY 391 AGACCTCTGGGGCAGCGGCGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 450  
Db 138 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTrpPheProGluPro 157  
QY 451 GTACGGTGTCTGGAACTCAGCGGCGCTGACAGCGGGGTGCACACCTTCCCGGCTGTC 510  
Db 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177  
QY 511 CTACAGTCCCTCAGGACTCTACTCCCTCAGCAGGCTGTGACCGTCCCTCCAGCAGCTG 570  
Db 178 LeuGlnSerSerGlyLeuTrpSerLeuSerSerValValThrValProSerSerLeu 197  
QY 571 GGCACCCAGCCTACATCTGCAACGTAATCAACAGCCCAAGCAACCAAGGTGGACAA 630  
Db 198 GlyThrGlnThrTrpIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217  
QY 631 AAAGTGGAGCCCAATCTGTGACAACTCAGACATGCCACCGTCCCGCAGCCTGAA 690  
Db 218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237  
QY 691 CTCGCGGGGCGCACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 750



Db 238 LeuLeuGlyGlyProSerValPheLeuPheProLysProLysProLysAspThrLeuMetIle 257  
QY 751 TCCCGACCCCTGAGGTACATGCGGTGGTGGAGCGTGGAGCCAGCAAGACCCCTGAGTTC 810  
Db 258 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 277  
QY 811 AGTTCAACTGGTACGTGACCGGTGGAGTGGATGATATGCAAGCAAGACCGCGGAG 870  
Db 278 LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297  
QY 871 GAGCAGTCAACAGCAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 930  
Db 298 GluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrp 317  
QY 931 CTGAATGGCAAGAGTACAAAGTCTCCAAAGGCTCTCCAAAGGCTCTCCAAAGGCTCTCC 990  
Db 318 LeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337  
QY 991 AAAACCATCTCCAAAGCCAAAGGAGCGCCGAGAACACACAGTGTACACCTGCGCCCA 1050  
Db 338 LysThrIleSerLysAlaLysGlyGlnProAsgGluProGlnValTyrThrLeuProPro 357  
QY 1051 TCCCGGATGAGTGTACCAAGAACCAAGGTACAGCTGACCTGCTGGTCAAGGCTTCAT 1110  
Db 358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 377  
QY 1111 CCCAGGACATCCCGTGGAGTGGAGACCAATGGCAGCCGAGAACCAACTACAGACC 1170  
Db 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnTyrLysThr 397  
QY 1171 ACCTCTCCCGTGTGACTCCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230  
Db 398 ThrProValLeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAsp 417  
QY 1231 AAGAGAGTGGCAGCAGGGGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1290  
Db 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437  
QY 1291 AACCACTACAGCAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332  
Db 438 AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 451

RESULT 9  
US-09-054-255-2

; Sequence 2, Application US/09054255  
; Patent No. 6242195  
; GENERAL INFORMATION:  
; APPLICANT: Esone Ekinaduse Idusogie et al.  
; TITLE OF INVENTION: Polypeptide Variants  
; FILE REFERENCE: P1266  
; CURRENT APPLICATION NUMBER: US/09/054,255  
; CURRENT FILING DATE: 1998-04-02  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 2  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: E27 anti-IgE antibody heavy chain  
US-09-054-255-2

## Alignment Scores:

Pred. No.: 8,02e-152 Length: 451  
Score: 2150.50 Matches: 408  
Percent Similarity: 92.51% Conservative: 12  
Best Local Similarity: 89.87% Mismatches: 21  
Query Match: 89.42% Indels: 13  
DB: 3 Gaps: 3

US-09-674-716b-18 (1-1335) x US-09-054-255-2 (1-451)

QY 1 GAGTGGAGCTGTGGAGTCTGGGAGGCTTGTAAAGCCCGGGGCTCCCTTAGACTC 60  
|||||

Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
QY 61 TCCTGTGCAGTACGGGATTCACCTTTC---AGTGGCTACTGGATGTCTCGGTCCGCCAG 117  
Db 21 SerCysAlaValSerGlyTyrSerIleThrSerGlyTyrSerTrpAsnTrpIleArgGln 40  
QY 118 GCTCCAGGAGGGCTCGAGTGGTGGTGAATAGATTGAATCTGATAATTATGCA 177  
Db 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTyrSerGlyGlu----- 57  
QY 178 ACATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCT 237  
Db 58 ThrLysTyrAsnProSerValLysGlyArgIleThrIleSerArgAspSerLysAsn 77  
QY 238 AGACTGTATCTGCAATTAACAGCTGAAACCGAGGACACAGCCGCTGTATTACTGTACA 297  
Db 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAla 97  
QY 298 -----GATTTCATAGACTGGGGCCAGGAACTAGTC 330  
Db 98 ArgGlySerHisTyrPheGlyHisTrpPheAlaValTrpGlyGlnGlyThrLeuVal 117  
QY 331 ACCGTCTCTCAGCTCCACCAAGGCCCAATCGGTCTTCCCTCTGGCACTCCCTCTCCAAG 390  
Db 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137  
QY 391 AGCACTCTGGGGCACAGCGCCCTGGCTGGTCAAGGACTACTTCCCGGAAACCG 450  
Db 138 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 157  
QY 451 GTGACGGTGTCTGGTGAATCTCAGCGCCCTGACCAAGCGCGTGCACACTTCCCGGCTGC 510  
Db 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177  
QY 511 CTACAGTCTCTCAGACTCTACTCCTCAGCAGCGTGTGACCGCTCCAGCAGCTTG 570  
Db 178 LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerLeu 197  
QY 571 GGCACCCAGACCTACATCTGCAAGCTGAATCACAAGCCCAAGCAGCACCAAGGTGACAAG 630  
Db 198 GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217  
QY 631 AAAGTGGAGCCCAATCTGTGACAAACTCACATGCCCGCCCGTGCAGCCAGCCTGAA 690  
Db 218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237  
QY 691 CTGCGGGGCGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCATGTC 750  
Db 238 LeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIle 257  
QY 751 TCCCGGACCCCTGAGGTACATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGC 810  
Db 258 SerArgThrProGluValThrCysValValAspValSerHisGluAspProGluVal 277  
QY 811 AAGTTCACTGTGACGTGGAGCGGTGGAGGTGATATGCAAGACCGCCGCGGAG 870  
Db 278 LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297  
QY 871 GAGCAGTCAACAGCAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGC 930  
Db 298 GluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrp 317  
QY 931 CTGAATGGCAAGAGTACAAAGTCTCCAAAGGCTCTCCAAAGGCTCTCCAGCCCGCCATCGAG 990  
Db 318 LeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337  
QY 991 AAAACCATCTCCAAAGCCAAAGGAGCGCCGAGAACCAAGTGTACACCTGCGCCCA 1050  
Db 338 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro 357  
QY 1051 TCCCGGATGAGTGTACCAAGAACCAAGTGTGAGCTGACCTGCTGGTCAAGGCTTCAT 1110  
Db 358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 377

QY 1111 CCAGCGACATCCCGTGGAGTGGAGCAATGGCGGAGAGCAACTACAGACC 1170  
 Db 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnSerTrpLysThr 397  
 QY 1171 ACGCCTCCCGTGGACTCCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGGAC 1230  
 Db 398 ThrProValLeuAspSerAspGlySerPhePheLeuTrpSerLysLeuThrValAsp 417  
 QY 1231 AAGACAGTGGCAGCAGGGAACGGTCTTCTCTATGCTCCGTGTGATGATGAGCTTCGCAC 1290  
 Db 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437  
 QY 1291 AACCACTACAGCAGAGACCTCTCCCTGTCTCCGGGTAAA 1332  
 Db 438 AsnHisTrpThrGlnLysSerLeuSerLeuSerProGlyLys 451

## RESULT 10

US-09-296-005-18  
 ; Sequence 18, Application US/09296005  
 ; Patent No. 6290957  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides  
 ; FILE REFERENCE: P1123C1r  
 ; CURRENT APPLICATION NUMBER: US/09/296,005  
 ; CURRENT FILING DATE: 1999-04-21  
 ; EARLIER APPLICATION NUMBER: US 08/887,352  
 ; EARLIER FILING DATE: 1997-07-02  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SEQ ID NO 18  
 ; LENGTH: 451  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: Artificial  
 ; LOCATION: 1-451  
 ; OTHER INFORMATION: Heavy chain sequence derived from MAB11  
 US-09-296-005-18

## Alignment Scores:

Pred. No.: 8 02e-152 Length: 451  
 Score: 2150.50 Matches: 408  
 Percent Similarity: 92.51% Conservative: 12  
 Best Local Similarity: 89.87% Mismatches: 21  
 Query Match: 89.42% Indels: 13  
 DB: 3 Gaps: 3

US-09-674-716b-18 (1-1335) x US-09-296-005-18 (1-451)

QY 1 GAGGTGAGCTGTGAGTCTGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTACATC 60  
 Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
 QY 61 TCCTGTGCAGTACGAGTTCACATTC---AGTGGTACTGGATGTCCTGGGTCCGCGCAG 117  
 Db 21 SerCysAlaValSerGlyTrpSerIleThrSerGlyTrpSerTrpAsnTrpIleArgGln 40  
 QY 118 GCTCCAGGGAAGGGTTCGAGTGGTGTCTGAAATPAGATTGAAATCTGATTAATTATCA 177  
 Db 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTrpSerGlyGlu----- 57  
 QY 178 ACACATTATCGGAGTCTGTGAGGGGAATTCACCATCTCAGAGATGATTCAAATCT 237  
 Db 58 ThrLysTrpAsnProSerValLysGlyArgIleThrIleSerArgAspSerLysAsn 77  
 QY 238 AGACTATCTGCAATGAACAGCTGAAACCGGAGCACACCGCTGTATTACTGTACA 297  
 Db 78 ThrPheTrpLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTrpTrpCysAla 97  
 QY 298 -----GATTTTCATAGACTGGGCGGAGGAACTAGTTC 330  
 Db 98 ArgGlySerHisTrpPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117

## RESULT 11

US-09-282-846-2  
 ; Sequence 2, Application US/09282846  
 ; Patent No. 6528624

QY 331 ACCGTCTCTCAGGCTCCACCAAGGGCCCATCGGTCTTCCCTTGGACCCCTCTCTCCAG 390  
 Db 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137  
 QY 391 AGCACCTCTGGGGGCACAGCGGCTGGGTCAAGTGTCAAGGACTACTTCCCGGAACCG 450  
 Db 138 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTrpPheProGluPro 157  
 QY 451 GTGACGGTGTCTGGAATCTCAGCGCCCTGACCAAGCGCGTGCACACCTTCCCGGTGTTC 510  
 Db 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177  
 QY 511 CTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTACCGTCCCTCCACGAGCTTG 570  
 Db 178 LeuGlnSerSerGlyLeuTrpSerLeuSerSerValValThrValProSerSerSerLeu 197  
 QY 571 GGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAAGCCCAACCAAGGTGGACAAG 630  
 Db 198 GlyThrGlnThrTrpIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217  
 QY 631 AAAGTGGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTCCCGGACCTGAA 690  
 Db 218 LysValGluProLysSerCysAspLysThrHisThrCysProCysProAlaProGlu 237  
 QY 691 CTCGGGGGGCACCGTCT 750  
 Db 238 LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIle 257  
 QY 751 TCCCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCACGACCAAGACCCCTCATGATC 810  
 Db 258 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 277  
 QY 811 AAGTTCAACTGGTACGTGGAGCGGTGGAGTGCATAATGCCAAGACCAAGCCCGGGAG 870  
 Db 278 LysPheAsnTrpTrpValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297  
 QY 871 GAGCAGTACAAACGACGTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 930  
 Db 298 GluGlnTrpAsnSerThrTrpArgValValSerValLeuThrValLeuHisGlnAspTrp 317  
 QY 931 CTGATGCGCAGGAGTACAAAGTCTCCAAAGCCCTCCCAAGCCCTCCCGCCCATCGAG 990  
 Db 318 LeuAsnGlyLysGluTrpLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337  
 QY 991 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCTGCCCCCA 1050  
 Db 338 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTrpThrLeuProPro 357  
 QY 1051 TCCCGGATGAGTGCACCAAGAACCGGTGAGTGCCTGACCTGCTGTGTGTGTGTGTGTGT 1110  
 Db 358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTrp 377  
 QY 1111 CCCAGCACATCCCGTGGAGTGGAGAGCAATGGGCGGCGGAGAACCAACTACAAGACC 1170  
 Db 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnSerTrpLysThr 397  
 QY 1171 ACGCCTCCCGTGTGAGTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230  
 Db 398 ThrProValLeuAspSerAspGlySerPhePheLeuTrpSerLysLeuThrValAsp 417  
 QY 1231 AAGACAGGTGGCAGAGGGGAACGCTTCTCTCATGTCTCGTGTGATGATGAGGTCTGCAC 1290  
 Db 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437  
 QY 1291 AACCACTACAGCAGAGACCT 1332  
 Db 438 AsnHisTrpThrGlnLysSerLeuSerLeuSerProGlyLys 451

; GENERAL INFORMATION:  
 ; APPLICANT: Esohe Ekinaduse Idusogie et al.  
 ; TITLE OF INVENTION: Polypeptide Variants  
 ; FILE REFERENCE: P1266R2  
 ; CURRENT APPLICATION NUMBER: US/09/282,846  
 ; CURRENT FILING DATE: 1999-03-31  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SEQ ID NO 2  
 ; LENGTH: 451  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: Artificial Sequence  
 ; LOCATION: 1-451  
 ; OTHER INFORMATION: Sequence is completely synthesized  
 ; Patent No. 6528624  
 US-09-282-846-2

Alignment Scores:  
 Pred. No.: 8,02e-152 Length: 451  
 Score: 2150.50 Matches: 408  
 Percent Similarity: 92.5% Conservatives: 12  
 Best Local Similarity: 89.8% Mismatches: 21  
 Query Match: 89.42% Indels: 13  
 DB: 4 Gaps: 3

US-09-674-716b-18 (1-1335) x US-09-282-846-2 (1-451)

QY 1 GAGGTGACGTGAGTCTGGGAGGCTGGTAAGCCCGGGGGTCCCTTAGATC 60  
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
 QY 61 TCCTGTGCAGCTAGCGGATTCACTTTC---AGTGGCTACTGGATGCTCTGGTCCGCCAG 117  
 Db 21 SerCysAlaValSerGlyTyrSerIleThrSerGlyTyrSerTrpAsnTrpIleArgGln 40  
 QY 118 GTCCAGGAAGGGCTCGAGTGGTGTCTGAATAGATTGAATCTGATTAATTGCA 177  
 Db 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTyrSerGlyGlu-----57  
 QY 178 ACACATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAATCT 237  
 Db 58 ThrLysTyrAsnProSerValLysGlyArgGileThrIleSerArgAspSerLysAsn 77  
 QY 238 AGACTGTATCTGCAATGAACCCCTGAAACCCAGGACACAGCCGTGTATTACTGTACA 297  
 Db 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAla 97  
 QY 298 -----GATTTCATAGCTGGGCCAGGGAACACTAGTC 330  
 Db 98 ArgGlySerHisTyrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117  
 QY 331 ACCGTCTCCCTCAGCTCCACCAAGGGCCCATCGTCTTCCCTCGCACCCTCCCTCCAG 390  
 Db 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerLys 137  
 QY 391 AGACCTCTGGGGGCACAGCGGCCCTGGGTGCTGCTCAAGACTACTTCCCGNACCG 450  
 Db 138 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 157  
 QY 451 GTGACGGTGTGCGGAACCTCAGCGCCCTCAGCAGCGGTGCACACCTTCCCGGTGTC 510  
 Db 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177  
 QY 511 CTACAGTCCTCAGACTCTACTCCCTCAGCAGCGTGTGACCTGCGCTCCAGCAGCTTG 570  
 Db 178 LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerLeu 197  
 QY 571 GGACCCAGACCTACATCTGCAAGCTGAATCAAGCCCGACCAACCCAGGTGGCAAG 630  
 Db 198 GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217  
 QY 631 AAAGTGGAGCCCAATCTTGTGCAAAAACCTCACACATGCCCCACCGCTGCCAGCACCTGAA 690

Db 218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237  
 QY 691 CTCGGGGGACACCGTCAGTCTTCTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGATC 750  
 Db 238 LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIle 257  
 QY 751 TCCGGACCCCTCAGGTTCACATCGGTGGTGGTGGAGCTGAGCCACGAGACCCCTGAGGTC 810  
 Db 258 SerArgThrProGluValThrCysValValValValValValValValValValVal 277  
 QY 811 AAGTTCAACTGGTACGTCGCGGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGGAG 870  
 Db 278 LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297  
 QY 871 GACAGTACACACGACGTACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 930  
 Db 298 GluGlnTyrAsnSerThrTyrArgValValValValValValValValValValVal 317  
 QY 931 CTGAATGGCAAGGAGTACAAAGTCTCAAAAGCCCTCCAGCCCTCCAGCCCTCCATCGAG 990  
 Db 318 LeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337  
 QY 991 AAAACCATCTCCAAAGCCAAAGGCGCCCGGAGAACCCAGAGTGTACACCTGCCCCCA 1050  
 Db 338 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro 357  
 QY 1051 TCCCGGATGAGTGCACCAAGAACCCAGGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1110  
 Db 358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 377  
 QY 1111 CCCAGGACATCGCGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGG 1170  
 Db 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr 397  
 QY 1171 ACGGCTCCCGTGGGACTCCGACGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1230  
 Db 398 ThrProProValLeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAsp 417  
 QY 1231 AAGAGCAGGTGGCAGCGGGAACGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1290  
 Db 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437  
 QY 1291 AACCATACACGCAAGAGCGCTCTCCCTGTCTCCGGGTAAA 1332  
 Db 438 AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 451

# RESULT 12

US-09-680-145-2  
 ; Sequence 2, Application US/09680145  
 ; Patent No. 6538124  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Esohe Ekinaduse Idusogie et al.  
 ; TITLE OF INVENTION: Polypeptide Variants  
 ; FILE REFERENCE: P1266R1  
 ; CURRENT APPLICATION NUMBER: US/09/680,145  
 ; CURRENT FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 09/282,505  
 ; PRIOR FILING DATE: 1999-03-13  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SEQ ID NO 2  
 ; LENGTH: 451  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: Artificial Sequence  
 ; LOCATION: 1-451  
 ; OTHER INFORMATION: Sequence is completely synthesized  
 ; Patent No. 6538124  
 US-09-680-145-2

Alignment Scores:  
 Pred. No.: 8,02e-152 Length: 451

Score: 2150.50 Matches: 408  
Percent Similarity: 92.51% Conservative: 12  
Best Local Similarity: 89.87% Mismatches: 21  
Query Match: 89.42% Indels: 13  
DB: 4 Gaps: 3

US-09-674-716B-18 (1-1335) x US-09-680-145-2 (1-451)

QY 1 GAGGTGAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
61 TCCTGTGACGTACGGATTCACTTC---AGTGGCTACTGGATGTCCTGGGTCCGCCAG 117  
DB 21 SerCysAlaValSerGlyThrSerGlyThrSerGlyThrSerTrpAsnTrpIleArgGln 40  
QY 118 GCTCCAGGGAAGGGCTCGAGTGGTGGTCTGAAATAGATTGAAATCTGATTAATTATGCA 177  
DB 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysThrSerGlyGlu-----57  
QY 178 ACACATTATCCGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATCAAAATCT 237  
DB 58 ThrLysThrAsnProSerValLysGlyArgIleThrIleSerArgAspSerLysAsn 77  
QY 238 AGACTGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCCGTGTATTACTGTACA 297  
DB 78 ThrPheThrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValThrCysAla 97  
QY 298 -----GATTTCATAGACTGGGCGCCAGGGAACACTAGTC 330  
DB 98 ArgGlySerHisThrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117  
QY 331 ACCGTCTCCCTCAGCTCCACCAAGGGCCATCGTCTCCCTGGACACCCCTCCCTCCAG 390  
DB 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137  
QY 391 AGCACTCTGGGGGCACAGGGCCCTGGGTCTGGTCAAGACTACTTCCCGCAACCG 450  
DB 138 SerThrSerGlyThrAlaAlaLeuGlyCysLeuValLysAspThrPheProGluPro 157  
QY 451 GTACGGTGTCTGGACTCAGGCGCCCTGACAGCGGGGTGACACCTTCCGGCTGTC 510  
DB 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177  
QY 511 CTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGGTCCCTCCAGCAGCTG 570  
DB 178 LeuGlnSerSerGlyLeuThrSerLeuSerSerValValThrValProSerSerLeu 197  
QY 571 GGCACCCAGACTACATCTGCAAGCTGAATCAAGCCCGAGCAACACCAAGTGGACAG 630  
DB 198 GlyThrGlnThrThrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217  
QY 631 AAAGTGAGCCCAAAATCTTGACAAACTCAACATGCCACCGTCCCGCCAGCACTGAA 690  
DB 218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237  
QY 691 CTGCGGGGGCCACCGTCACTTCTCTTCCCGCCCAAAACCAAGCAACCTCATGATC 750  
DB 238 LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIle 257  
QY 751 TCCCGGACCCCTGAGTCACTGCGTGGTGGTGGACGTGAGCCAGAGACCTGAGTC 810  
DB 258 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 277  
QY 311 AAGTCACTGCTGACGCGCGTGGAGGTGCATAATGCGCAAGCAAAAGCCGGGAG 870  
DB 278 LysPheAsnTrpThrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297  
QY 371 GAGCACTACAAGCAGCAGTACCGTGGTGGTCAAGCTCTCCCGTCTCCAGCAGACTGG 930  
DB 298 GluGlnThrAsnSerThrThrArgValValSerValLeuThrValLeuHisGlnAspTrp 317  
QY 931 CTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAAAGGCGCTCCCGAGCCCGCATCGAG 990

318 LeuAsnGlyLysGluThrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337  
QY 991 AAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGCAACACACAGGTGTACACCTGCCCCCA 1050  
DB 338 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValThrLeuProPro 357  
QY 1051 TCCCGGATGAGCTGACCAAGAACAGCTCAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1110  
DB 358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheThr 377  
QY 1111 CCCAGCACATCCGCTGGAGTGGAGAGCAATGGGAGCGGAGAGACAACTACAAGACC 1170  
DB 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnThrLysThr 397  
QY 1171 ACGCTCCCGTCTGGACTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230  
DB 398 ThrProValLeuAspSerAspGlySerPhePheLeuThrSerLysLeuThrValAsp 417  
QY 1231 AAGAGCGAGTGGACAGCGGGAACGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1290  
DB 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437  
QY 1291 AACCACTACAGCAGAGAGCGCT 1332  
DB 438 AsnHisThrThrGlnLysSerLeuSerLeuSerProGlyLys 451

RESULT 13  
US-09-920-171-18  
; Sequence 18, Application US/09920171  
; Patent No. 6682735  
; GENERAL INFORMATION:  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Lowe, John  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)  
; FILE REFERENCE: P1123C2US  
; CURRENT APPLICATION NUMBER: US/09/920,171  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: US 08/887,352  
; PRIOR FILING DATE: 1997-07-02  
; PRIOR APPLICATION NUMBER: US 09/296,005  
; PRIOR FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 18  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-920-171-18

Alignment Scores:  
Pred. No.: 8,02e-152 Length: 451  
Score: 2150.50 Matches: 408  
Percent Similarity: 92.51% Conservative: 12  
Best Local Similarity: 89.87% Mismatches: 21  
Query Match: 89.42% Indels: 13  
DB: 4 Gaps: 3

US-09-674-716B-18 (1-1335) x US-09-920-171-18 (1-451)

QY 1 GAGGTGAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
QY 61 TCCTGTGACGTACGGATTCACTTC---AGTGGCTACTGGATGTCCTGGGTCCGCCAG 117  
DB 21 SerCysAlaValSerGlyThrSerGlyThrSerGlyThrSerTrpAsnTrpIleArgGln 40  
QY 118 GCTCCAGGGAAGGGCTCGAGTGGTGGTCTGAAATAGATTGAAATCTGATTAATTATGCA 177  
DB 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysThrSerGlyGlu-----57  
QY 178 ACACATTATCCGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATCAAAATCT 237  
DB 58 ThrLysThrAsnProSerValLysGlyArgIleThrIleSerArgAspSerLysAsn 77  
QY 238 AGACTGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCCGTGTATTACTGTACA 297  
DB 78 ThrPheThrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValThrCysAla 97  
QY 298 -----GATTTCATAGACTGGGCGCCAGGGAACACTAGTC 330  
DB 98 ArgGlySerHisThrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117  
QY 331 ACCGTCTCCCTCAGCTCCACCAAGGGCCATCGTCTCCCTGGACACCCCTCCCTCCAG 390  
DB 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137  
QY 391 AGCACTCTGGGGGCACAGGGCCCTGGGTCTGGTCAAGACTACTTCCCGCAACCG 450  
DB 138 SerThrSerGlyThrAlaAlaLeuGlyCysLeuValLysAspThrPheProGluPro 157  
QY 451 GTACGGTGTCTGGACTCAGGCGCCCTGACAGCGGGGTGACACCTTCCGGCTGTC 510  
DB 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177  
QY 511 CTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGGTCCCTCCAGCAGCTG 570  
DB 178 LeuGlnSerSerGlyLeuThrSerLeuSerSerValValThrValProSerSerLeu 197  
QY 571 GGCACCCAGACTACATCTGCAAGCTGAATCAAGCCCGAGCAACACCAAGTGGACAG 630  
DB 198 GlyThrGlnThrThrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217  
QY 631 AAAGTGAGCCCAAAATCTTGACAAACTCAACATGCCACCGTCCCGCCAGCACTGAA 690  
DB 218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237  
QY 691 CTGCGGGGGCCACCGTCACTTCTCTTCCCGCCCAAAACCAAGCAACCTCATGATC 750  
DB 238 LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIle 257  
QY 751 TCCCGGACCCCTGAGTCACTGCGTGGTGGTGGACGTGAGCCAGAGACCTGAGTC 810  
DB 258 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 277  
QY 311 AAGTCACTGCTGACGCGCGTGGAGGTGCATAATGCGCAAGCAAAAGCCGGGAG 870  
DB 278 LysPheAsnTrpThrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297  
QY 371 GAGCACTACAAGCAGCAGTACCGTGGTGGTCAAGCTCTCCCGTCTCCAGCAGACTGG 930  
DB 298 GluGlnThrAsnSerThrThrArgValValSerValLeuThrValLeuHisGlnAspTrp 317  
QY 931 CTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAAAGGCGCTCCCGAGCCCGCATCGAG 990

Db 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleTyrSerGlyGlu----- 57  
QY 178 ACACATTATGCGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCT 237  
Db 58 ThrLysTyrAsnProSerValLysGlyArgIleThrIleSerArgAspSerLysAsn 77  
QY 238 AGACTGTATCTGCAATGAACAGCCTGAAACCCGAGGACACAGCCGTGTATTACTGTACA 297  
Db 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyr-TyrCysAla 97  
QY 298 -----GATTTCATAGACTGGGCCAGGACACACTAGTC 330  
Db 98 ArgGlySerHisTyrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117  
QY 331 ACCGTCCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCTCCGACACCTCTCTCCAAAG 390  
Db 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137  
QY 391 AGCAGCTCTGGGGGACAGCGCCCTGGCGTCCCTGTCAGGACTACTTCCCGGAACCG 450  
Db 138 SerThrSerGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 157  
QY 451 GTGACGGTGTCTGGAACCTCAGCGCCCTGACACGCGGTGCACACCTTCCCGCTGTC 510  
Db 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177  
QY 511 CTACAGTCTCAGGACTCTACTCCTCAGCAGCGGTGACGCTGCCCTCCAGCAGCTTG 570  
Db 178 LeuGlnSerSerGlyLeuTyrSerLeuSerValValThrValProSerSerSerLeu 197  
QY 571 GACACCCAGACTACATCTGCAACGTGATCAACAGCCAGCAACACCAAGGTGACAAAG 630  
Db 198 GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217  
QY 631 AAAGTGGAGCCCAATCTTGTGACAAACTCACATGCCACCGTCCCGACCACTGAA 690  
Db 218 LysValGluProLysSerCysAspLysThrHisThrCysProCysProAlaProGlu 237  
QY 691 CTCGCGGGGACCGTCAGTCTTCTCTTCCCGCCCAACCCCAAGCACCTCATGTC 750  
Db 238 LeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIle 257  
QY 751 TCCGAGACCCCTGAGTTCATGCGTGGTGGAGCTGAGCAGCAGCAAGACCTCAGTGC 810  
Db 258 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 277  
QY 811 AAGTTCACCTGCTGACGCGGTGGAGGTGATATGATGCAAGACAAAGCCGCGGAG 870  
Db 278 LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297  
QY 871 GAGCAGTCAACAGCAGTACGCTGTGTCAGCTCTCAGCTCTCAGCTGTCAGCAGACTGG 930  
Db 298 GluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrp 317  
QY 931 CTGAATGGCAAGGAGTACAGTCAAGTCTCCAAAGCCCTCCAGCCCTCCAGCCCTCAG 990  
Db 318 LeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaIleGlu 337  
QY 991 AAAACATCTCCAAAGCCAAAGGGAGCCCGGAGAACCAACAGGTGTACACCTGCCCCCA 1050  
Db 338 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro 357  
QY 1051 TCCCGGGATGAGTGCACCAAGAACCAAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1110  
Db 358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 377  
QY 1111 CCAGCGACATCCCGGTGAGTGGAGAGCAATGGCGAGCCGAGAACCAACTACAGACC 1170  
Db 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr 397  
QY 1171 ACCGTCCTCCGTGTCAGCTCCGAGCTCTCTCTCTCTACAGCAAGCTCACCGTGGAC 1230  
Db 398 ThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAsp 417

QY 1231 AAGAGCAGGTGGCAGCAGCGGAAAGCTTTCTCATGCTCCGTGATGATGAGGCTCTGCAC 1290  
Db 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437  
QY 1291 AACCATACACGACGAGAGCCTCTCCCTGCTCCCGGTAAA 1332  
Db 438 AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 451  
RESULT 14  
US-09-027-449-71  
; Sequence 71, Application US/09027449  
; Patent No. 6025158  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027,449  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074,330  
; FILING DATE: 22-Jan-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/038,664  
; FILING DATE: 21-Feb-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-027-449-71  
Alignment Scores:  
Pred. No.: 1,23e-151 Length: 452  
Score: 2148.00 Matches: 407  
Percent Similarity: 92.73% Conservative: 14  
Best Local Similarity: 89.65% Mismatches: 21  
Query Match: 89.31% Indels: 12  
DB: 3 Gaps: 3  
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QY 1 GAGGTGACGCTGGTGGAGCTGTGGGGAGGCTGTGTAAGCCCGGGGGTCCCTTAGACTC 60  
Db 1 GluValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
QY 61 TCCTGTGACGTAGCGGATTCACATTTTCAGTGCCTACTGATGCTCTGGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyTyr-SerPheSerSerHisTyrMetHisTrpValArgGlnAla 40



Db	41	ProGlyLysGlyLeuGluTrpValGlyTyrIle-----AspProSerAsnGlyGluThr	58
Qy	181	CATATGCGGAGTGTGTAAGGGGAATTCACATCTCAGAGATGATTCAAAATCTAGA	240
Db	59	ThrTyrAsnGlnLysPheLysGlyArgPheThrLeuSerArgAspAsnSerLysAsnThr	78
Qy	241	CTGTATCTGCAATCAACAGCCTGAAACACGAGGACACAGCCGTGTTATTACTGTACAGAT	300
Db	79	AlaTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAlaArg	98
Qy	301	-----TTCATAGAC-----TGGGGCCAGGGACACTAGTC	330
Db	99	GlyAspTyrArgTyrAsnGlyAspTrpPheAspValTrpGlyGlnGlyThrLeuVal	118
Qy	331	ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCACCCCTCCTCCAAG	390
Db	119	ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys	138
Qy	391	AGCACTCTGGGGGACAGCGGCCCTGGGCTGCTGCTCAAGACTACTTCCCGCAACCG	450
Db	139	SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro	158
Qy	451	GTGAGGCTGTGCGTAACCTCAGGCGCCCTGACGCGCGTGCACACCTTCCCGCTGTC	510
Db	159	ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal	178
Qy	511	CTACAGTCTCCTCAGGACTTACTCTCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAGCTTG	570
Db	179	LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeu	198
Qy	571	GGCACCACGACCTACATCTGCAACGTGAATCACAAGCCGACCAACCAAGGTGGACAAG	630
Db	199	GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys	218
Qy	631	AAAGTGGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGTGGCCCGACCTGAA	690
Db	219	LysValGluProLysSerCysAspLysThrHisThrCysProCysProAlaProGlu	238
Qy	691	CTCGCGGGGACCGTACGTCTTCTTCTTCCCTCCCAAAACCAAGACACCTCATGATC	750
Db	239	LeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIle	258
Qy	751	TCCCGGACCCCTGAGTGCATCGTGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTC	810
Db	259	SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal	278
Qy	811	AAATTCACTGGTACGTGACCGCGTGGAGTGCATATGCCAAGAACAGCCCGGGAG	870
Db	279	LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu	298
Qy	871	GAGCAGTACAACAGCAGTACCGTGTGTCAGCGTCTCACCCTGCTGCACCCAGGACTGG	930
Db	299	GluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrp	318
Qy	931	CTGAATGGCAAGGAGTACAAGTCAAGTCTCCAACAAAGCCCTCCAGCCCCCATCGAG	990
Db	319	LeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu	338
Qy	991	AAACCATCTCCAAGCCAAAGGGAGCCCGGAGAACCAACAGGTGTACACCTGGCCCCCA	1050
Db	339	LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro	358
Qy	1051	TCCCGGGATGAGTGCACCAAGACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT	1110
Db	359	SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr	378
Qy	1111	CCAGGCGACATCCCGTGGAGTGGGAGAGCAATGGCGAGCCCGGAGAACCACTACAGACC	1170
Db	379	ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr	398
Qy	1171	ACCGTCCCGTGTGAGTCCGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1230
Db	399	ThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAsp	418

Qy	1231	AAGAGCAGGTGGCAGCAGGGGAACGCTTCTCTCATGCTCGTGCATGAGGCTCTGCAC	1290
Db	419	LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis	438
Qy	1291	AACCATACACGACAGAGAGCCTCTCCCTGTCTCCGGGTAAA	1332
Db	439	AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys	452

Search completed: September 30, 2004, 09:32:00  
Job time : 54.6509 secs

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